

KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 530 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.
FT DOMAIN 32 351 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 352 372 POTENTIAL.
FT DOMAIN 373 530 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 147 IG-LIKE V-TYPE.
FT DOMAIN 153 247 IG-LIKE C2-TYPE 1.
FT DOMAIN 252 337 IG-LIKE C2-TYPE 2.
FT DISULFID 54 131 BY SIMILARITY.
FT DISULFID 174 229 BY SIMILARITY.
FT DISULFID 274 320 BY SIMILARITY.
FT CARBOHYD 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 339 467 ESPSTAGAGATGGIIGGIIAIIATAVAGTGILICRQRKE
FT ORLQAADDEEELEGGPPSYKPTPKAKLEPEMPMSQLFTLGA
FT SEHSPVKTPYFDAGVSCADQEMPRYHELPTEERSGPELLLG
FT ATGLGP -> DTPQASRDVGLVWGA VGTLLVLLAGGFL
FT ALILLRRRRKSPGGNGDRGSDYDKTQVFGNGGPFVFW
FT RSASPEPMRPDGREDEEHEEMKAEGLMLPPHESPKDDM
FT ESHLDGSLISRRAYV (in isoform Alpha).
FT /FTid=VSP 002630.
FT Missing (in isoform Alpha).
FT /FTid=VSP 002631.
FT SEQUENCE 530 AA; 57317 MW; 0ED71BFA2B231BBE CRC64;
SQ
Query Match 25.1%; Score 434.5; DB 1; Length 530;
Best Local Similarity 31.3%; Pred. No. 3.3e-27;
Matches 107; Conservative 57; Mismatches 145; Indels 33; Gaps 11;
QY 1 VSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVQGEY--QGRVLF----- 50
Db 50 VELPCHLLPPTTTERVSVQVTWQRLDG---TVVAAFHPSPFGVDFPNQFSKDRLSFVRARPE 106
QY 51 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEP-----TVSLIKGP 105
Db 107 TNADLRDATLAFRGLRVEDEGNYTCEFAFPNGTRRGVTWLRVIAQPENHAEAEQVETIGP 166
QY 106 DSLIDGGNETVAAICATGKPVAHIDWEGDLGEMESTTSPFN---ETATIISQYKLFPP 162
Db 167 QSV-----AVARCSTGGRPPARITWISSLGG-EAKDTQEPGIOAGTVTIISRYSLVP 218
QY 163 TRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNFWFVGRKGVNLIKCNADA 222
Db 219 VGRADGVKVTCTRVEHESFEPIILLPVTLVSRYPPEVSIISGDDNWNWYLGSRSEAILTCDVRS 278
QY 223 NPPPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVVICKVTNSLQSRSDQKVIYI 282
Db 279 NPEPTDYDWSTTSVGFPAVAQAQSQL-LVHSDVRMWNVTTFICTATNAVGTGRAEQVILV 337
QY 283 SDVPFKQTSSIAVAGAVIGAVLALFI-IAIFVTVLLTPRKKR 323
Db 338 RESP--STAGAGATGGIIGGIIAIIATAVAGTGILICRQR 377
RESULT 5
PVR2_HUMAN
ID_PVR2_HUMAN STANDARD; PRT; 538 AA.
AC Q92692; O75455; Q96J29;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Herpes virus entry mediator B) (HvEB) (Nectin 2) (CD112 antigen).
DE PVR2 OR PRR2 OR HVEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).

RX MEDLINE=95347610; PubMed=7622062;
RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
RT "The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the true homolog of the murine MPH gene.";
RL Gene 159:267-272(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98321161; PubMed=9657005;
RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
RT "A cell surface protein with herpesvirus entry activity (HvEB) confers susceptibility to infection by mutants of herpes simplex virus type 1, herpes simplex virus type 2, and pseudorabies virus.";
RT Virology 246:179-189(1998).
RL [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX TISSUE=Brain;
MEDLINE=2238257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Sodergren E.J., Lu X., Gibbs R.A.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 31-538 FROM N.A.
RA Yoshiura K., Murray J.C.;
RT "A transcriptional map in the region of 19ql3 derived using direct sequencing and exon trapping.";
RT Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RL [5]
RP SEQUENCE OF 449-538 FROM N.A.
RX MEDLINE=99449047; PubMed=10520737;
RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
RA Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;
RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene: PEREC1.";
RL DNA Seq. 9:89-101(1998).
CC -!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND
CC PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Delta;
CC IsoId=Q92692-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:74-77(2000);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/204270028_g.htm".

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CC modified and this statement is not removed. Usage by and for commercial
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FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 515
FT DOMAIN 31 141
FT DOMAIN 145 243
FT DOMAIN 247 334
FT DOMAIN 437 443
FT DOMAIN 444 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
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FT CARBOHYD 332 332
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;

Query Match 32.5%; Score 561.5; DB 1; Length 515;
Best Local Similarity 36.4%; Pred. No. 2.3e-37;
Matches 118; Conservative 61; Mismatches 126; Indels 19; Gaps 6;

Qy 13 ITQISWEKIHGKSSQTVAVHPHQYGVSGVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGK 72
Db 62 ITQVTWKATNGSKQNVAIYNPAMGVSVLAPYRVERVEFLRPSFTDGTIRLSRLEDEGV 121

Qy 73 YICKAVTFPLGNAQSSTVTTLVPEPTVSLIKGPDSLIDG---GNETVAAICIAATGKPV 128
Db 122 YICEFATFPAGNRESQNLNLTVMKPT-NWIEGTQAVLRAKKGDKDKVLVATCTSANGKPP 180

Qy 129 AHIDWEGDL-GEMESTTTSFPNETATISQYKLFPTFRFARGRRITCVVKHPALEKDIRYS 187
Db 181 SVVSWETHLKGEAEYQEIIRNPNGTIVISRYRLVPSREDHRSQSLACIVNYHM--DRFRES 238

Qy 188 FILDIOYAPEVSVTGYDGNWVFGKGVNLCNADANPPPKSVWSRLDGQWPDGLLASDN 247
Db 239 LTLNVQVEFEVTIEGFDGNWYLQRMVVKLTCKADANPPATEYHWITLNGSLPKGVAEQNR 298

Qy 248 TLHFVHLTFNYSYGVYICKVTNSLQSRSDQKVYIYISDVPFKQTS-----SIAVAG 297
Db 299 TLFFRGPIYNSMAGTYICEATNPIGTRSGQVEVNITEFPYTPSPHGRAGQVPTAIIG 358

Qy 298 AVIGAV-LALPIIAIFVTVLLTPR 320
Db 359 GVGVSILLVFFVVGIVVALCRRR 382

RESULT 4

PVR2 MOUSE
ID PVR2_MOUSE STANDARD; PRT; 530 AA.
AC P32507; Q62096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).
GN PVR2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human poliovirus receptor gene."
RL J. Virol. 66:2807-2813(1992).

RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in interaction with poliovirus."
RL J. Biol. Chem. 269:8431-8438(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hsieh F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L., Diatchenko L., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Stapleton M., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Brownstein M.J., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Bosak S.A., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Richards S., Sodergren E.J., Lu X., Gibbs R.A., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Rodriguez A.C., Krzywinski M.I., Skalski U., Smallos D.E., Butterfield Y.S.N., Jones S.J.M., Marra M.A.;
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99214397; PubMed=10196354;
RA Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB) mediates entry of pseudorabies virus but not herpes simplex virus types 1 and 2."
RL J. Virol. 73:4493-4497(1999).
CC -!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P32507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P32507-2; Sequences=VSP_002630, VSP_002631;
CC -!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and liver.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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CC EMBL; M80206; AAA39734.1; -.
CC EMBL; D26107; BAA05103.1; -.
CC EMBL; BC059941; AAH59941.1; -.
CC PIR; A38211; HLMSP3.
CC PIR; A53437; A53437.
CC MGD; MGI:97822; Pvr12.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig_3.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS50835; IG_LIKE; 3.

; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match 13.2%; Score 228.5; DB 4; Length 432;
Best Local Similarity 25.8%; Pred. No. 1.3e-14;
Matches 83; Conservative 61; Mismatches 155; Indels 23; Gaps 13;

Qy	1	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDA	TI	60
Db	80	VVLKCVKDHED-SSLQWS---NPAQQTIL-----YFGEKRALRDNRIQLVTSTPHEL	SI	129
Qy	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDLSLIDGGNETV	AAIC	120
Db	130	SISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REKDTAT	LNC	186
Qy	121	IAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLPTRFARGRRITC	VVK	176
Db	187	QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKFTTVSSSVTFQVTREDDGASIV	CSVN	246
Qy	177	HPALE-KDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGNLKNADANPPPKSVWSRLD		235
Db	247	HESLKGADRSTSQRIEVLVYPTAMIRPDPPHPREGQK-LLHCEGRGNPVPVPPQYLW	EK-E	304
Qy	236	GQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSS	IAV	295
Db	305	GSVPPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSKAYYTLNVND-PSPVPSS	SST	362
Qy	296	AGAVIGAVLALFIIAIFVTVLL		317
Db	363	YHAIIGGIVA-FIVFLLIMLI		383

Search completed: April 12, 2004, 09:49:30
Job time : 11.9264 secs

Query Match	13.2%;	Score 228.5;	DB 4;	Length 398;
Best Local Similarity	25.8%;	Pred. No. 1.1e-14;		
Matches	83;	Conservative 61;	Mismatches 155;	Indels 23; Gaps 13;
QY	1	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFVSQGEYQGRVLFKNYSLNDATI	60	
Db	46	VVLKCVKHED--SSLQWS---NPAQQT-----YFGEKRALRDNRIQLVTSTPHEL	95	
QY	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC	120	
Db	96	SISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPOKPIITGYKSSL-REKDTATLNC	152	
QY	121	IAATGKPAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTRFARGRRITCVVK	176	
Db	153	QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFTVSSSVTFQVTRDDGASIVCSVN	212	
QY	177	HPALE-KDIRYSFILDIOYAPEVSVTYGDGNWFVGRKGNLKNADANPPPKSVMSRLD	235	
Db	213	HESLKGADRSTSQRIEVLVYPTAMIRPDPPHPREGOK-LLHCEGRGNVPVQQYLWEK-E	270	
QY	236	GQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPFKQTSSIAV	295	
Db	271	GSVPPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYKAYYTLNVND-PSPVPSSSST	328	
QY	296	AGAVIGAVLALFIIAIFVTVLL	317	
Db	329	YHAIIGGIVA-FIVFLLIMLI	349	

RESULT 14
US-09-902-775A-84

Sequence 84, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transferred
TITLE OF INVENTION: Acids Encoding
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/90000000
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/00000000
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,143
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,145
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,146
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20000000

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; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/209444
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-902-775A-84

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Query Match	13.2%	Score 228.5	DB 4	Length 398
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Best Local Similarity 25.8%; Pred. No. 1.1e-14;

Matches	83	Conservative	61	Mismatches	155	Indels	23	Gaps	13
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QY	1	VSLKCLIEVNETTQISWEKIHGKSSQTVAVHHPOYGFVSQGHEYQGRVLFXNYSLNDATI	60
Dd	46	VWLKCQVKDHED--SSLQWS---NPAQQTL-----YFGEKRALRDNRIQLVTSTPHELSI	95
QY	61	TLHNIGFSDSGKYICKAVTFPLGLNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC	120
Dd	96	SISNALADEGEYTCISFTMPVRTAKS--LVTVLGIPOKPPIITGYKSSL-REKDTATLNC	152
QY	121	IAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIISOYKLFPTRFARGRRITCVVK	176
Dd	153	QSSGSKPAARLLTRWKGDQQLHGEPTRIQEDPNGKTFTVSSSVTFQVTRDDGASIVCSVN	212
QY	177	HPALE-KDIRYSFILDIQYAPEVSVTYDGNWFVGKGVNLKNADANPPFKSVMSRLD	235
Dd	213	HESLKGA DRSTSQR IEVLYTP TAMIRPD PPHPREGOK-LLLHC EGRGNVPVQQYLWEK-E	270
QY	236	GOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSDDQVIYISDVFPFKOTSSIAV	295
Dd	271	GSVPPLKMTQESALIIPP-F-LNKSDSGTYGCTATSNMGSYKAYYTTLNVND-PSPVPSSSST	328
QY	296	AGAVIGAVLALEFIAlFVTVLL	317
Dd	329	YHAILGGIVA-FIVFLLLIIMLI	349

RESULT 15

US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05

; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-84

Query Match 13.2%; Score 228.5; DB 4; Length 398;
Best Local Similarity 25.8%; Pred. No. 1.1e-14;
Matches 83; Conservative 61; Mismatches 155; Indels 23; Gaps 13;

QY 1 VSLKCLIEVNETITQISWEKHGKSSQTVAVHPQYGFSGVQGEYQGRVLFKNYSLNDAI 60
Db | | | :
46 VVLKQVKDHED-SSLQWS---NPAQOTL-----YFGEKRALRDNRQLVTSSTPHELSI 95
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db :
96 SISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REKDTATLNC 152
QY 121 IAATGKPVAHIDWEGDLGEMESTTSF---PN-ETATISQYKLFPTRFARGRRITCVVK 176
Db :
153 QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTRDDGASIVCSVN 212
QY 177 HPALE-KDIRYSFILDIQAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPKSVWSRLD 235
Db | : | : | :
213 HESLKGADRSTQRIEVLTYPTAMIRPDPPHPREGQK-LLHCEGRGNPVPQQYLWEK-E 270
QY 236 GQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVPFKQTSIAV 295
Db | : | :
271 GSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSKAYTYTLNVND-PSVPVSSST 328
QY 296 ACAVIGAVLALFIIAIFVTLL 317
Db :
329 YHAIIGGIVA-FIVFLLLIMLI 349

RESULT 13
US-09-905-125A-84
; Sequence 84, Application US/09905125A

; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-905-125A-84


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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match      24.4%; Score 422; DB 4; Length 479;
Best Local Similarity 29.4%; Pred. No. 3e-34;
Matches 101; Conservative 63; Mismatches 135; Indels 44; Gaps 10;

QY 13 ITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEYQG--RVLF-----KNYSLNDAT 59
Db 65 ISLVTWQRPDAPANHQNVAAFHPKMGPSFFPSKPGSERLSFVSAKQSTQDTEAELQDAT 124

QY 60 ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP-----TVSLIKGPDSDLIDGG 112
Db 125 LALHGLTVEDEGNYTCEPATFPKGSVRGWTWLRVIAKPKNQAEAKQVTFSDP----- 177

QY 113 NETVAAICIAATKCPVAHI-----DWEGDLGEMESTTTTFPNETATIIISQYKLFPTREFA 166
Db 178 --TTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAG----TVTVTSRFTLVPSGRA 231

QY 167 RGRRTTCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPP 226
Db 232 DGVTVTCKVBHESFEPEPALIPVTLTVRYPPEVVISGYDDNWYLGRTDATLSCDVRNPEP 291

QY 227 FKSVMRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVP 286
Db 292 TGYDWSSTTSGFPTSAVAQSQL-VIHAVDSLFTTFVCTVTNAVGMGRABQVIFVRETP 350

QY 287 FKQTSSIA--VAGAVIGAVLALFIIA--IFTVLLTPRKKRPS 325
Db 351 RASPRDVGPLVWGAVGTTLLVLLLAGGSLAFILLRVRRRKS 393

RESULT 5
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62

Query Match      21.6%; Score 374; DB 4; Length 408;
Best Local Similarity 31.0%; Pred. No. 1.8e-29;
Matches 104; Conservative 57; Mismatches 153; Indels 22; Gaps 10;

QY 2 SLKCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDA 58
Db 47 TLHCSLTSNENVTTITQITWMKSDSGSHALVAVFHPKKGPNIKEPERVKFLAAQQDLRNA 106

QY 59 TITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSLI--DGGNE 114
Db 107 SLAISNLVEDEGIYECQIATFPRGRSTNAWLKVQARPKNATAEALPSPPTLILQD---- 162

QY 115 TVAAICIAATKCPVAHIDW----EGDLGEMESTTTTFPNETATIIISQYKLFPTREARGRR 170
Db 163 --VAKCISANGHPPGPRISWPSNVNMGSHREMKE-PGSQPG-TTIVTSYLSMVPVSRQADGKN 218
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QY 171 ITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFGVGRKGVNLCNADANPPPEKS 229
Db 219 ITCTVEHESLQELDQLLVTLTSQYPPPENVISISGYDGNWYVGLTNLTLTCEAHSKPAPDMA 278

QY 230 --VWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVPF 287
Db 279 GYNWSTNTGDFPNFSVKRQGNMLLISTVEDGLNNTVIVCEVTNALSGSGQGVHIIIVKEKPE 338

QY 288 KQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKR 323
Db 339 NMQONTRLHLGYIFLIVFVLAVVIIIAALYTIRRCR 374

RESULT 6
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match      16.0%; Score 276; DB 4; Length 440;
Best Local Similarity 26.4%; Pred. No. 1.9e-19;
Matches 81; Conservative 57; Mismatches 121; Indels 48; Gaps 9;

QY 52 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLID 110
Db 99 NFSSSELKVSLTNVSISDEGRYFCQLYTDP--POESYTTITVLVPPRNLMIDIQKDTAVE 156

QY 111 GGNETVAAICIAATGKPVAHIDW-EGDL-----GEMESTTTFPNETATIIISQYKLFPTR 164
Db 157 G--EEIEVNCTAMASKPATTTIRWFKGNTLKGKSEVEWSDMY-----TVTSQLMLKVHK 209

QY 165 FARGRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKG--VNLKCNADA 222
Db 210 EDDGVPIQVEHPAVTGNLTQRYLEVQYKPVHQVHIQMTYPLQGLTREGDALELTCEAIG 269

QY 223 NPPPFKSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYI 282
Db 270 KPQPMVMTWVRVDDMPQHAHLVSGPNL-FINNLNKTNDNGYRCEASNIVGKAHSDYMLYV 328

QY 283 SDVPF-----KQTSIAVAGAVIGAVLALFIIAIFV 313
Db 329 YDPTTIPPPPTTTTTTTTTTTTTTTTTTTTTTTTTTTTDSRAGEEGSRAVDHAVIGGVAVVVFAMLC 388

QY 314 TVLLTPR 320
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Db 239 LTLNVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEYHWTTLNGSLPKGVEAQR 298
QY 248 TLHFVHPLTFNYSVYICKVTNSLQORSQDKVIYISDVPFKQTS-----SIAVAG 297
Db 299 TLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYTPSPPEHGRAGVPVPTAIIG 358
QY 298 AVIGAVLALFIALFVTVLLTPRKKRPSY 326
Db 359 GVAGSILLVIVGGIVVAL--RRRRHTF 385

RESULT 2
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: HIGR and Related v Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 32.2%; Score 557; DB 4; Length 458;
Best Local Similarity 36.8%; Pred. No. 5.2e-48;
Matches 119; Conservative 59; Mismatches 135; Indels 10; Gaps 5;

QY 13 ITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDAITLHNIGFSDSGK 72
Db 62 ITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPSFTDGTIRLSRLEDEGV 121
QY 73 YICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG---GNETVAAICIAATGKPV 128
Db 122 YICGFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAKKGDDKVLVATCTSANGKPP 180
QY 129 AHIDWEGDL-GEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVXHPALEKDIRYS 187
Db 181 SVVSWETRLKGEAEYQEIIRNPNGTIVTISRVLVPSREAHQQLACIVNYHM--DRFKES 238
QY 188 FILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANPPFPKSVWSRLDQWPDGLLASDN 247
Db 239 LTLNVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEYHWTTLNGSLPKGVEAQR 298
QY 248 TLHFVHPLTFNYSVYICKVTNSLQORSQDKVIYISDVPFKQTS-----SIAVAGVIGAVLALF 307
Db 299 TLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEKPRPQRLGSAARLLAGTVAVFL 358
QY 308 IIAIFVTV--LLTPRKKRPSYLD 328
Db 359 ILVAVLTVFFLYNRQKSPPETD 381

RESULT 3
US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:

; APPLICANT: Faria, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CDI
US-09-919-172-20

Query Match 31.4%; Score 542.5; DB 4; Length 518;
Best Local Similarity 34.0%; Pred. No. 1.9e-46;
Matches 115; Conservative 66; Mismatches 120; Indels 37; Gaps 7;

QY 13 ITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDAITLHNIGFSDSGK 72
Db 62 ITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPSFTDGTIRLSRLEDEGV 121
QY 73 YICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG---GNETVAAICIAATGKPV 128
Db 122 YICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAKKGDDKVLVATCTSANGKPP 180
QY 129 AHIDWE-----GDLGEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVXHP 178
Db 181 SVVSWETRLKGEARVPDGSCT-----PMAPVTVISRYRLVPSREAHQQLACIVNYH 232
QY 179 ALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANPPFPKSVWSRLDQW 238
Db 233 M--DRFKESLTLNVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEYHWTTLNGSL 290
QY 239 PDGLLASDNTLHFVHPLTFNYSVYICKVTNSLQORSQDKVIYISDVPFKQTS----- 291
Db 291 PKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYTPSPPEHGRRA 350
QY 292 ---SIAVAGVIGAVLALFIIAIFVTVLLTPRKKRPSY 326
Db 351 GPVPTAIIGVAGSILLVIVGGIVVAL--RRRRHTF 386

RESULT 4
US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 10.9264 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-31_COPY_74_404

Perfect score: 1728

Sequence: 1 VSLKCLIEVNETITQISWEK.....FVTVLLTPRKRPSTYLDKVI 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	565	32.7	517	4	US-09-723-368-4
2	557	32.2	458	4	US-09-435-956A-1
3	542.5	31.4	518	4	US-09-919-172-20
4	422	24.4	479	4	US-09-723-368-2
5	374	21.6	408	4	US-09-724-864-62
6	276	16.0	440	4	US-09-866-028-61
7	276	16.0	442	4	US-09-778-510-20
8	276	16.0	442	4	US-09-930-803-1
9	272	15.7	423	4	US-09-778-510-22
10	238.5	13.8	398	4	US-09-778-510-4
11	228.5	13.2	398	4	US-09-778-510-6
12	228.5	13.2	398	4	US-09-907-794A-84
13	228.5	13.2	398	4	US-09-905-125A-84
14	228.5	13.2	398	4	US-09-902-775A-84
15	228.5	13.2	432	4	US-09-778-510-2
16	223	12.9	421	2	US-08-659-984A-1
17	223	12.9	421	3	US-08-660-531-1
18	223	12.9	444	2	US-08-659-984A-5
19	223	12.9	444	3	US-08-660-531-5
20	190.5	11.0	227	4	US-09-205-258-947
21	187.5	10.9	274	4	US-09-570-367C-19
22	187.5	10.9	274	4	US-09-915-524-19
23	169.5	9.8	1101	3	US-08-986-485-2
24	164	9.5	467	3	US-09-046-736-2
25	158.5	9.2	278	4	US-09-570-367C-2
26	158.5	9.2	278	4	US-09-915-524-2
27	157.5	9.1	365	2	US-08-979-424-3

28	157.5	9.1	365	3	US-08-928-383B-2	Sequence 2, Appli
29	157.5	9.1	365	3	US-09-272-496-2	Sequence 2, Appli
30	155.5	9.0	278	4	US-09-570-367C-21	Sequence 21, Appl
31	155.5	9.0	278	4	US-09-915-524-21	Sequence 21, Appl
32	155	9.0	365	3	US-08-928-383B-23	Sequence 23, Appl
33	155	9.0	365	3	US-08-928-383B-24	Sequence 24, Appl
34	153.5	8.9	642	1	US-08-217-299-1	Sequence 1, Appli
35	153.5	8.9	698	2	US-08-602-725-36	Sequence 36, Appl
36	153.5	8.9	734	2	US-08-389-459A-17	Sequence 17, Appl
37	153.5	8.9	734	3	US-08-987-867A-17	Sequence 17, Appl
38	153	8.9	365	3	US-08-928-383B-26	Sequence 26, Appl
39	149	8.6	1651	3	US-09-540-245A-18	Sequence 18, Appl
40	147	8.5	477	2	US-08-432-016-3	Sequence 3, Appli
41	147	8.5	477	2	US-08-684-594-3	Sequence 3, Appli
42	142	8.2	387	4	US-09-175-928-2	Sequence 2, Appli
43	141.5	8.2	464	2	US-08-602-725-32	Sequence 32, Appl
44	140	8.1	643	5	PCT-US93-00031-19	Sequence 19, Appl
45	140	8.1	644	5	PCT-US93-00031-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1

US-09-723-368-4
; Sequence 4, Application US/097233368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match 32.7%; Score 565; DB 4; Length 517;
Best Local Similarity 35.9%; Pred. No. 9.6e-49;
Matches 118; Conservative 66; Mismatches 125; Indels 20; Gaps 6;

QY	13	ITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNVSLNDATITLHNIGFSDSGK	72
Db	62	ITQVTQKSTNGSKONVAIYNPSMGVSLAPYRERVEFLRPSFTDGTIRLSRLEDEGV	121
QY	73	YICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG----GNETVAAICIAATGKPV	128
Db	122	YICEFATFPTGNRESQNLNTVMAKPT-NWIEGTQAVLRAKQGDQDKVLVATCTSANGKPP	180
QY	129	AHIDWEGDL-GEMESTTTSFNETATIIISQKLFPTFRFARRRITCVVKHPALEKDIRYS	187
Db	181	SVVSWETRLKGEAEYQEIERNPENGTVTVISRYRLVPSREAHQOQSLACIVNYHM--DRFKES	238
QY	188	FILDIQYAPEVSVTGYDGNWFVGRKGVNLCNADANPPFKSVWSRLDGQWPDGLLASDN	247


```
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

Query Match      87.5%; Score 1512; DB 10; Length 426;
Best Local Similarity 98.6%; Pred. No. 4.4e-134;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDA 60
Db 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDA 60
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSLIDGGNETVAA 120
Db 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSLIDGGNETVAA 120
QY 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSLIDGGNETVAA 193
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSLIDGGNETVAA 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRITCVVKHP 180
Db 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRITCVVKHP 180
QY 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRITCVVKHP 253
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRITCVVKHP 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPD 240
Db 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPD 240
QY 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPD 313
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPEKQT 290
Db 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPEKQT 290
QY 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTT 363
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTT 363
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Search completed: April 12, 2004, 10:25:31
Job time : 27.6628 secs

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP----- 286
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPPTTTTLQPTIQWHP 373
QY 287 -----FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK- 322
Db 374 TADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIVLSVLAGIFCYRRRT 433
QY 323 -RPSYLDK 329
Db 434 FRGDYFAK 441

RESULT 13
US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-6

Query Match 87.9%; Score 1519.5; DB 10; Length 549;
Best Local Similarity 79.6%; Pred. No. 1.2e-134;
Matches 293; Conservative 12; Mismatches 24; Indels 39; Gaps 2;
QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDAI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP----- 286
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPPTTTTLQPTIQWHP 373

QY 287 -----FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK- 322
Db 374 TADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIVLSVLAGIFCYRRRT 433
QY 323 -RPSYLDK 329
Db 434 FRGDYFAK 441
RESULT 14
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 87.9%; Score 1519.5; DB 14; Length 549;
Best Local Similarity 79.6%; Pred. No. 1.2e-134;
Matches 293; Conservative 12; Mismatches 24; Indels 39; Gaps 2;
QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDAI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP----- 286
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPPTTTTLQPTIQWHP 373
QY 287 -----FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK- 322
Db 374 TADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIVLSVLAGIFCYRRRT 433
QY 323 -RPSYLDK 329
Db 434 FRGDYFAK 441
RESULT 15
US-09-972-268-15


```

; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-4

Query Match      97.0%; Score 1677; DB 10; Length 510;
Best Local Similarity 95.5%; Pred. No. 1.5e-149;
Matches 316; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY      1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 60
      |||||||
Db      74 VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHHPQYGFSGVQGDYQGRVLFKNYSLNDAI 133
      |||||||

QY      61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
      |||||||
Db      134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC 193
      |||||||

QY      121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVKHPAL 180
      |||||||
Db      194 VAATGKPVQAIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFARGRRITCVVKHPAL 253
      |||||||

QY      181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 240
      |||||||
Db      254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 313
      |||||||

QY      241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPEFKQTSSIAVAGAVI 300
      |||||||
Db      314 GLLASDNTLHFVHPLTFNYSGVYCKVNSLQGRSDQKVIYISDIPLTQTSSIAVAGAVI 373
      |||||||

QY      301 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 331
      |||||||
Db      374 GAVLALFIIITVFVTVLLTPRKKRPSYLDKVI 404
      |||||||

RESULT 8
US-09-972-268-18
; Sequence 18, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 510
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-18

Query Match      97.0%; Score 1677; DB 10; Length 510;
Best Local Similarity 95.5%; Pred. No. 1.5e-149;
Matches 316; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY      1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 60
      |||||||
Db      74 VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHHPQYGFSGVQGDYQGRVLFKNYSLNDAI 133
      |||||||

QY      61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
      |||||||
Db      134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC 193
      |||||||

QY      121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVKHPAL 180
      |||||||
Db      194 VAATGKPVQAIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFARGRRITCVVKHPAL 253
      |||||||

QY      181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 240
      |||||||
Db      254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 313
      |||||||

QY      241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPEFKQTSSIAVAGAVI 300
      |||||||
Db      314 GLLASDNTLHFVHPLTFNYSGVYCKVNSLQGRSDQKVIYISDIPLTQTSSIAVAGAVI 373
      |||||||

QY      301 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 331
      |||||||
Db      374 GAVLALFIIITVFVTVLLTPRKKRPSYLDKVI 404
      |||||||

RESULT 8
US-09-972-268-18
; Sequence 18, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 510
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-18

Query Match      97.0%; Score 1677; DB 10; Length 510;
Best Local Similarity 95.5%; Pred. No. 1.5e-149;
Matches 316; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY      1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 60
      |||||||
Db      74 VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHHPQYGFSGVQGDYQGRVLFKNYSLNDAI 133
      |||||||

QY      61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
      |||||||
Db      134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
      |||||||

QY      121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVKHPAL 180
      |||||||
Db      194 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVKHPAL 253
      |||||||

QY      181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 240
      |||||||
Db      254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 313
      |||||||

QY      241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPEFKQTSS 292
      |||||||
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QY      1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 60
      |||||||
Db      74 VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHHPQYGFSGVQGDYQGRVLFKNYSLNDAI 133
      |||||||

QY      61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
      |||||||
Db      134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC 193
      |||||||

QY      121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVKHPAL 180
      |||||||
Db      194 VAATGKPVQAIDWEGDLGEMESSTTSPNETATIVSQYKLFPTFRFARGRRITCVVKHPAL 253
      |||||||

QY      181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 240
      |||||||
Db      254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 313
      |||||||

QY      241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPEFKQTSSIAVAGAVI 300
      |||||||
Db      314 GLLASDNTLHFVHPLTFNYSGVYCKVNSLQGRSDQKVIYISDIPLTQTSSIAVAGAVI 373
      |||||||

QY      301 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 331
      |||||||
Db      374 GAVLALFIIITVFVTVLLTPRKKRPSYLDKVI 404
      |||||||

RESULT 9
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

Query Match      89.5%; Score 1546; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.4e-137;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 60
      |||||||
Db      74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 133
      |||||||

QY      61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
      |||||||
Db      134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
      |||||||

QY      121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVKHPAL 180
      |||||||
Db      194 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRITCVVKHPAL 253
      |||||||

QY      181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 240
      |||||||
Db      254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANPPPFKSVWSRLDGQWPD 313
      |||||||

QY      241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPEFKQTSS 292
      |||||||
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US-09-972-268-12

Query Match	100.0%;	Score 1728;	DB 10;	Length 510;
Best Local Similarity	100.0%;	Pred. No. 2.2e-154;		
Matches 331; Conservative	0;	Mismatches 0;	Indels 0;	

[illegible]

RESULT 5

US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US2003008334A1

GENERAL INFORMATION:

; APPLICANT: Yoshimi TAKAI
 ; APPLICANT: Hiroyuki NAKANISHI
 ; APPLICANT: Keiko SATO
 ; APPLICANT: Kenichi TAKAHASHI
 ; TITLE OF INVENTION: Protein Nectin-3
 ; FILE REFERENCE: 2001-1678A/LC/00653
 ; CURRENT APPLICATION NUMBER: US/09/959,845
 ; CURRENT FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: PCT/JP01/01871
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: JP 2000-065595
 ; PRIOR FILING DATE: 2000-03-09
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6

; LENGTH: 438

TYPE: PRT

ORGANISM: Mollusc

TTS-09-959-845-6

Query Match	97.0%;	Score 1677;	DB 10;	Length 438;
Best Local Similarity	95.5%;	Pred. No. 1.2e-149;		
Matches 316:	Conservative	10;	Mismatches 5;	Indels 0;
	Gaps	0;		

Qy	1	VSLKCLIEVN	ETITQISWEKIHGKSSQTVAHHPOYGFSVQGEYQGRVLFPKNYSUNDATI	60
Dd	74	VSLKCLIEVN	ETITQISWEKIHGKSTQTVAHHPOYGFSVQGDYQGRVLFPKNYSUNDATI	133
Qy	61	TLHNIGFSDS	GKYICKAVTFPLGNAQSSITTIVLVEPTVSLLIKGPDLSLIDGGNETVAAIC	120
Dd	134	TLHNIGFSDS	GKYICKAVTFPLGNAQSSITTIVLVEPTVSLLIKGPDLSLIDGGNETVAAVC	193
Qy	121	IAATGKPVAH	IDWEGDLGEMESSTTSFPNETATTISQYKLFPTRFARGRRITCVVKHPAL	180
Dd	194	VAAATGKPVA	IDWEGDLGEMESSTTSFPNETATTISQYKLFPTRFARGRRITCVVKHPAL	253
Qy	181	EKDIRYSFIL	DIQYAPEVSVTGYDGNWFVGXKGWNLCNADANPPPFKSVMWSRLDGQWPD	240

Db	254	EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPFKSVWSRLDGQWPD	313
QY	241	GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPEFKQTSSIAVAGAVI	300
Db	314	GLLASDNTLHFVHPLTFNYSGVYCKVSVNSLQORSQDKVIYISDIPLTQTSSIAVAGAVI	373
QY	301	GAVLALFIIAIFVTVLLTPRKKRPPSYLDKVI	331
Db	374	GAVLALFIITVFVTVLLTPRKKRPPSYLDKVI	404

RESULT 6

US-09-972-268-19
; Sequence 19, Application US/09972268
; Publication No. US20030044893A1

: GENERAL INFORMATION:

```

1 / APPLICANT: Baum, Peter R.
2 /
3 / APPLICANT: Fanslow, William C.
4 /
5 / APPLICANT: Lofton, Timothy E.
6 /
7 / APPLICANT: Sorensen, Eric A.
8 /
9 / APPLICANT: Youakim, Adel
10 /
11 / TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES AND COMPOSITIONS THEREOF
12 /
13 / FILE REFERENCE: 3101-A
14 /
15 / CURRENT APPLICATION NUMBER: US/09/972,268
16 /
17 / CURRENT FILING DATE: 2001-10-05
18 /
19 / PRIOR APPLICATION NUMBER: 60/238,557
20 /
21 / PRIOR FILING DATE: 2000-10-05
22 /
23 / NUMBER OF SEQ ID NOS: 39
24 /
25 / SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 19

LENGTH: 4

TYPE: PRT

ORGANISM: *MUSCIVORA*

Query Match	97.0%;	Score 1677;	DB 10;	Length 438;
Best Local Similarity	95.5%;	Pred. No. 1.2e-149;		
Matches 316:	Conservative	10;	Mismatches	5;
	Indels			

QY	1	VSLKCLIEVN	ETITQISWEKIHGKSSQTVAVHH	PQYGFVSQGEYQGRVLFKNYS	LNDATI	60
Db	74	VSLKCLIEVN	ETITQISWEKIHGKSTQTVAVHH	PQYGFVSQGEYQGRVLFKNYS	LNDATI	133
QY	61	TLHNIGFSD	SGKYICKAVTFPLGNAQSSTTVTL	VEPTVSLIKGPDSLIDGGNETVAA	IC	120
Db	134	TLHNIGFSD	SGKYICKAVTFPLGNAQSSTTVTL	VEPTVSLIKGPDSLIDGGNETVAA	VC	193
QY	121	IAATGKPV	AHIDWEGDLGEMESTTSPNETATI	ISQYKLFPTFRFARGRRITCVVK	HPAL	180
Db	194	VAATGKPV	AQIDWEGDLGEMESTTSPNETATI	VSQYKLFPTFRFARGRRITCVVK	HPAL	253
QY	181	EKDIRYS	FILDIQYAPEVSVTGYDGNWFVGR	KGVLKCNADANPPPKSVWSRLDG	QWPD	240
Db	254	EKDIRYS	FILDIQYAPEVSVTGYDGNWFVGR	KGVLKCNADANPPPKSVWSRLDG	QWPD	313
QY	241	GLLASDNT	LHFVHPLTFNYSGVYICKVTNSL	QORSQDKVIYISDVPFKQTSSIA	VAGAVI	300
Db	314	GLLASDNT	LHFVHPLTFNYSGVYICKVTNSL	QORSQDKVIYISDIPLTQTSSIA	VAGAVI	373
QY	301	GAVLALF	IIAIFVTVLLTPRKKRPSYLDKVI			331
Db	374	GAVLALF	IIITVFTVLLTPRKKRPSYLDKVI			404

RESULT 7

US-09-959-845-4
; Sequence 4, Application US/09959845
; Publication No. US20030008334A1

: GENERAL INFORMATION:

APPLICANT: YOSHIKI TAKAI

APPLICANT: HJ TOYLIK; NAKANT SHT
 APPLICANT: HJ TOYLIK; NAKANT SHT

APPLICANT: KEIJO SATO

Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253
Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGNLKNADANPPPKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGNLKNADANPPPKSVWSRLDGQWPD 313
Qy 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPFKQTSSIAVAGAVI 300
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPFKQTSSIAVAGAVI 373
Qy 301 GAVLALFIIAIFVTVLLTPRKRPSYLDKVI 331
Db 374 GAVLALFIIAIFVTVLLTPRKRPSYLDKVI 404

RESULT 2

US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

Query Match 100.0%; Score 1728; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.2e-154;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI 60
Db 68 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI 127
Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 128 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 187
Qy 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 188 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 247
Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGNLKNADANPPPKSVWSRLDGQWPD 240
Db 248 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGNLKNADANPPPKSVWSRLDGQWPD 307
Qy 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPFKQTSSIAVAGAVI 300
Db 308 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPFKQTSSIAVAGAVI 367
Qy 301 GAVLALFIIAIFVTVLLTPRKRPSYLDKVI 331
Db 368 GAVLALFIIAIFVTVLLTPRKRPSYLDKVI 398

RESULT 3

US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are from human Nectin-3 beta
US-09-972-268-10

Query Match 100.0%; Score 1728; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.2e-154;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI 133
Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
Qy 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253
Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGNLKNADANPPPKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGNLKNADANPPPKSVWSRLDGQWPD 313
Qy 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPFKQTSSIAVAGAVI 300
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPFKQTSSIAVAGAVI 373
Qy 301 GAVLALFIIAIFVTVLLTPRKRPSYLDKVI 331
Db 374 GAVLALFIIAIFVTVLLTPRKRPSYLDKVI 404

RESULT 4

US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 27.6628 Seconds
(without alignments)
3146.189 Million cell updates/sec

Title: US-09-972-268-31_COPY_74_404
Perfect score: 1728
Sequence: 1 VSLKCLIEVNETITQISWEK.....FVTVLLTPRKRPYSYLDKVI 331

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1728	100.0	437	10	US-09-972-268-31 Sequence 31, Appl
2	1728	100.0	504	10	US-09-972-268-8 Sequence 8, Appli
3	1728	100.0	510	10	US-09-972-268-10 Sequence 10, Appl
4	1728	100.0	510	10	US-09-972-268-12 Sequence 12, Appl
5	1677	97.0	438	10	US-09-959-845-6 Sequence 6, Appli
6	1677	97.0	438	10	US-09-972-268-19 Sequence 19, Appl
7	1677	97.0	510	10	US-09-959-845-4 Sequence 4, Appli
8	1677	97.0	510	10	US-09-972-268-18 Sequence 18, Appl
9	1546	89.5	387	10	US-09-972-268-16 Sequence 16, Appl
10	1546	89.5	595	10	US-09-972-268-14 Sequence 14, Appl
11	1519.5	87.9	542	10	US-09-972-268-2 Sequence 2, Appli
12	1519.5	87.9	549	10	US-09-972-268-4 Sequence 4, Appli
13	1519.5	87.9	549	10	US-09-972-268-6 Sequence 6, Appli
14	1519.5	87.9	549	14	US-10-161-572-45 Sequence 45, Appl
15	1512	87.5	426	10	US-09-972-268-15 Sequence 15, Appl

16	1512	87.5	634	10	US-09-972-268-13 Sequence 13, Appl
17	1490.5	86.3	549	10	US-09-959-845-2 Sequence 2, Appli
18	1490.5	86.3	549	10	US-09-972-268-17 Sequence 17, Appl
19	565	32.7	514	14	US-10-161-572-60 Sequence 60, Appl
20	565	32.7	517	10	US-09-972-268-20 Sequence 20, Appl
21	560	32.4	458	10	US-09-972-268-21 Sequence 21, Appl
22	542.5	31.4	518	9	US-09-919-172-20 Sequence 20, Appl
23	483	28.0	479	10	US-09-766-511B-35 Sequence 35, Appl
24	483	28.0	497	10	US-09-972-268-37 Sequence 37, Appl
25	483	28.0	510	10	US-09-766-511B-33 Sequence 33, Appl
26	483	28.0	510	12	US-10-058-270A-54 Sequence 54, Appl
27	483	28.0	510	14	US-10-161-572-55 Sequence 55, Appl
28	483	28.0	510	14	US-10-241-220-94 Sequence 94, Appl
29	483	28.0	510	15	US-10-295-027-66 Sequence 66, Appl
30	483	28.0	510	15	US-10-173-999-76 Sequence 76, Appl
31	481.5	27.9	498	10	US-09-972-268-39 Sequence 39, Appl
32	481.5	27.9	511	10	US-09-972-268-34 Sequence 34, Appl
33	481	27.8	510	10	US-09-972-268-24 Sequence 24, Appl
34	481	27.8	510	14	US-10-161-572-54 Sequence 54, Appl
35	450.5	26.1	314	10	US-09-766-511B-36 Sequence 36, Appl
36	446.5	25.8	580	10	US-09-972-268-36 Sequence 36, Appl
37	426.5	24.7	538	10	US-09-972-268-23 Sequence 23, Appl
38	426.5	24.7	538	10	US-09-984-130-138 Sequence 138, App
39	426.5	24.7	538	10	US-09-836-353A-138 Sequence 138, App
40	426.5	24.7	538	14	US-10-161-572-61 Sequence 61, Appl
41	426.5	24.7	538	15	US-10-411-010-17 Sequence 17, Appl
42	422	24.4	479	10	US-09-972-268-22 Sequence 22, Appl
43	422	24.4	479	14	US-10-161-572-62 Sequence 62, Appl
44	420	24.3	522	15	US-10-264-049-2969 Sequence 2969, Ap
45	407.5	23.6	458	12	US-10-296-115-1150 Sequence 1150, Ap

ALIGNMENTS

RESULT 1
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match 100.0%; Score 1728; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.8e-154;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDA	60
Db	74	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDA	133
QY	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC	120
Db	134	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC	193
QY	121	IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRARGRRITCVVKHPAL	180

Search completed: April 12, 2004, 09:38:39
Job time : 40.9767 secs

QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPPFKSVMSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPPFKSVMSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQDKVIYISDVP----- 286
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QY 287 -----FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK- 322
Db 374 TADIEDLATEPKKLPFPLSLATIKDDTIATIIASVVGALFIVLSVLGIFCYRRRT 433
QY 323 -RPSYLDK 329
Db 434 FRGDYFAK 441

RESULT 14
ABJ20222
ID ABJ20222 standard; protein; 549 AA.
XX
AC ABJ20222;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human IG gene related protein SEQ ID No 45.
XX
KW Breast cancer; p53 pathway modulating agent; IG; colon cancer;
KW kidney cancer; lung cancer; ovary cancer; human.
XX
OS Homo sapiens.
XX
PN WO200299040-A2.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017313.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 22-OCT-2001; 2001US-0338733P.
PR 15-FEB-2002; 2002US-0357253P.
PR 15-FEB-2002; 2002US-0357600P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Lioubin MN;
XX
DR WPI; 2003-148660/14.
XX
PT Identifying a candidate p53 pathway modulators that are useful as targets
PT for therapeutics or for diagnosing cancers associated with defective p53
PT function, by providing an assay system having a purified IG polypeptide
PT or nucleic acid.
XX
PS Claim 13; Page 206-209; 248pp; English.
XX

CC The invention relates to a novel method for identifying a candidate p53
CC pathway modulating agent. The method comprises providing an assay system
CC having a purified IG polypeptide or nucleic acid, or their functionally
CC active fragment or derivative. The method is useful for identifying
CC modulators of the p53 pathway, particularly for identifying agents for
CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
CC cancer or cancer of the ovary) associated with defective p53 function.
CC The identified modulators are useful as targets for novel therapeutics.
CC The method is also useful for diagnosing disorders associated with
CC defective p53 function. The IG proteins or nucleic acids are useful as
CC modifiers of the p53 pathway, and as therapeutic targets for disorders
CC associated with defective p53 function. This sequence represents a human
CC protein relating to the human IG genes used in the assay for identifying
CC modulators of the p53 pathway of the invention
XX

SQ Sequence 549 AA;
Query Match 87.9%; Score 1519.5; DB 6; Length 549;
Best Local Similarity 79.6%; Pred. No. 1.2e-128;
Matches 293; Conservative 12; Mismatches 24; Indels 39; Gaps 2;
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Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPPFKSVMSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQDKVIYISDVP----- 286
Db 314 GLLASDNTLHFVHPLTFNYSVGVICKVTNSLQORSQDKVIYISDVP----- 373
QY 287 -----FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK- 322
Db 374 TADIEDLATEPKKLPFPLSLATIKDDTIATIIASVVGALFIVLSVLGIFCYRRRT 433
QY 323 -RPSYLDK 329
Db 434 FRGDYFAK 441

RESULT 15
AAM39143
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XX
AC AAM39143;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2288.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC FLAGpolyHis fusion protein
XX
SQ Sequence 387 AA;
Query Match 89.5%; Score 1546; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.9e-131;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYSINDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYSINDATI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANPPFPKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANPPFPKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIYISDVVPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIYISDVVPFKQTSS 365

RESULT 10
AAE23288
ID AAE23288 standard; protein; 595 AA.
XX
AC AAE23288;
XX
DT 27-AUG-2002 (first entry)
XX Human nectin-3beta-IgG1Fc region fusion protein.
DE
XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX

PA (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 102-104; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 595 AA;
Query Match 89.5%; Score 1546; DB 5; Length 595;
Best Local Similarity 100.0%; Pred. No. 5.2e-131;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYSINDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYSINDATI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANPPFPKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANPPFPKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIYISDVVPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIIYISDVVPFKQTSS 365
RESULT 11
AAE23281
ID AAE23281 standard; protein; 542 AA.
XX
AC AAE23281;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3alpha protein.
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW

QY	301	GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI	331	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC	120
Db	374	GAVLALFIITVFVTVLLTPRKKRPSYLDKVI	404	134	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC	193
RESULT 8						
AAE23292	ID AAE23292 standard; protein; 510 AA.					
AC	AAE23292;					
XX	27-AUG-2002 (first entry)					
DT	Mouse nectin-3beta protein.					
DE	XX					
XX	KW Mouse; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;					
KW	paracellular transport disorder; kidney; diabetic retinopathy; allergy;					
KW	alllograft rejection; metastasis; restenosis; inflammatory bowel disease;					
KW	oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;					
KW	stroke; tumour; cancer; herpesvirus infection; asthma.					
XX	OS Mus musculus.					
OS	XX					
PN	WO200228902-A2.					
XX	PD 11-APR-2002.					
XX	PF 05-OCT-2001; 2001WO-US031392.					
XX	PR 05-OCT-2000; 2000US-0238557P.					
XX	(IMMV) IMMUNEX CORP.					
PA	Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;					
XX	WPI; 2002-426103/45.					
DR	Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,					
XX	useful for treating or preventing heart failure, malaria,					
PT	glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,					
PT	sepsis, stroke.					
XX	PS Disclosure; Page 109-110; 14lpp; English.					
PS	CC The invention relates to a substantially purified nectin3alpha, beta,					
XX	gamma and nectin-4 polypeptides and their corresponding polynucleotides.					
CC	Nectin DNA and protein are useful for treating a disease associated with					
CC	cell adhesion activity, adherens junction formation activity, epithelial					
CC	or endothelial barrier function activity, endothelial proliferation or					
CC	migration activity, viral polypeptide binding activity. The epithelial or					
CC	endothelial barrier function disorder which is treated by the above					
CC	mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,					
CC	asthma, allergy, allograft rejection, metastasis of cancer cells,					
CC	paracellular transport disorders such as magnesium transport defects in					
CC	the kidney or inflammatory bowel disease. Nectin DNA is also useful for					
CC	inhibiting angiogenesis in a mammal and treating endothelial migration,					
CC	proliferation or angiogenic condition of a tissue or a subject, such as					
CC	ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,					
CC	stroke, restenosis, tumour growth and treating herpesvirus infection.					
CC	Nectin is also useful for modulating proliferation or migration of an					
CC	endothelial cell, an epithelial cell or a smooth muscle cell (vascular					
CC	smooth muscle cell). The present sequence is mouse nectin-3beta protein					
XX	SQ Sequence 510 AA;					
QY	1	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI	60	121	IAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPPTRFARRRITCVVKHPAL	180
Db	74	VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGDYQGRVLFKNYSLNDATI	133	194	VAATGKPVQAIDWEGDLGEMESTTTSFPNETATIVSQYKLPPTRFARRRITCVVKHPAL	253

KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..6
FT /note= "Mouse nectin-3 pprotein"
FT Region 7..510
FT /note= "Human nectin-3beta protein"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37444.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 94-95; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 510 AA;

Query Match 100.0%; Score 1728; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. NO. 1.4e-147;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 60
Db |
74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 133

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db |
134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 193

QY 121 IAAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db |
194 IAAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGNLKNADANPPPFKSVWSRLDGQWPD 240
Db |
254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGNLKNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIISDVPEFKQTSSIAVAGAVI 300
Db |
314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIISDVPEFKQTSSIAVAGAVI 373
QY 301 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 331
Db |
374 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 404

RESULT 4
AAE23286
ID AAE23286 standard; protein; 510 AA.
XX
AC AAE23286;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 73
FT /note= "N-glycosylated"
FT Domain 74..152
FT /note= "Extracellular Ig domain"
FT Modified-site 83
FT /note= "N-glycosylated"
FT Modified-site 125
FT /note= "N-glycosylated"
FT Modified-site 186
FT /note= "N-glycosylated"
FT Domain 189..250
FT /note= "Extracellular Ig domain"
FT Modified-site 222
FT /note= "N-glycosylated"
FT Domain 287..342
FT /note= "Extracellular Ig domain"
FT Modified-site 331
FT /note= "N-glycosylated"
FT Domain 386..510
FT /note= "Intracellular C-terminal domain"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37445.
XX

CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3gamma protein.
CC Human nectin-3gamma gene is located on chromosome 3
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 1728; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.1e-147;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI 133
Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
Qy 121 IAATGKPVAHIDWEGDLGEMESTTTTFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTTFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253
Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANPPPKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANPPPKSVWSRLDGQWPD 313
Qy 241 GLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIYISDVFPFKQTSSIAVAGAVI 300
Db 314 GLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIYISDVFPFKQTSSIAVAGAVI 373
Qy 301 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 331
Db 374 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 404

RESULT 2
AAE23284
ID AAE23284 standard; protein; 504 AA.
XX
AC AAE23284;
XX

DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3beta protein.
XX

KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX

OS Homo sapiens.
XX
FN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX

PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX

DR WPI; 2002-426103/45.
DR N-PSDB; AAD37443.
XX

PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX

PS Claim 1; Page 89-91; 141pp; English.
XX

CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX

SQ Sequence 504 AA;

Query Match 100.0%; Score 1728; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 331; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI 60
Db 68 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI 127
Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 128 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 187
Qy 121 IAATGKPVAHIDWEGDLGEMESTTTTFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 188 IAATGKPVAHIDWEGDLGEMESTTTTFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 247
Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANPPPKSVWSRLDGQWPD 240
Db 248 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANPPPKSVWSRLDGQWPD 307
Qy 241 GLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIYISDVFPFKQTSSIAVAGAVI 300
Db 308 GLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIYISDVFPFKQTSSIAVAGAVI 367
Qy 301 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 331
Db 368 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 398

RESULT 3
AAE23285
ID AAE23285 standard; protein; 510 AA.
XX

AC AAE23285;
XX

DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX

DE Mouse nectin-3-human nectin-3beta fusion protein.
XX

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 39.9767 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-31_COPY_74_404
Perfect score: 1728
Sequence: 1 VSLKCLIEVNETITQISWEK.....FVTVLLTPRKRPYSYLDKVI 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1728	100.0	437	5 AAE23299	Aae23299 Human nec
2	1728	100.0	504	5 AAE23284	Aae23284 Human del
3	1728	100.0	510	5 AAE23285	Aae23285 Mouse nec
4	1728	100.0	510	5 AAE23286	Aae23286 Human nec
5	1677	97.0	438	4 AAG63984	Aag63984 Amino aci
6	1677	97.0	438	5 AAE23293	Aae23293 Mouse nec
7	1677	97.0	510	4 AAG63983	Aag63983 Amino aci
8	1677	97.0	510	5 AAE23292	Aae23292 Mouse nec
9	1546	89.5	387	5 AAE23290	Aae23290 Human nec
10	1546	89.5	595	5 AAE23288	Aae23288 Human nec
11	1519.5	87.9	542	5 AAE23281	Aae23281 Human del
12	1519.5	87.9	549	5 AAE23283	Aae23283 Human nec
13	1519.5	87.9	549	5 AAE23282	Aae23282 Mouse nec
14	1519.5	87.9	549	6 ABJ20222	Abj20222 Human IG
15	1519.5	87.9	555	4 AAM39143	Aam39143 Human pol
16	1512	87.5	426	5 AAE23289	Aae23289 Human nec
17	1512	87.5	634	5 AAE23287	Aae23287 Human nec
18	1490.5	86.3	549	4 AAG63982	Aag63982 Amino aci
19	1490.5	86.3	549	4 AAG63985	Aag63985 Amino aci
20	1490.5	86.3	549	5 AAE23291	Aae23291 Mouse nec
21	1444.5	83.6	559	4 AAM40929	Aam40929 Human pol
22	1128	65.3	267	4 AAM93536	Aam93536 Human pol
23	565	32.7	514	6 ABJ20237	Abj20237 Human IG
24	565	32.7	517	3 AAY32390	Aay32390 Herpesvir
25	565	32.7	517	5 AAE23294	Aae23294 Human nec

26	560	32.4	458	5 AAE23295	Aae23295 Human nec
27	542.5	31.4	518	5 ABG77170	Abg77170 Prostate
28	483	28.0	497	5 AAE23303	Aae23303 Human nec
29	483	28.0	510	4 AAB93365	Aab93365 Human pro
30	483	28.0	510	4 AAU00471	Aau00471 Human TAN
31	483	28.0	510	5 ABJ05562	Abj05562 Breast ca
32	483	28.0	510	6 ABJ20232	Abj20232 Human IG
33	483	28.0	510	6 ABR48229	Abr48229 Human bla
34	483	28.0	510	6 ABU56613	Abu56613 Lung canc
35	483	28.0	510	6 ABP97212	Abp97212 Tumour-as
36	483	28.0	510	7 ADB80512	Adb80512 Ovarian c
37	481.5	27.9	498	5 AAE23305	Aae23305 Human nec
38	481.5	27.9	511	5 AAE23301	Aae23301 Human nec
39	481	27.8	510	5 AAE23300	Aae23300 Human nec
40	481	27.8	510	6 ABJ20231	Abj20231 Human IG
41	446.5	25.8	580	5 AAE23302	Aae23302 Human nec
42	426.5	24.7	538	5 AAE23297	Aae23297 Human nec
43	426.5	24.7	538	6 ABJ20238	Abj20238 Human IG
44	426.5	24.7	538	8 ADE86687	Ade86687 Human pol
45	422	24.4	479	3 AAY32389	Aay32389 Herpesvir

ALIGNMENTS

RESULT 1
AAE23299
ID AAE23299 standard; protein; 437 AA.
XX

AC AAE23299;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3gamma protein.
XX

KW Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37450.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 125-126; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

Search completed: April 12, 2004, 09:45:16
Job time : 26.8824 secs

Db	356	IAALLFCLLVVVVLMRSYHR	376	
Db	128	LPSGVRVKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQVTVEVLDPEDPGKQVDLVA	346	
QY	296	AGAVIGAVLALFIIAIFVTVLLTPRKKR	323	
Db	347	SVIIVGVIAALLFCLLVVVVLMRSYHR	374	
RESULT 14				
Q9DBP8				
ID	Q9DBP8	PRELIMINARY;	PRT;	483 AA.
AC	Q9DBP8;			
DT	01-JUN-2001 (TReMBLrel. 17, Created)			
DT	01-JUN-2001 (TReMBLrel. 17, Last sequence update)			
DT	01-OCT-2003 (TReMBLrel. 25, Last annotation update)			
DE	1200017F15Rik protein.			
GN	PVRL4 OR 1200017F15RIK.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C57BL/6J; TISSUE=Lung;			
RX	MEDLINE=21085660; PubMed=11217851;			
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,			
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,			
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,			
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,			
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,			
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,			
RA	Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,			
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,			
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,			
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,			
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,			
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,			
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,			
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,			
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,			
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,			
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,			
RA	Hayashizaki Y.;			
RT	"Functional annotation of a full-length mouse cDNA collection.";			
RL	Nature 409:685-690(2001).			
DR	EMBL; AK004821; BAB23592.1; -.			
DR	MGI; MGI:1918990; Pvrl4.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003598; IG_c2.			
DR	Pfam; PF00047; IG; 3.			
DR	SMART; SM00408; IGC2; 1.			
DR	PROSITE; PS50835; IG LIKE; 3.			
KW	Immunoglobulin domain.			
SQ	SEQUENCE 483 AA; 53030 MW; F8F0466C000852E8 CRC64;			
Query Match 27.2%; Score 470.5; DB 11; Length 483;				
Best Local Similarity 33.5%; Pred. No. 4.7e-32;				
Matches 110; Conservative 60; Mismatches 133; Indels 25; Gaps 9;				
QY	10	NETITQISWEKIH-GKSSQTVAVHHPOYGFVSQGEYQGRV-----LFKNYSLNDA	59	
Db	58	DEQVQVAVARVDPNEGIRELALLHSKYGLHVNPAVEDRVEQPPPRDPL-----DGS	110	
QY	60	ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGNETVAAI	119	
Db	111	VLLRNAVQADEGEYECRVSTFPAGSFQARMRLRVLPPLPSLNPGP-PLIEGQGLTLAAS	169	
QY	120	CIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPA	179	
Db	170	C-TAEGSPAPSVTWDTEVKGTSQSSRSTHPRSAAVTSEFHLVPSRMNGQPLTCVVSHPG	228	
QY	180	LEKDIRYSFILDIOYAPEVSVTGYDGN--WFVGRKGVNLKCNADANPPPFKSVWSRLDQ	237	
Db	229	LLQDRRITHTLQVAFLAEASVRGLEQNLWQVGREGATLKCLSEGQPPP-KYNWTRLDGP	287	
QY	238	WPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDV--PFKQTSSIAV	295	
Db	288	LPSGVRVKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQVTVEVLDPEDPGKQVDLVA	346	
QY	296	AGAVIGAVLALFIIAIFVTVLLTPRKKR	323	
Db	347	SVIIVGVIAALLFCLLVVVVLMRSYHR	374	
Query Match 27.2%; Score 470.5; DB 11; Length 508;				
Best Local Similarity 33.5%; Pred. No. 5e-32;				
Matches 110; Conservative 60; Mismatches 133; Indels 25; Gaps 9;				
QY	10	NETITQISWEKIH-GKSSQTVAVHHPOYGFVSQGEYQGRV-----LFKNYSLNDA	59	
Db	58	DEQVQVAVARVDPNEGIRELALLHSKYGLHVNPAVEDRVEQPPPRDPL-----DGS	110	
QY	60	ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGNETVAAI	119	
Db	111	VLLRNAVQADEGEYECRVSTFPAGSFQARMRLRVLPPLPSLNPGP-PLIEGQGLTLAAS	169	
QY	120	CIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPA	179	
Db	170	C-TAEGSPAPSVTWDTEVKGTSQSSRSTHPRSAAVTSEFHLVPSRMNGQPLTCVVSHPG	228	
QY	180	LEKDIRYSFILDIOYAPEVSVTGYDGN--WFVGRKGVNLKCNADANPPPFKSVWSRLDQ	237	
Db	229	LLQDRRITHTLQVAFLAEASVRGLEQNLWQVGREGATLKCLSEGQPPP-KYNWTRLDGP	287	
QY	238	WPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDV--PFKQTSSIAV	295	
Db	288	LPSGVRVKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQVTVEVLDPEDPGKQVDLVA	346	
QY	296	AGAVIGAVLALFIIAIFVTVLLTPRKKR	323	
Db	347	SVIIVGVIAALLFCLLVVVVLMRSYHR	374	

QY 287 -----FKQTSSIAVAGAVIGAVLALFIIAIFVTV 315
DB 121 PTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIATIIASVVGALFIVLSVLGI 180
QY 316 LLTPRKK--RPSYLDK 329
DB 181 FCYRRRTFRGDYFAK 196

RESULT 9
Q9ERF5 PRELIMINARY; PRT; 295 AA.
AC Q9ERF5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308634; AAG30283.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1 295
FT NON_TER 295
SQ SEQUENCE 295 AA; 33112 MW; 03E5C4DCB5032E7F CRC64;

Query Match 30.8%; Score 533; DB 11; Length 295;
Best Local Similarity 39.4%; Pred. No. 9.5e-38;
Matches 109; Conservative 56; Mismatches 104; Indels 8; Gaps 5;

QY 13 ITQISWEKIHKSSQTAVVHHPOYGFSGVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGK 72
DB 21 ITQVTWQKATNGSKQNMAIYNPTMGVSVLPPEYKRVFLRPSFDIGTIRLSHLEDEGM 80
QY 73 YICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG----GNETVAAICIAATGKPV 128
DB 81 YICEFATPTGNRESQLNLITVMAKPT-NWIEGTQAVLRARKGQDDKVVVATCTSANGKPP 139
QY 129 AHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTTRFARRRITCVVKHPALEKDIYS 187
DB 140 SVVSWETRLKGEAEYQEIIRNPNGTIVISRYRLVPSREAHRSQSLACIVNY-HLDR-FRES 197
QY 188 FILDIOYAPEVSVTGVDGNWFGVGRKGNLKNADANPPPFKSVWSRLDGQWPDGLLASDN 247
DB 198 LTLNVQYEPEVTIEGFDGNWYLQRTDVLTCKADANPPATEYHHTWTLNGLPKGVEAQR 257
QY 248 TLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 284
DB 258 TLFFRGPINYSLAGTYICEATNPIGTRSGQVEVNITE 294

RESULT 10
Q9GL74 PRELIMINARY; PRT; 298 AA.
ID Q9GL74
AC Q9GL74;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308635; AAG30284.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1 298
FT NON_TER 298
SQ SEQUENCE 298 AA; 33309 MW; AEAD41842B8CA200 CRC64;

Query Match 30.5%; Score 526.5; DB 6; Length 298;
Best Local Similarity 38.6%; Pred. No. 3.5e-37;
Matches 108; Conservative 55; Mismatches 106; Indels 11; Gaps 5;

QY 13 ITQISWEKI---HGKSSQTAVVHHPOYGFSGVQGEYQGRVLFKNYSLNDATITLHNIGFSD 69
DB 21 ITQVTWQKITQATNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPSFTDGTIRLSRLELED 80
QY 70 SGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG----GNETVAAICIAATG 125
DB 81 EGVYICEFATPTGNRESQLNLITVMAKPT-NWIEGTQAVLRARKGQDDKVLVATCTSANG 139
QY 126 KPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTTRFARRRITCVVKHPALEKDI 184
DB 140 KPPSVVSWETRLKGEAEYQEIIRNPNGTIVISRYRLVPSREAHRSQSLACIVNYHM--DRF 197
QY 185 RYSFILDIOYAPEVSVTGVDGNWFGVGRKGNLKNADANPPPFKSVWSRLDGQWPDGLLA 244
DB 198 KESLTNLNVQYEPEVTIEGFDGNWYLQRMVDVLTCKADANPPATEYHHTWTLNGLPKGVEA 257
QY 245 SDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 284
DB 258 QNRTLFFKGPISYSLAGTYICEATNPIGTRSGQVEVNITE 297

RESULT 11
Q9GL75 PRELIMINARY; PRT; 295 AA.
ID Q9GL75
AC Q9GL75;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308633; AAG30282.1; -.

Db 374 PADVQDIATEHKKLPFPLSTLATLKDDTIGTIIASVVGALFVLVNSILAGVFCYRRRT 433

QY 323 -RPSYLDK 329

Db 434 FRGDYFAK 441

RESULT 6

Q9Y412 PRELIMINARY; PRT; 407 AA.

AC Q9Y412;

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).

GN DKFZP566B0846.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AL050071; CAB43256.1; -.

DR PIR; T08732; T08732.

DR InterPro; IPR007110; IG-LIKE.

DR PROSITE; PS50835; IG-LIKE; 2.

KW Hypothetical protein.

FT NON_TER 1

SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;

Query Match 66.9%; Score 1156.5; DB 4; Length 407;

Best Local Similarity 74.9%; Pred. No. 2.1e-91;

Matches 224; Conservative 12; Mismatches 24; Indels 39; Gaps 2;

QY 70 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAICIAATGKPPVA 129

Db 1 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAICIAATGKPPVA 60

QY 130 HIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFI 189

Db 61 HIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFI 120

QY 190 LDIQYAPEVSTGYDGNWFVGRKGVNLKCNADANPPFKSVWSRLDGQWPDGGLASDNTL 249

Db 121 LDIQYAPEVSTGYDGNWFVGRKGVNLKCNADANPPFKSVWSRLDGQWPDGGLASDNTL 180

QY 250 HFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVP----- 286

Db 181 HFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDPTTTTLQPTIQWHPSTADIEDLAT 240

QY 287 -----FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLDK 329

Db 241 EPKKLPPPLSTLATIKDDTIATIIASVVGALFVLVNSILAGVFCYRRRRTFRGDYFAK 299

RESULT 7

Q8NC05 PRELIMINARY; PRT; 267 AA.

AC Q8NC05;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein FLJ90624.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,

RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,

RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,

RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,

RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;

RT "NEDO human cDNA sequencing project.";

RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK075105; BAC11404.1; -.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR Pfam; PF00047; ig; 1.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG-LIKE; 2.

KW Hypothetical protein.

SQ SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;

Query Match 65.3%; Score 1128; DB 4; Length 267;

Best Local Similarity 99.5%; Pred. No. 3.3e-89;

Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVGEYQGRVLFKNYSLNDATI 60

Db 51 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVGEYQGRVLFKNYSLNDATI 110

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAIC 120

Db 111 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAIC 170

QY 121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARRRITCVVKHPAL 180

Db 171 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARRRITCVVKHPAL 230

QY 181 EKDIRYSFILDIOYAPEVSTGYDGNWFVGRKGVNLK 217

Db 231 EKDIRYSFILDIOYAPEVSTGYDGNWFVGRKGVNLK 267

RESULT 8

Q9BVA9 PRELIMINARY; PRT; 304 AA.

AC Q9BVA9;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Similar to nectin 3, DKFZP566B0846 protein (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Cervix;

RA Strausberg R.;

RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC001336; AAH01336.1; -.

DR InterPro; IPR007110; IG-LIKE.

DR PROSITE; PS50835; IG-LIKE; 1.

FT NON_TER 1

SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 36.3%; Score 627.5; DB 4; Length 304;

Best Local Similarity 61.7%; Pred. No. 6.8e-46;

Matches 121; Conservative 12; Mismatches 24; Indels 39; Gaps 2;

QY 173 CVVKHPALEKDIRYSFILDIOYAPEVSTGYDGNWFVGRKGVNLKCNADANPPFKSVWS 232

Db 1 CVVKHPALEKDIRYSFILDIOYAPEVSTGYDGNWFVGRKGVNLKCNADANPPFKSVWS 60

QY 233 RLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVP----- 286

Db 61 RLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDPTTTTLQ 120

Db 434 FRGDYFAK 441

RESULT 4

Q9JLB9 PRELIMINARY; PRT; 549 AA.

AC Q9JLB9; 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Cell adhesion molecule nectin-3 alpha.

GN PVRL3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20209403; PubMed=10744716;

RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,

RA Tachibana K., Mizoguchi A., Takai Y.;

RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules

RT that shows homophilic and heterophilic cell-cell adhesion

RT activities.";

RL J. Biol. Chem. 275:10291-10299 (2000).

DR EMBL; AF195833; AAF63685.1; --

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005913; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;

Query Match 86.3%; Score 1490.5; DB 11; Length 549;

Best Local Similarity 78.3%; Pred. No. 4.4e-120;

Matches 288; Conservative 18; Mismatches 23; Indels 39; Gaps 3;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60

Db 74 VSLKCLIEVNETITQISWEKIHGKSTQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120

Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC 193

QY 121 IAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARGRRITCVVKHPAL 180

Db 194 VAATGKPVQAIDWEGDLGEMESTTSPFNETATIVSQYKLPFTRFARGRRITCVVKHPAL 253

QY 181 EKDIRYSFILDIIQYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPD 240

Db 254 EKDIRYSFILDIIQYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPD 313

QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPEFKQT----- 290

Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPEFKQT----- 322

QY 291 -----SSIA-----VAGAVIGAVLALFIIAIFVTVLLTPRKK- 322

Db 374 PADVQDIATEHKKLPFLSTLATLKDITIGTIIASVVGALFLVLISLAGVFCYRRRT 433

QY 323 -RPSYLDK 329

Db 434 FRGDYFAK 441

RESULT 5

Q9D006

ID Q9D006 PRELIMINARY; PRT; 549 AA.

AC Q9D006;

DT 01-JUN-2001 (TrEMBLrel. 17, Created)

DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE 2610301B19Rik protein.

GN PVRL3 OR 2610301B19RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK011949; BAB27933.1; --

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005913; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;

Query Match 83.7%; Score 1446.5; DB 11; Length 549;

Best Local Similarity 76.1%; Pred. No. 2.8e-116;

Matches 280; Conservative 21; Mismatches 28; Indels 39; Gaps 3;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60

Db 74 VSLKCLIEVNETITQISWEKIHGKSTQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120

Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC 193

QY 121 IAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARGRRITCVVKHPAL 180

Db 194 VSSTGKPVQAIDWEGDLGEREPSTISFLNETATIVSQYELFPTRFARGRRITCVVKHPAL 253

QY 181 EKDIRYSFILDIIQYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPD 240

Db 254 EKDIRYSFILDIIQYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPD 313

QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPEFKQT----- 290

Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPEFKQT----- 373

QY 291 -----SSIA-----VAGAVIGAVLALFIIAIFVTVLLTPRKK- 322

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 194 VAATGKPVQAIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTFRFARRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVPPFKQTSSIAVAGAVI 300
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVPPFKQTSSIAVAGAVI 373
QY 301 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 331
Db 374 GAVLALFIIITVFTVLLTPRKKRPSYLDKVI 404

RESULT 2

Q9JLB8 PRELIMINARY; PRT; 510 AA.
AC Q9JLB8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 beta.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA SatoH-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities."
RL J. Biol. Chem. 275:10291-10299 (2000).
DR EMBL; AF195834; AAF63686.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;

Query Match 97.0%; Score 1677; DB 11; Length 510;
Best Local Similarity 95.5%; Pred. No. 3.1e-136;
Matches 316; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180

Db 194 VAATGKPVQAIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTFRFARRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVPPFKQTSSIAVAGAVI 300
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVPPFKQTSSIAVAGAVI 373
QY 301 GAVLALFIIAIFVTVLLTPRKKRPSYLDKVI 331
Db 374 GAVLALFIIITVFTVLLTPRKKRPSYLDKVI 404

RESULT 3

Q9NQS3 PRELIMINARY; PRT; 549 AA.
AC Q9NQS3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Reymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin."
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;

Query Match 87.9%; Score 1519.5; DB 4; Length 549;
Best Local Similarity 79.6%; Pred. No. 1.4e-122;
Matches 293; Conservative 12; Mismatches 24; Indels 39; Gaps 2;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVPPFKQTSSIAVAGAVI 300
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVPPFKQTSSIAVAGAVI 373
QY 287 -----FKQTSSIAVAGAVI GAVLALFIIAIFVTVLLTPRKK- 322
Db 374 TADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFVLVSLAGIFCYRRRT 433
QY 323 -RPSYLDK 329

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 26.8824 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-31_COPY_74_404
Perfect score: 1728
Sequence: 1 VSLKCLIEVNETITQISWEK.....FVTVLLTPRKRPSPYLDKVI 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1677	97.0	438	11 Q9JLB7	Q9jlb7 mus musculu
2	1677	97.0	510	11 Q9JLB8	Q9jlb8 mus musculu
3	1519.5	87.9	549	4 Q9NQS3	Q9nqs3 homo sapien
4	1490.5	86.3	549	11 Q9JLB9	Q9jlb9 mus musculu
5	1446.5	83.7	549	11 Q9D006	Q9d006 mus musculu
6	1156.5	66.9	407	4 Q9Y412	Q9y412 homo sapien
7	1128	65.3	267	4 Q8NC05	Q8nc05 homo sapien
8	627.5	36.3	304	4 Q9BVA9	Q9bva9 homo sapien
9	533	30.8	295	11 Q9ERF5	Q9erf5 mesocricetu
10	526.5	30.5	298	6 Q9GL74	Q9gl74 cercopithec
11	526	30.4	295	6 Q9GL75	Q9gl75 bos taurus
12	483	28.0	510	4 Q96NY8	Q96ny8 homo sapien
13	483	28.0	510	4 Q96K15	Q96k15 homo sapien
14	470.5	27.2	483	11 Q9DBP8	Q9dbp8 mus musculu
15	470.5	27.2	508	11 Q8R007	Q8r007 mus musculu
16	470.5	27.2	508	11 Q8CED8	Q8ced8 mus musculu

17	436	25.2	467	11	Q91VT9	Q91vt9 mus musculu
18	436	25.2	467	11	Q8C6F2	Q8c6f2 mus musculu
19	434.5	25.1	530	11	Q80XJ5	Q80xj5 mus musculu
20	422	24.4	449	4	Q9UEI6	Q9uei6 homo sapien
21	395	22.9	412	11	Q9RIE1	Q9rie1 rattus norv
22	390	22.6	412	11	Q63611	Q63611 rattus norv
23	387	22.4	417	4	Q96BJ1	Q96bj1 homo sapien
24	380	22.0	400	6	Q8HY16	Q8hy16 cebus apell
25	378	21.9	403	6	Q8HY15	Q8hy15 lemur catta
26	376	21.8	408	11	Q91WPI	Q91wp1 mus musculu
27	374	21.6	408	11	Q8K094	Q8k094 mus musculu
28	373	21.6	401	6	Q08835	Q08835 cercopithec
29	373	21.6	408	11	Q8BVF6	Q8bvf6 mus musculu
30	347	20.1	412	6	Q8HY14	Q8hy14 oryctolagus
31	343	19.8	415	11	Q60977	Q60977 mus musculu
32	283	16.4	394	13	Q7ZXX1	Q7zxx1 xenopus lae
33	282	16.3	417	11	Q7TNL1	Q7tnl1 mus musculu
34	275	15.9	442	4	Q9BY67	Q9by67 homo sapien
35	275	15.9	445	11	Q8K3T6	Q8k3t6 mus musculu
36	272	15.7	445	11	Q8R4L1	Q8r4l1 mus musculu
37	269.5	15.6	443	4	Q8N2F4	Q8n2f4 homo sapien
38	266.5	15.4	456	11	Q8R5M8	Q8r5m8 mus musculu
39	249.5	14.4	333	4	Q86WB8	Q86wb8 homo sapien
40	246.5	14.3	336	11	Q9D6E7	Q9d6e7 mus musculu
41	246.5	14.3	336	11	Q80VG4	Q80vg4 mus musculu
42	238.5	13.8	396	11	Q99N28	Q99n28 mus musculu
43	238.5	13.8	800	5	Q86LF9	Q86lf9 drosophila
44	238.5	13.8	801	5	Q86LF8	Q86lf8 drosophila
45	228.5	13.2	398	4	Q8N126	Q8n126 homo sapien

ALIGNMENTS

RESULT 1
Q9JLB7
ID Q9JLB7 PRELIMINARY; PRT; 438 AA.
AC Q9JLB7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 gamma.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195835; AAF63687.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 3.
SQ SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;

Query Match 97.0%; Score 1677; DB 11; Length 438;
Best Local Similarity 95.5%; Pred. No. 2.5e-136;
Matches 316; Conservative 10; Mismatches 5; Indels 0; Gaps 0;

DR Siena-2DPAGE; P98160; -.
DR Genew; HGNC:5273; HSPG2.
DR MIM; 142461; -.
DR MIM; 255800; -.
DR InterPro; IPR008985; ConA_like_lect_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00047; ig; 22.
DR Pfam; PF00052; laminin_B; 3.
DR Pfam; PF00053; laminin_EGF; 7.
DR Pfam; PF00054; laminin_G; 3.
DR Pfam; PF00057; ldl_recept_a; 4.
DR Pfam; PF01390; SEA; 1.
DR PRINTS; PR00261; LDLRECEPTOR.
DR ProDom; PD003031; Laminin_B; 3.
DR SMART; SM00181; EGF; 15.
DR SMART; SM00180; EGF_Lam; 12.
DR SMART; SM00409; IG_22.
DR SMART; SM00408; IGC2; 21.
DR SMART; SM00406; IGV; 7.
DR SMART; SM00281; LamB; 3.
DR SMART; SM00282; LamG; 3.
DR SMART; SM00192; LDLa; 4.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01196; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 4.
DR PROSITE; PS50835; IG_LIKE; 22.
DR PROSITE; PS50025; LAM_G_DOMAIN; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
DR PROSITE; PS01209; LDLRA_1; 4.
DR PROSITE; PS50068; LDLRA_2; 4.
DR PROSITE; PS50024; SEA; 1.
KW Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; EGF-like domain; Disease mutation.
FT SIGNAL 1 21
FT CHAIN 22 4391
FT
FT
FT DOMAIN 80 194
FT DOMAIN 198 235
FT DOMAIN 284 320
FT DOMAIN 324 360
FT DOMAIN 367 404
FT DOMAIN 405 504
FT DOMAIN 521 530
FT DOMAIN 531 730
FT DOMAIN 731 763
FT DOMAIN 764 813
FT DOMAIN 814 871
FT DOMAIN 879 923
FT DOMAIN 924 933
FT DOMAIN 934 1125
FT DOMAIN 1126 1158
FT DOMAIN 1159 1208
FT DOMAIN 1209 1265
FT DOMAIN 1275 1324
FT DOMAIN 1325 1334
FT DOMAIN 1335 1529
FT DOMAIN 1530 1562
FT DOMAIN 1563 1612
FT DOMAIN 1613 1670

FT	DOMAIN	1677	1771	IG-LIKE C2-TYPE 2.
FT	DOMAIN	1772	1865	IG-LIKE C2-TYPE 3.
FT	DOMAIN	1866	1955	IG-LIKE C2-TYPE 4.
FT	DOMAIN	1956	2051	IG-LIKE C2-TYPE 5.
FT	DOMAIN	2052	2151	IG-LIKE C2-TYPE 6.
FT	DOMAIN	2152	2244	IG-LIKE C2-TYPE 7.
FT	DOMAIN	2245	2340	IG-LIKE C2-TYPE 8.
FT	DOMAIN	2341	2436	IG-LIKE C2-TYPE 9.
FT	DOMAIN	2437	2533	IG-LIKE C2-TYPE 10.
FT	DOMAIN	2534	2629	IG-LIKE C2-TYPE 11.
FT	DOMAIN	2630	2726	IG-LIKE C2-TYPE 12.

Query Match 9.8%; Score 169.5; DB 1; Length 4391;
Best Local Similarity 23.2%; Pred. No. 6.7e-05;
Matches 69; Conservative 48; Mismatches 128; Indels 53; Gaps 13;

QY	1	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDATI	60
Db	2942	LDLNCVVP-GQAHQVTVYKRGG-----SLPARHQTHG-----SQL	2976
QY	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVV-----LVEPTVSLIKGPDSDLIDG	111
Db	2977	RHLVSPADSGEYVVCRAASGCPGEQEAFTVTPPSESSYRLRSPVIS-IDPPSSTVQQ	3035
QY	112	GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIIISQYKLPTRFARGRI	171
Db	3036	GQD-ASFCKLIHDGAAPISLEWKTNRQLEDNVHISPNGSIIIT---IVGTRPSNHGT	3089
QY	172	TCVVKHPALEKDIRYSFI-LDIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPKSV	230
Db	3090	RCVASN---AYGVAQSVVNLSVHGPPPTVSVLPEGPVWVKVKAVTLEC-VSAGEPRSSAR	3145
QY	231	WSRLDG-----QWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYI	282
Db	3146	WTRISSTPAKLEQRTYGLMDSHAVLQ-ISSAKPSDAGTYVCLAQNALGTAQKQVEVIV	3202

Search completed: April 12, 2004, 09:39:54
Job time : 6.28976 secs

FT CONFLICT 309 310 NA -> KS (IN REF. 4, 5 AND 6).
SQ SEQUENCE 626 AA; 69352 MW; E97998E280ECD635 CRC64;

Query Match 9.9%; Score 170.5; DB 1; Length 626;
Best Local Similarity 24.9%; Pred. No. 4.9e-06;
Matches 74; Conservative 40; Mismatches 132; Indels 51; Gaps 14;

QY 26 SQTAVVHPQYGFSGYQGRV-LFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGN 84
Db 76 SRTQVVHE-----SFQGRSRLLDGLRLNCTLLSLSPELGKGYFR-----GD 120

QY 85 AQSSTTVTLVETVSLIKGPDLSLID----GGNETVAAICIAATGKPV--AHIDWEGDLG 138
Db 121 LGGYNQYTFSEHSVLDIINTPNIVPPEVVAGTE-VEVSCMVPDNCPELRPELSWLHGEG 179

QY 139 EMESTTTSFPNE---TATIIQYKLFPTFRFARGRRITCVKHPALEKDIRYSPILDIQYA 195
Db 180 LGEPTVLGRLEDEGTWVQVSLHFFVPTREANGHRLGCGQAAPNTTLQFEGYASLDVKYP 239

QY 196 PEV-----SVTGYDGNWVGRKGNLKNADANPPPKSVMSRLDQWPDGILL---ASDN 247
Db 240 PVIVEMNNSVEAIEGS-----HVSLLCGADSNPPPLLT-WMR-----DGMVLEAEVAE 286

QY 248 TLHF-VHPLTFNYSYGVYICKVTNSLQSRSDQKVIYISDVPPFKQT---SSIAVAGAVI 300
Db 287 SLYLDLEEVTPAEDGIYACLAENAYGQDNRTVELSWMYAPWKPTVNGTVVAVEGETV 343

RESULT 15
PGBM HUMAN
ID PGBM HUMAN STANDARD; PRT; 4391 AA.
AC P98160; Q16287; Q9H3V5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basement membrane heparan sulfate proteoglycan core protein: a
RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Skin;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple
RT domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
RX MEDLINE=20553141; PubMed=11101850;
RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissbach J.,
RA Hentati F., Fontaine B.;
RT "Perlecan, the major proteoglycan of basement membranes, is altered in
RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";
RL Nat. Genet. 26:480-483(2000).
RN [4]
RP SEQUENCE OF 1016-1470 FROM N.A.

RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [5]
RP SEQUENCE OF 890-1396 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to 1p36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [6]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
RN [7]
RP CARBOHYDRATE-LINKAGE SITE ASN-2121.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel
CC syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder
CC characterized by permanent myotonia (prolonged failure of muscle
CC relaxation) and skeletal dysplasia, resulting in reduced stature,
CC kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.
CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 3 laminin IV domains.
CC -!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X62515; CAA44373.1; -.
CC EMBL; M85289; AAA52700.1; -.
CC EMBL; AL445795; CAC18534.1; -.
CC EMBL; M64283; AAA52699.1; -.
CC EMBL; S76436; AAB21121.2; -.
CC EMBL; L22078; -; NOT_ANNOTATED_CDS.
CC PIR; A38096; A38096.
CC HSSP; P00740; 1EDM.

RP SEQUENCE FROM N.A. (ISOFORM S-MAG).
RC TISSUE=Brain;
RX MEDLINE=91298961; PubMed=1712586;
RA Nakano R., Fujita N., Sato S., Inuzuka T., Sakimura K.,
RA Ishiguro H., Mishina M., Miyatake T.;
RT "Structure of mouse myelin-associated glycoprotein gene.";
RL Biochem. Biophys. Res. Commun. 178:282-290(1991).
RN [3]
RP TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX MEDLINE=91366725; PubMed=1716323;
RA Pedraza L., Frey A.B., Hempstead B.L., Colman D.R., Salzer J.L.;
RT "Differential expression of MAG isoforms during development.";
RL J. Neurosci. Res. 29:141-148(1991).
RN [4]
RP SIALIC ACID BINDING.
RX MEDLINE=95179521; PubMed=7533044;
RA Kelm S., Pelz A., Schauer R., Filbin M.T., Tang S., de Bellard M.E.,
RA Schnaar R.L., Mahoney J.A., Hartnell A., Bradfield P., Crocker P.R.;
RT "Sialoadhesin, myelin-associated glycoprotein and CD22 define a new
RT family of sialic acid-dependent adhesion molecules of the
RT immunoglobulin superfamily.";
RL Curr. Biol. 4:965-972(1994).
RN [5]
RP FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=20090811; PubMed=10625334;
RA Schachner M., Bartsch U.;
RT "Multiple functions of the myelin-associated glycoprotein MAG
RT (siglec-4a) in formation and maintenance of myelin.";
RL Glia 29:154-165(2000).
RN [6]
RP INTERACTION WITH RTN4R.
RX MEDLINE=22171378; PubMed=12089450;
RA Liu B.P., Fournier A., GrandPre T., Strittmatter S.M.;
RT "Myelin-associated glycoprotein as a functional ligand for the Nogo-66
RT receptor.";
RL Science 297:1190-1193(2002).
CC -!- FUNCTION: Adhesion molecule in postnatal neural development that
CC mediates sialic-acid dependent cell-cell interactions between
CC neuronal and myelinating cells. Preferentially binds to alpha2,3-
CC linked sialic acid. Isoform L-MAG is critical for the formation of
CC myelin in the CNS, whereas isoform S-MAG is sufficient to maintain
CC the integrity of myelin in PNS.
CC -!- SUBUNIT: Binds to RTN4R.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=L-MAG;
CC IsoId=P20917-1; Sequence=Displayed;
CC Name=S-MAG;
CC IsoId=P20917-2; Sequence=VSP 002527, VSP 002528;
CC -!- TISSUE SPECIFICITY: Expressed by myelinating glial cells in the
CC central and peripheral nervous system. Detected in oligodendrocyte
CC processes before formation of compact myelin. Restricted to the
CC periaxonal space after myelination. Isoform S-MAG is the
CC predominant isoform in CNS and PNS of the adult.
CC -!- DEVELOPMENTAL STAGE: In CNS isoform L-MAG is the major form
CC synthesized early in development, and it persists as a significant
CC proportion of the MAG present in the adult. In the PNS isoform L-
CC MAG is expressed at modest levels during development; it is absent
CC in the adult.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; M31811; AAA39487.1; --
DR EMBL; M74793; AAA91743.1; --
DR EMBL; M74783; AAA91743.1; JOINED.
DR EMBL; M74784; AAA91743.1; JOINED.
DR EMBL; M74785; AAA91743.1; JOINED.
DR EMBL; M74786; AAA91743.1; JOINED.
DR EMBL; M74787; AAA91743.1; JOINED.
DR EMBL; M74788; AAA91743.1; JOINED.
DR EMBL; M74790; AAA91743.1; JOINED.
DR EMBL; M74791; AAA91743.1; JOINED.
DR HSSP; Q62230; IQFP.
DR MGD; MGI:96912; Mag.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Palmitate; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 626 MYELIN-ASSOCIATED GLYCOPROTEIN.
FT DOMAIN 20 516 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 517 536 POTENTIAL.
FT DOMAIN 537 626 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 120 IG-LIKE V-TYPE.
FT DOMAIN 139 237 IG-LIKE C2-TYPE 1.
FT DOMAIN 241 325 IG-LIKE C2-TYPE 2.
FT DOMAIN 327 412 IG-LIKE C2-TYPE 3.
FT DOMAIN 413 508 IG-LIKE C2-TYPE 4.
FT DISULFID 37 165 BY SIMILARITY.
FT DISULFID 42 100 BY SIMILARITY.
FT DISULFID 159 217 BY SIMILARITY.
FT DISULFID 261 305 BY SIMILARITY.
FT DISULFID 347 392 BY SIMILARITY.
FT DISULFID 421 430 BY SIMILARITY.
FT DISULFID 432 488 BY SIMILARITY.
FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 531 531 S-palmitoyl cysteine (By similarity).
FT VARSPLIC 574 582 EKRLGSERR -> REVSTRDCH (in isoform
FT S-MAG).
FT FTId=VSP 002527.
FT VARSPLIC 583 626 Missing (in isoform S-MAG).
FT FTId=VSP 002528.
SQ SEQUENCE 626 AA; 69259 MW; 9C797BD6B52B6057 CRC64;
Query Match 10.0%; Score 172.5; DB 1; Length 626;
Best Local Similarity 26.4%; Pred. No. 3.4e-06;
Matches 78; Conservative 42; Mismatches 127; Indels 49; Gaps 16;
QY 26 SQTAVVHHFQYGFVSQGEYQGRV-LFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLG- 83
Db 76 SRTQVVHE-----SFQGRSRLGLDLRLNCTLLSTLSPELGKYYFRG---DLGG 123
QY 84 -NAQSSITVTVL-VEPTVSLIKGPDSLIDGGNETVAAICIAATGKPV--AHIDWEGDLGE 139
Db 124 YNQYTFSEHSVLDIVNTPNIVVPE--VVAGTE-VEVSCWVPDNCPELRPELSWLHGEG 180
QY 140 MESTTTSFPNE---TATIISQYKLPFTRFARRRITCVVXHPALEKDIRYSFILDIOYAP 196
Db 181 GEPTVLGLRLREDEGTWVQVSLHLHFVPTREANGHRLGCAAFNTTLQFEGYASLDVKYPP 240
QY 197 EV-----SVTGYDGNWFVGRKGVNLIKCNADANPPPKSVWSRLDQWPDGLL---ASDNT 248
Db 241 VIVEMNSSVEAIEGS-----HVSLLCGADSNPPPLLT-WMR-----DGMVLEAVAKS 287

RP SEQUENCE FROM N.A.
RX MEDLINE=89392063; PubMed=2476987;
RA Sato S., Fujita N., Kurihara T., Kuwano R., Sakimura K., Takahashi Y.,
RA Miyatake T.;
RT "cDNA cloning and amino acid sequence for human myelin-associated
RT glycoprotein.";
RL Biochem. Biophys. Res. Commun. 163:1473-1480(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Adamson A.W., Burkhardt-Schultz K.,
RA Kyle A., Ramirez M., Stilwagen S.A., Garnes J., Danganan L.,
RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnercher A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Adhesion molecule in postnatal neural development that
CC mediates sialic-acid dependent cell-cell interactions between
CC neuronal and myelinating cells. Preferentially binds to alpha2,3-
CC linked sialic acid (By similarity).
CC -!- SUBUNIT: Binds to RTN4R (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL; M29273; AAA59545.1; -.
DR EMBL; AC002132; AAB58805.1; -.
DR EMBL; BC053347; AAH53347.1; -.
DR PIR; A61084; A61084.
DR HSSP; Q62230; 1QFP.
DR Genew; HGNC:6783; MAG.
DR MIM; 159460; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Cell adhesion; lectin; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Palmitate; Lipoprotein.
FT SIGNAL 1 19
FT CHAIN 20 626 MYELIN-ASSOCIATED GLYCOPROTEIN.

FT DOMAIN 20 516 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 517 536 POTENTIAL.
FT DOMAIN 537 626 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 120 IG-LIKE V-TYPE.
FT DOMAIN 139 237 IG-LIKE C2-TYPE 1.
FT DOMAIN 241 325 IG-LIKE C2-TYPE 2.
FT DOMAIN 327 412 IG-LIKE C2-TYPE 3.
FT DOMAIN 413 508 IG-LIKE C2-TYPE 4.
FT DISULFID 37 165 BY SIMILARITY.
FT DISULFID 42 100 BY SIMILARITY.
FT DISULFID 159 217 BY SIMILARITY.
FT DISULFID 261 305 BY SIMILARITY.
FT DISULFID 347 392 BY SIMILARITY.
FT DISULFID 421 430 BY SIMILARITY.
FT DISULFID 432 488 BY SIMILARITY.
FT CARBOHYD 99 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 531 S-palmitoyl cysteine (By similarity).
SQ SEQUENCE 626 AA; 69068 MW; ED2D36B24F21CAAA CRC64;

Query Match 10.0%; Score 172.5; DB 1; Length 626;
Best Local Similarity 25.7%; Pred. No. 3.4e-06;
Matches 76; Conservative 43; Mismatches 128; Indels 49; Gaps 15;

QY 26 SQTVAVHPQYGFSGVQGEYQGRV-LFKNYSINDATITLHNIGFSDSGKYICKAVTFPLG- 83
Db 76 SRTQVVHE-----SFQGRSRLGLDLGLNCTLLLSNVSPELGGKYVFRG---DLGG 123

QY 84 -NAQSSTTVTVL-VEPTVSLIKGPDSLIDGGNETVAAICIAATGKPV--AHIDWEGDLGE 139
Db 124 YNQYTFSEHSVLDIVNTPNIVPPE--VVAGTE-VEVSCMVDPNCPRLPELSWLHGEL 180

QY 140 MESTTTSFPNE---TATIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIQYAP 196
Db 181 GEPAVLGRRLREDEGTWVQVSLHFPVPTREANGHRLGCGASFNTTLQFEGVASMVDVKYPP 240

QY 197 EV-----SVTGYDGNWVGRKGNLKNADANPPFPKSVWSRLDGQWPDGULL----ASDN 247
Db 241 VIVEMNSSVEAIEGS-----HVSLLCGADSNPPPLLT-WMR-----DGTVLREAVAES 287

QY 248 TLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVFPKQT---SSIAVAGAVI 300
Db 288 LLELEEVTPAEDGVYACLAENAYGQDNRTVGLSVMYAPWKPTVNGTMVAVEGETV 343

RESULT 13
MAG_MOUSE
ID MAG_MOUSE STANDARD; PRT; 626 AA.
AC P20917; P16880;
DT 01-AUG-1990 (Rel. 15, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-associated glycoprotein precursor (Siglec-4a).
GN MAG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS L-MAG AND S-MAG).
RX MEDLINE=90121220; PubMed=2482022;
RA Fujita N., Sato S., Kurihara T., Kuwano R., Sakimura K., Inuzuka T.,
RA Takahashi Y., Miyatake T.;
RT "cDNA cloning of mouse myelin-associated glycoprotein: a novel
RT alternative splicing pattern.";
RL Biochem. Biophys. Res. Commun. 165:1162-1169(1989).
RN [2]

QY 62 LHNIGFSDSGKICKAVTFPLGNAQSSTTVTLVVEPTVSL-IGKPDSDLIDGNETVAAIC 120
Db 108 FWNITLEDGCMCLFNTFGFKISGTACLTVVYQPIVSLHYKFSSEHLN-----IT 159
QY 121 IAATGKPVAHIDWEGDLGEMESTTT--SFPNETATIIISQYKLFPTFRFARGPRITCVVKHP 178
Db 160 CSATARPAPMVFWKVPKRSIENSTVTLSHPNGTSTVTSILHIKDPKNQVSKVICOVLHL 219
QY 179 ALEKDIRYSFILDIOYAPEVSVTGYDGNWF 208
Db 220 GTVTDFKQ-----TVNKGYNWF 235

RESULT 11
NCM2 HUMAN
ID NCM2 HUMAN STANDARD; PRT; 837 AA.
AC O15394;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (NCAM 2).
GN NCAM2 OR NCAM21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369930; PubMed=9226371;
RA Paoloni-Giacobino A., Chen H., Antonarakis S.E.;
RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2)
RT that maps to chromosome region 21q21 and is potentially involved in
RT Down syndrome.";
RL Genomics 43:43-51(1997).
RN [2]

RP CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal
CC brain.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC
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CC
CC
CC EMBL; U75330; AAB80803.1; -.
DR Genew; HGNC:7657; NCAM2.
DR MIM; 602040; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0005896; C:plasma membrane; TAS.
DR GO; GO:0007158; P:neuronal cell adhesion; TAS.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.

DR PROSITE; PS50835; IG LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 837 NEURAL CELL ADHESION MOLECULE 2.
FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 698 718 POTENTIAL.
FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 108 IG-LIKE C2-TYPE 1.
FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
FT DOMAIN 482 581 FIBRONECTIN TYPE-III 1.
FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
FT DISULFID 42 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 281 PROBABLE.
FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 837 AA; 92932 MW; C3D034106C5741C1 CRC64;

Query Match 10.1%; Score 175; DB 1; Length 837;
Best Local Similarity 22.5%; Pred. No. 3.1e-06;
Matches 72; Conservative 50; Mismatches 102; Indels 96; Gaps 16;

QY 30 AVHHPQYGFVSQGE-----YQGRVLFKN--YSL--NDATITLH 63
Db 210 AISMPQKSFNATAERGEEMTFSCRASGSPESAISWFRNGKLIENEKYILKGSNTELTVR 269
QY 64 NIGFSDSGKICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDGNETVAAICIAA 123
Db 270 NIINSDGGPYVCRA-TNKAGEDEKQAFQVQFVQPHIIQLKNETTYENG---QVTLVC-DA 324
QY 124 TGPVVAHIDW-----EGDLGEMESTTTSFPNETATIIISQY-----KLFPTFRFARG 168
Db 325 EGEPIPEITWKRAVDGFTFTGED-----KSPDGRIEVKGQHGSSSLHIKDVKLSGS 375
QY 169 RRITC-----VVKHPALEKDIRYSFILDIOYAP-----EVSVTGYDGNWVFGKGVNLKC 218
Db 376 GRVDCEAASRIGGH-----QKSMYLDIEYAPKFIISQTIYYSWEGN-----PINISC 422
QY 219 NADANPPPFKSVWSRLDQWPDGLLASDNTLHF-----VHPLTFNYSGVYICK 266
Db 423 DVKSNPP--ASIHWRDKL-----VLPKNTTLKTYSTGRKMIETAPTSDNDFGRYNCT 476
QY 267 VTNSLGQRSDQKVIYISDVP 286
Db 477 ATNHIGTRFQEIYALADVP 496

RESULT 12
MAG HUMAN
ID MAG HUMAN STANDARD; PRT; 626 AA.
AC P20916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-associated glycoprotein precursor (Siglec-4a).
GN MAG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

FT DISULFID 166 221 BY SIMILARITY.
FT DISULFID 266 312 BY SIMILARITY.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 386 392 EHASASA -> HHQSCHN (in isoform Delta).
FT VARSPLIC 393 417 /FTID=VSP_002622.
FT VARSPLIC 393 417 Missing (in isoform Delta).
FT VARSPLIC 393 417 /FTID=VSP_002623.
SQ SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6E1F CRC64;

Query Match 23.0%; Score 398; DB 1; Length 417;
Best Local Similarity 30.3%; Pred. No. 2e-24;
Matches 99; Conservative 62; Mismatches 144; Indels 22; Gaps 10;

QY 1 VSLKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---POYGFVQGEYQGRVLFKNY 53
Db 45 VTLPYQLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTOGPNYSEPKRLEFVAARL--GT 101

QY 54 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSLIKGPDSDLIDG 111
Db 102 ELRDASLRMFGLRVEDEGNYTCLFVTFPQGRSVDIWLRLVLAKPQNTAEVQKVQLT--- 157

QY 112 GNETVAAICIAATGKPKVAHIDWEGDLGEMESTTTS--FPNETATIISQVKLFPTFRFARGR 169
Db 158 GKVPVVARCVSTGGRPPAHITWHSIDLGMPTNSQAPGFLSGTIVTVTSLWILVPSSQVDGK 217

QY 170 RITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNVFWGRKGVNLCNADANPPPEKS 229
Db 218 SVTCKVEHSEFEKPKQLLTVNLTVYYPPEVSIISGYDNNWYLSQNEATLTCDARSNPEPTGY 277

QY 230 VWSRLDQWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVYIISDVPEKQ 289
Db 278 NWSTTMGRLPPFAVAQGAQL-LIRPVDKPINTTFICNVTNALGARQAEALTVPVKEGPPSE 336

QY 290 TSSIA---VAGAVIGAVLALFIIAIFV 313
Db 337 PSMSSNNIIIFILGIVILLTLIGIV 363

RESULT 7

PVR HUMAN
ID PVR HUMAN STANDARD; PRT; 417 AA.
AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168426; PubMed=2538245;
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
RT sequence, and expression of a new member of the immunoglobulin
RT superfamily.";
RL Cell 56:855-865(1989).
RN [2]
RP REVISIONS.
RA Racaniello V.R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91006015; PubMed=2170108;
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RA Takeuchi K., Takegami T., Nomoto A.;
RT "The poliovirus receptor protein is produced both as membrane-bound
RT and secreted forms.";
RL EMBO J. 9:3217-3224(1990).
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyanni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
RA Shannon M., Brower A., Olsen A.S., Smith L.M.;
RT "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger
RT gene cluster.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS.
RX MEDLINE=91239515; PubMed=1851992;
RA Koike S., Ise I., Nomoto A.;
RT "Functional domains of the poliovirus receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N glycosylation of the virus binding domain is not essential for
RT function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P15151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P15151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
CC VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".

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CC EMBL; M24407; AAA36461.1; -.
CC EMBL; M24406; AAA36462.1; -.
CC EMBL; X64116; CAA45478.1; -.
CC EMBL; X64117; CAA45478.1; JOINED.
CC EMBL; X64118; CAA45478.1; JOINED.
CC EMBL; X64119; CAA45478.1; JOINED.
CC EMBL; X64120; CAA45478.1; JOINED.
CC EMBL; X64121; CAA45478.1; JOINED.
CC EMBL; X64122; CAA45478.1; JOINED.
CC EMBL; X64123; CAA45478.1; JOINED.
CC EMBL; X64116; CAA45479.1; -.
CC EMBL; X64117; CAA45479.1; JOINED.
CC EMBL; X64118; CAA45479.1; JOINED.
CC EMBL; X64119; CAA45479.1; JOINED.
CC EMBL; X64120; CAA45479.1; JOINED.
CC EMBL; X64121; CAA45479.1; JOINED.
CC EMBL; X64122; CAA45479.1; JOINED.
CC EMBL; X64123; CAA45479.1; JOINED.
CC EMBL; X64116; CAA45480.1; -.
CC EMBL; X64117; CAA45480.1; JOINED.


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EMBL; X80038; CAA56342.1; -.
DR EMBL; AF058448; AAC23797.1; -.
DR EMBL; BC003091; AAH03091.1; -.
DR EMBL; AF044968; AAC82348.1; -.
DR EMBL; AF044962; AAC82348.1; JOINED.
DR EMBL; AF044963; AAC82348.1; JOINED.
DR EMBL; AF044964; AAC82348.1; JOINED.
DR EMBL; AF044966; AAC82348.1; JOINED.
DR EMBL; AF044967; AAC82348.1; JOINED.
DR EMBL; AF050154; AAD02503.1; -.
DR PIR; I68093; I68093.
DR Genew; HGNC:9707; PVRL2.
DR MIM; 600798; -.
DR GO; GO:0005886; C:plasma membrane; TAS.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 538 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.
FT DOMAIN 32 360 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 361 381 POTENTIAL.
FT DOMAIN 382 538 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 156 IG-LIKE V-TYPE.
FT DOMAIN 162 256 IG-LIKE C2-TYPE 1.
FT DOMAIN 261 345 IG-LIKE C2-TYPE 2.
FT DISULFID 54 140 BY SIMILARITY.
FT DISULFID 183 238 BY SIMILARITY.
FT CARBOHYD 137 137 BY SIMILARITY.
FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 351 479 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT QGAEDEDELGPPSYKPTPKAKLEAQEMPSQLFTLGASEH
FT SPLKTPYFDAGASCTQEMPRYHELPTLEERSGPHPGATS
FT LGSPIP -> RASPRDVGLVWGVGTTLLVLLLAGGSLA
FT FILLRVRRRRKSPGGAGGASGDGGFYDPKQAVLGNDDPVF
FT WTPVVPGMPEPDGKDEEEEEEEKAEKGLMLPPPALEDDM
FT ESQLDGSLISRRAVYV (in isoform Alpha).
FT /FTId=VSP_002628.
FT Missing (in isoform Alpha).
FT /FTId=VSP_002629.
FT SEQUENCE 538 AA; 57742 MW; 3AE4F83E92F6F624 CRC64;
Query Match 24.7%; Score 426.5; DB 1; Length 538;
Best Local Similarity 29.3%; Pred. No. 1.5e-26;
Matches 99; Conservative 64; Mismatches 132; Indels 43; Gaps 10;
QY 13 ITQISWEKIHGKSS-QTVAVHHPOYGFVSQGEYQG--RVLF-----KNYSINDAT 59
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 ISLVTWQRPDAPANHQNVAAPHKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAEIQDAT 124
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPE-----TVSLIKGPDSLIDGG 112
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 LALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNAEAKQVTFSDP----- 177
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 NETVAAICIAATGKPVAAHI-----DWEGDLGEMESTTSPNETATIISQYKLFPRFA 166
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 178 --TTVALCISKEGRPPARISWLSLDWEAKETQVSGTLAG---TVTVTSRFTLVPSGRA 231
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 RGRITCVVVKHPALEKDIRYSFILLDIQYAPEVSVTGYDGNWPFVGRKGVNLCNADANPPP 226
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 DGVTVTCKVEHESFEPEPALIPVTLVRYRPEVSVISGYDDNWVLGRTDATLSCDVRSNPEP 291
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 227 FKSVWSRLDGQWPDGLLASDNLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVP 286
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 292 TGYDWSSTTSGTFTSAVAQGSQQL-VIHAVDSLFTNTTFCVTVTNAVGMGRAEQVIFVRETP 350
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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```
QY 287 FKQTSSIAVAGAVIGAVLALFI-IAIFVTVLLTPRK 323
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 351 --NTAGAGATGGIIGGIIAIIATAVAATGILICRQOR 386
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
| : : : : : : : : : : : : : : : : : : : : : : : : : : : :
RESULT 6
PVR_CERAE
ID PVR_CERAE STANDARD; PRT; 417 AA.
AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
GN PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RX MEDLINE=93059651; PubMed=1331508;
RA Koike S.; Ise I.; Sato Y.; Yonekawa H.; Gotoh O.; Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
RT has no putative N-glycosylation site in the functional N-terminal
RT immunoglobulin-like domain.";
RL J. Virol. 66:7059-7066(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-2; Sequence=VSP_002622, VSP_002623;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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EMBL; D12611; BAA02136.1; -.
DR EMBL; D12612; BAA02137.1; -.
DR PIR; A44194; A44194.
DR PIR; B44194; B44194.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 417 POLIOVIRUS RECEPTOR.
FT DOMAIN 21 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 367 POTENTIAL.
FT DOMAIN 368 417 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 139 IG-LIKE V-TYPE.
FT DOMAIN 145 237 IG-LIKE C2-TYPE 1.
FT DOMAIN 244 328 IG-LIKE C2-TYPE 2.
FT DISULFID 49 123 BY SIMILARITY.
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 5.28976 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-31_COPY_74_404
Perfect score: 1728
Sequence: 1 VSLKCLIEVNETITQISWEK.....FVTVLLTPRKRPSPYLDKVI 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues 141681
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	578.5	33.5	515	1	PVR1_MOUSE	Q9jkf6 mus musculu
2	565	32.7	517	1	PVR1_HUMAN	Q15223 homo sapien
3	561.5	32.5	515	1	PVR1_PIG	Q9gl76 sus scrofa
4	434.5	25.1	530	1	PVR2_MOUSE	P32507 mus musculu
5	426.5	24.7	538	1	PVR2_HUMAN	Q92692 homo sapien
6	398	23.0	417	1	PVR_CERAE	P32506 cercopithec
7	390	22.6	417	1	PVR_HUMAN	P15151 homo sapien
8	211.5	12.2	764	1	ICCR_DROME	Q08180 drosophila
9	199	11.5	837	1	NCM2_MOUSE	Q35136 mus musculu
10	187.5	10.9	278	1	OX2G_HUMAN	P41217 homo sapien
11	175	10.1	837	1	NCM2_HUMAN	O15394 homo sapien
12	172.5	10.0	626	1	MAG_HUMAN	P20916 homo sapien
13	172.5	10.0	626	1	MAG_MOUSE	P20917 mus musculu
14	170.5	9.9	626	1	MAG_RAT	P07722 rattus norv
15	169.5	9.8	4391	1	PGBM_HUMAN	P98160 homo sapien
16	164.5	9.5	853	1	NCA1_BOVIN	P31836 bos taurus
17	160	9.3	858	1	NCA1_RAT	P13596 rattus norv
18	158.5	9.2	278	1	OX2G_MOUSE	O54901 mus musculu
19	158.5	9.2	278	1	OX2G_RAT	P04218 rattus norv
20	157.5	9.1	365	1	NCAR_HUMAN	P78310 homo sapien
21	157	9.1	1091	1	NCA1_CHICK	P13590 gallus gall
22	156	9.0	847	1	CD22_HUMAN	P13593 mus musculu
23	154	8.9	467	1	SIL7_HUMAN	P20273 homo sapien
24	154	8.9	509	1	SHS1_RAT	Q9y286 homo sapien
25	153.5	8.9	702	1	CEA5_HUMAN	P97710 r protein-t
26	153	8.9	365	1	NCAR_MOUSE	P06731 homo sapien
27	152	8.8	739	1	VCA1_MOUSE	P97792 mus musculu
28	152	8.8	761	1	NCA2_HUMAN	P29533 mus musculu
29	152	8.8	848	1	NCA1_HUMAN	P13592 homo sapien
30	149.5	8.7	725	1	NCA2_MOUSE	P13591 homo sapien
31	149.5	8.7	1115	1	NCA1_MOUSE	P13594 mus musculu
32	149	8.6	353	1	CEPU_CHICK	P13595 mus musculu
33	148	8.6	2012	1	DSCA_HUMAN	Q90773 gallus gall
						O60469 homo sapien

34	147.5	8.5	1088	1	NCA1_XENLA	P16170 xenopus lae
35	147	8.5	588	1	CL66_CHICK	P42292 gallus gall
36	147	8.5	1709	1	SN_HUMAN	Q9bzz2 homo sapien
37	146.5	8.5	1051	1	PTK7_CHICK	Q91048 gallus gall
38	145	8.4	330	1	CD22_PONPY	Q9nle3 pongo pygma
39	145	8.4	359	1	LACH_MOUSE	Q24372 drosophila
40	143.5	8.3	569	1	SILF_MOUSE	Q920g3 mus musculu
41	143.5	8.3	1092	1	NCA2_XENLA	P36335 xenopus lae
42	143	8.3	337	1	OPCM_CHICK	Q98892 gallus gall
43	142.5	8.2	332	1	CD22_PANPA	Q9nles pan paniscu
44	142.5	8.2	332	1	CD22_PANTR	Q9nle6 pan troglod
45	142	8.2	519	1	ECTO_RAT	P16573 rattus norv

ALIGNMENTS

RESULT 1
PVR1_MOUSE STANDARD; PRT; 515 AA.
ID Q9JKF5; Q9ERL5; Q9JIL7;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1).
GN PVRL1 OR PRR1 OR HVEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,
RA Lecocq E., Dubreuil P., Campadelli-Fiume G.;
RT "The murine homolog of human nectin1 delta serves as a species
RT nonspecific mediator for entry of human and animal alpha herpesviruses
RT in a pathway independent of detectable binding to gD";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-lalpha to human nectin-lalpha
RT (HvEC) in sequence and activity as a glycoprotein D receptor for
RT alphaherpesvirus entry";
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the
RT floor plate during embryogenesis, suggesting a role in neural
RT development";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAPERPEPVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF239762; AAF60333.1; -.

Query Match		10.7%;	Score 184.5;	DB 2;	Length 5198;
Best Local Similarity		25.9%;	Pred. No. 3.4e-05;		
Matches		82;	Conservative 40;	Mismatches 131;	Indels 63; Gaps 17;
Qy	1	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLPKNYSLNDATI	60		
Db	810	VTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG-----NLLITDAQI	856		
Qy	61	TLHNIGFSDGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSLIKGPDSDLIDGGNETVAA	118		
Db	857	-----EDQQQFTCIARN-TYGOQSQSSTLMTGLVSPVLGHVPPFEQLIEGQDLTLS-	907		
Qy	119	ICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTRFARGR---RITCVV	175		
Db	908	-CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSLRLRGGNPKDEGKYTCIA	960		
Qy	176	KHPALEKDIRYSFIL----DIQYAPE-----VSVTGYDGNW-----FVGRKGVNL	216		
Db	961	VSPAGNSTLHINVQLIKKPEFVYKPEGGIVFKPTISGMDEKHVAVVNSTHVDVLDGEGFAI	1020		
Qy	217	KCNADANPPPFKSVMWSRLDGQWP-----DGLLASDNTLHFVHPLTFNYSGVYICKVTNS	270		
Db	1021	PCVVSCTPPPI-ITW-YLDGR-PITPNSRDFTVTADNTL-IVRKADKSYSGVYTCQATNS	1076		
Qy	271	LGQRSDQKVIYISDVP	286		
Db	1077	AGDNEQKTTIRIMNTP	1092		

Search completed: April 12, 2004, 09:47:09
Job time : 9.75845 secs

Db 264 HMSTGSRIVEHSQVRLECRADANPSDVYRWFINDEPIIGGQKTEMVIRNVRKFKH 319

QY 261 GVIYI-CKVTNSLQGRSDQKVIYISDVP-FKQTSSIAVAGAVIGAVLAL 306

Db 320 DAIVKCEVQNSVGKSEDTLDISYAPSRQRPOSMEADVGSVVS 365

RESULT 13

A47639

OX-2 membrane glycoprotein precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000

C;Accession: A47639

R;McCaughan, G.W.; Clark, M.J.; Barclay, A.N.

Immunogenetics 25, 329-335, 1987

A;Title: Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein

A;Reference number: A47639; MUID:87192943; PMID:3032785

A;Accession: A47639

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-274 <MCC>

A;Cross-references: GB:X05323; NID:g34742; PIDN:CAA28943.1; PID:g1335216; GB:M17226; GB:

C;Superfamily: MRC OX-2 antigen; immunoglobulin homology

C;Keywords: glycoprotein; membrane protein

F;40-119/Domain: immunoglobulin homology <IMM>

Query Match 10.9%; Score 187.5; DB 2; Length 274;

Best Local Similarity 24.8%; Pred. No. 5.4e-07;

Matches 52; Conservative 36; Mismatches 97; Indels 25; Gaps 4;

QY 2 SLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGSVQGEYQGRVLFKNSLNDATIT 61

Db 44 SLKCSLQNAQEALIVTWQKKAVSPENMVTFSENHGVIQPAYKDKINITQLGLQNSTIT 103

QY 62 LHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSL-IKGPDSLIDGGNETVAAIC 120

Db 104 FWNITLEDGECYMCLENTFGFGKISGTACLTVYVQPIVSLHYKFSEDLN-----IT 155

QY 121 IAATGKPVAHIDWEGDLGEMESTTT--SFPNETATIIISQYKLPFTRFARGRRITCVVKHP 178

Db 156 CSATARAPAPMFWKVPKRSKIENSTVTLSPNGTTSVTSILHIKDPKNQVGKEVICQVLHL 215

QY 179 ALEKDIRYSFILDIOYAPEVSVTYGDNWF 208

Db 216 GTVTDKQ-----TVNKGYWF 231

RESULT 14

T20992

hypothetical protein F15G9.4a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T20992; T24733

R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20992

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5175 <WIL>

A;Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone F15G9

R;Kershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24733

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5175 <WI2>

A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: CESP:F15G9.4a

A;Map position: x

A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3

; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/

1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077

Query Match 10.7%; Score 184.5; DB 2; Length 5175;

Best Local Similarity 25.9%; Pred. No. 3.4e-05;

Matches 82; Conservative 40; Mismatches 131; Indels 63; Gaps 17;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGSVQGEYQGRVLFKNSLNDATI 60

Db 810 VTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG-----NLLITDAQI 856

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAA 118

Db 857 -----EDQGQFTCIARN-TYQQSQSSTTLMVTGLVSPVLGHVPPEEQDLIEGQDLTIS- 907

QY 119 ICIAATGKPVAHIDWEGDLGEMESTTTTSFPNETATIIISQYKLPFTRFARGR---RITCVV 175

Db 908 -CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSLRLRGGNPKDGEKYTCIA 960

QY 176 KHPALEKDIRYSFIL---DIQYAPE-----VSVTYGDNW-----FVGRKGVNL 216

Db 961 VSPAGNSTLHINVQLIKKPEFVYKPEGGIVFKPTISGMDEKHVAVVNSTHVDLDGEGFAI 1020

QY 217 KCNADANPPPFKSVWSRLDGQWP-----DGLLASDNTLHFVHPLTFNYSGVYICKVTNS 270

Db 1021 PCVVSGETPPI-ITW-YLDGR-PITPNSRDFVTADNTL-IVRKADKSYSGVYTCQATNS 1076

QY 271 LGQRSDQKVIYISDVP 286

Db 1077 AGDNEQKTTIRIMNTP 1092

RESULT 15

T43290

hemicentin precursor - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000

C;Accession: T43290; T20993; T24734

R;Vogel, B.E.; Hedgcock, E.M.

submitted to the EMBL Data Library, June 1998

A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ

A;Reference number: Z22396

A;Accession: T43290

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-5198 <VOG>

A;Cross-references: EMBL:AF074901; PIDN:AAC26792.1

R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20993

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5198 <WIL>

A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

A;Experimental source: clone F15G9

R;Kershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24734

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5198 <WI2>

A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: him-4; F15G9.4b

A;Map position: x

A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3

; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/

1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100

Db 338 RESP--STAGAGATGGIIGGIIAAIIATAVAGTGILICRQR 377

RESULT 5

I68093

PRR2 delta - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000

C:Accession: I68093

R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.

Gene 159, 267-272, 1995

A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th

A:Reference number: I53960; MUID:95347610; PMID:7622062

A:Accession: I68093

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-538 <RES>

A:Cross-references: GB:S79172; NID:g1042204; PID:g1042205

C:Genetics:

A:Gene: PRR2delta

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 24.7%; Score 426.5; DB 2; Length 538;

Best Local Similarity 29.3%; Pred. No. 7.2e-25;

Matches 99; Conservative 64; Mismatches 132; Indels 43; Gaps 10;

QY 13 ITQISWEKIHGKSS-QTVAVHHPQYGFSGVEYQG--RVLF-----KNYSLNDAT 59

Db 65 ISLVTWQRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDAT 124

QY 60 ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEP-----TVSLIKGPDSDLIDGG 112

Db 125 LALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQAEAKQVTFSQDP----- 177

QY 113 NETVAAICIAATGKPVVAHI-----DWEGLGEMESTTTSFPNETATISQYKLFPTRFA 166

Db 178 --TTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAG----TVTTSRFTLVPSGRA 231

QY 167 RGRRIITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPP 226

Db 178 --TTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAG----TVTTSRFTLVPSGRA 231

QY 167 RGRRIITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPP 226

Db 232 DGVTVTKVEHESFEERALIPVTLVRYPPPEVSIISGDDNWYLGRTDATLSCDVRSNPEP 291

QY 227 FKSVMRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 286

Db 292 TGYDWSSTSGTFTSAVAQSQL-VIHAVDSLNTTFVCTVTNAVGMGRAEQVIFVRETP 350

QY 13 ITQISWEKIHGKSS-QTVAVHHPQYGFSGVEYQG--RVLF-----KNYSLNDAT 59

Db 65 ISLVTWQRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDAT 124

QY 60 ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEP-----TVSLIKGPDSDLIDGG 112

Db 125 LALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQAEAKQVTFSQDP----- 177

QY 113 NETVAAICIAATGKPVVAHI-----DWEGLGEMESTTTSFPNETATISQYKLFPTRFA 166

Db 178 --TTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAG----TVTTSRFTLVPSGRA 231

QY 167 RGRRIITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPP 226

Db 232 DGVTVTKVEHESFEERALIPVTLVRYPPPEVSIISGDDNWYLGRTDATLSCDVRSNPEP 291

QY 227 FKSVMRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 286

Db 292 TGYDWSSTSGTFTSAVAQSQL-VIHAVDSLNTTFVCTVTNAVGMGRAEQVIFVRETP 350

QY 287 FKQTSSIAVAGAVIGAVLALFI-IAIFVTVLLTPRKKR 323

Db 351 --NTAGAGATGGIIGGIIAAIIATAVAGTGILICRQR 386

RESULT 6

I53960

PRR2 alpha - human

C:Species: Homo sapiens (man)

C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

C:Accession: I53960

R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.

Gene 159, 267-272, 1995

A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th

A:Reference number: I53960; MUID:95347610; PMID:7622062

A:Accession: I53960

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-478 <RES>

A:Cross-references: GB:S79171; NID:g1042202; PID:g1042203

C:Genetics:

A:Gene: PRR2alpha

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 24.2%; Score 418.5; DB 2; Length 478;

Best Local Similarity 29.5%; Pred. No. 2.5e-24;

Matches 101; Conservative 64; Mismatches 134; Indels 43; Gaps 10;

QY 13 ITQISWEKIHGKSS-QTVAVHHPQYGFSGVEYQG--RVLF-----KNYSLNDAT 59

Db 65 ISLVTWQRPDAPANHQNVAAFHPKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDAT 124

QY 60 ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEP-----TVSLIKGPDSDLIDGG 112

Db 125 LALHGLTVEDEGNYTCEFATFPKGSVRGMTWLRVIAKPKNQAEAKQVTFSQDP----- 177

QY 113 NETVAAICIAATGKPVVAHI-----DWEGLGEMESTTTSFPNETATISQYKLFPTRFA 166

Db 178 --TTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAG----TVTTSRFTLVPSGRA 231

QY 167 RGRRIITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPP 226

Db 232 DGVTVTKVEHESFEERALIPVTLVRYPPPEVSIISGDDNWYLGRTDATLSCDVRSNPEP 291

QY 227 FKSVMRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 286

Db 292 TGYDWSSTSGTFTSAVAQSQL-VIHAVDSLNTTFVCTVTNAVGMGRAEQVIFVRETP 350

QY 287 F-KQTSSIAVAGAVIGAVLALFIIA--IFVTVLLTPRKKRPS 325

Db 351 RPRRDVGPLVMGAVGGTLLVLLLAGGSLAFILLRVRRRRKS 392

RESULT 7

B44194

poliovirus receptor (clone AGM-delta-1) - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: B44194

R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A:Title: A second gene for the African green monkey poliovirus receptor that has no put

A:Reference number: A44194; MUID:93059651; PMID:1331508

A:Accession: B44194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <KOI>

A:Cross-references: GB:S48817

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 23.0%; Score 398; DB 2; Length 392;

Best Local Similarity 30.3%; Pred. No. 7.3e-23;

Matches 99; Conservative 62; Mismatches 144; Indels 22; Gaps 10;

QY 1 VSLKCLIEV--NET-ITQISWEKIHGKSSQTVAVHH---PQYGFSGVEYQGRVLFKNY 53

Db 45 VTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQIQGPNYSEPKRLEFVAARL--GT 101

QY 54 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEP--TVSLIKGPDSDLIDG 111

Db 102 ELRDASLRMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVLAKPQNTAEVQKQLT---- 157

QY 112 GNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTS--FPNETATISQYKLFPTREARGR 169

Db 158 GKPVPVARCVSTGGRPPAHITWHSDLGGMPTNSQAPGLSGTIVTSLMWILVPSSQVDGK 217

QY 170 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 229

Db 218 SVTCKVEHESFEKPOLLTVNLTVVYPPPEVSIISGDDNWYLSQNEATLTCDARSNPEPTGY 277

QY 230 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVPFKQ 289

Db 278 NWSTTMGLPLPPFAVAQQAQL-LIRPVDKPINTTFCINVTNALGARQAELTVQKEGPPSE 336

QY 290 TSSIA---VAGAVIGAVLALFIIAIFV 313

Db 337 PSGMSSNIIFLILGIVILLTLIGIV 363

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 8.75845 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-31_COPY_74_404
Perfect score: 1728
Sequence: 1 VSLKCLIEVNETITQISWEK.....FVTVLLTPRKKRPSYLDKVI 331

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1156.5	66.9	407	2 T08732	hypothetical prote
2	542.5	31.4	518	2 JC4024	poliovirus recepto
3	436	25.2	467	1 HLMSP3	poliovirus recepto
4	434.5	25.1	530	2 A53437	poliovirus recepto
5	426.5	24.7	538	2 I68093	PRR2 delta - human
6	418.5	24.2	478	2 I53960	PRR2 alpha - human
7	398	23.0	392	2 B44194	poliovirus recepto
8	398	23.0	417	2 A44194	poliovirus recepto
9	387	22.4	392	1 RWHUPD	poliovirus recepto
10	387	22.4	417	1 RWHUPA	poliovirus recepto
11	310	17.9	416	2 A54017	colon carcinoma-as
12	211.5	12.2	764	2 A49448	irregular chiasm C
13	187.5	10.9	274	2 A47639	OX-2 membrane glyc
14	184.5	10.7	5175	2 T20992	hypothetical prote
15	184.5	10.7	5198	2 T43290	hemichentin precurs
16	172.5	10.0	626	1 A61084	myelin-associated
17	172.5	10.0	637	2 B33785	myelin-associated
18	170.5	9.9	582	1 BNRT3S	myelin-associated
19	170.5	9.9	626	1 BNRT3	myelin-associated
20	169.5	9.8	4391	2 A38096	perlecan precursor
21	164.5	9.5	853	1 IJBONC	neural cell adhesi
22	161	9.3	765	2 C42632	cell adhesion mole
23	161	9.3	812	2 B42632	cell adhesion mole
24	161	9.3	932	2 A42632	cell adhesion mole
25	160	9.3	858	1 IJRTNC	neural cell adhesi
26	158.5	9.2	278	1 TDRTOX	OX-2 membrane glyc
27	157	9.1	365	2 JC7780	coxsackie- and ade
28	157	9.1	1091	1 IJCHNL	neural cell adhesi
29	156	9.0	847	2 JH0371	B-cell adhesion pr

30	155	9.0	7962	2 I38346	elastic titin - hu
31	153.5	8.9	702	2 A36319	carcinoembryonic a
32	152	8.8	739	2 JN0581	vascular cell adhe
33	152	8.8	761	1 IJHUNG	neural cell adhesi
34	152	8.8	1612	2 T30805	du1t1 protein - mo
35	149.5	8.7	725	1 IJMSNG	neural cell adhesi
36	149.5	8.7	1115	1 IJMSNL	neural cell adhesi
37	148	8.6	1651	2 T14160	transmembrane rece
38	148	8.6	1896	2 T08851	Down syndrome cell
39	147.5	8.5	725	2 JE0099	neural cell adhesi
40	147.5	8.5	1088	1 IJXLNL	neural cell adhesi
41	147	8.5	588	2 JH0506	adhesion molecule
42	147	8.5	588	2 A45254	surface glycoprote
43	146.5	8.5	1051	2 A39712	kinase-like protei
44	146	8.4	647	2 A35648	B-cell adhesion pr
45	145.5	8.4	725	2 JE0100	neural cell adhesi

ALIGNMENTS

RESULT 1

T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08732
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732
A;Molecule type: mRNA
A;Residues: 1-407 <OTT>
A;Cross-references: EMBL:AL050071
A;Experimental source: fetal kidney; clone DKFZp566B0846
C;Genetics:
A;Note: DKFZp566B0846.1

Query Match 66.9%; Score 1156.5; DB 2; Length 407;
Best Local Similarity 74.9%; Pred. No. 1e-80;
Matches 224; Conservative 12; Mismatches 24; Indels 39; Gaps 2;

QY	70	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAICIAATGK PVA	129
Db	1	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAICIAATGK PVA	60
QY	130	HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFI	189
Db	61	HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFI	120
QY	190	LDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPKSVWSRLDQWPDLASDNTL	249
Db	121	LDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPKSVWSRLDQWPDLASDNTL	180
QY	250	HFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP-----	286
Db	181	HFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT	240
QY	287	-----FKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLDK	329
Db	241	EPKKLPFLPLSLTIKDDTIATIIASVVGALFIVLVSLAGIFCYRRRRRTFRGDYFAK	299

RESULT 2

JC4024
poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, C.; Dubre
Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene
A;Reference number: JC4024; MUID:95237621; PMID:7721102

Db 206 SIVCSVNHESLKGADRSTSQRIEVLVYFTAMIRPDPPHREGQK-LLLHCEGRGNPVPQQ 264
Qy 245 SVWSRLDGQWPDGLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQSDQKVIYISDVPEK 304
Db 265 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSKAYYTLNVND-PSP 321
Qy 305 QTSSIAVAGAVIGAVLALFIIAIFVTVLL 333
Db 322 VPSSSTYHAIIGGIVA-FIVFLLIMLI 349

RESULT 15

US-09-778-510-2
; Sequence 2, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 432
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-2

Query Match 11.9%; Score 238.5; DB 4; Length 432;
Best Local Similarity 26.1%; Pred. No. 7.6e-15;
Matches 86; Conservative 61; Mismatches 159; Indels 23; Gaps 13;
Qy 10 TAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQGFVSQGEYQGRVLFKNY 69
Db 73 TVVAGGTIVLKCQVKDHED-SSLQWS----NPAQQT-----YFGEKRALRDNRIQLVTS 122
Qy 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGNN 129
Db 123 TPHELSISINVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 179
Qy 130 ETVAAICIAATGKPVAHIDWEGDLGEMESTTSF---PN-ETATIIISQYKLFPTRFARGR 185
Db 180 DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPENGKFTVSSSVTFQVTREDDGA 239
Qy 186 RITCVVXHPALE-KDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFK 244
Db 240 SIVCSVNHESLKGADRSTSQRIEVLVYFTAMIRPDPPHREGQK-LLLHCEGRGNPVPQQ 298
Qy 245 SVWSRLDGQWPDGLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQSDQKVIYISDVPEK 304
Db 299 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSKAYYTLNVND-PSP 355
Qy 305 QTSSIAVAGAVIGAVLALFIIAIFVTVLL 333
Db 356 VPSSSTYHAIIGGIVA-FIVFLLIMLI 383

Search completed: April 12, 2004, 09:49:29
Job time : 13.5439 secs


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; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/907,794A
; CURRENT FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-907-794A-84

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Query Match      11.9%; Score 238.5; DB 4; Length 398;
Best local Similarity 26.1%; Pred. No. 6.7e-15;
Matches 86; Conservative 61; Mismatches 159; Indels 23; Gaps 13;

QY 10 TAVWGNVSLKCLIEVNETITQISWEKIHGSSQTVAVHHPQYGFSGVQGEYQGRVLFKNY 69
Db 39 TVVAGGTVVVKCQVKDHED-SSLQWS----NPAQOTL-----YFGEKRALRDNRILQVTS 88

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QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNQAQSTTVTVLVEPTVSLIKGPDSDLIDGN 129
Db 89 TPHELSISINVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145
QY 130 ETVAAICIAATGKPVAHIDWEGDLGEMESTTSF---PN-ETATISQYKLFPTTRFARGR 185
Db 146 DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGA 205
QY 186 RITCVVXHPALE-KDIRYSFILDIQYAPEVSVTYGDNWFVGRKGVNLKCNADANPPPFK 244
Db 206 SIVCSVNHESLKGADRSTSORIEVLVYFTAMIRDPDPPHREGQK-LLHCEGRGNVPVQQ 264
QY 245 SVWSRLDGQWPDGCLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPFK 304
Db 265 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSKAYYTLNVND-PSP 321
QY 305 QTSSIAVAGAVIGAVLALFIIAIFVTVLL 333
Db 322 VPSSSSTYHAIGGIVA-FIVFLLLIMLI 349

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RESULT 13
US-09-905-125A-84
; Sequence 84, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/23089

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Db 211 DDGVPVICQVEHPAVTGNLQTRYLEVQYKPVQVHIQMTYPLQGLTREGDALELTCEAIGK 270
QY 240 PPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYIS 299
Db 271 POPVMVTWVRVDDDEMPQHAVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 329
QY 300 DVPF-----KQTSSIAVAGAVIGAVLALFIIAIFVT 330
Db 330 DPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTIITDSRAGEEGSIRAVDHAVIGGVAVVVFAMLC 389
QY 331 VLLTPR 336
Db 390 LIILGR 395

RESULT 7
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-20

Query Match 14.1%; Score 283; DB 4; Length 442;
Best Local Similarity 24.9%; Pred. No. 3.3e-19;
Matches 91; Conservative 70; Mismatches 147; Indels 58; Gaps 12;
QY 9 VTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKN 68
Db 52 VTVIEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YFRDRLKDSRFQLLN 101
QY 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIK-GPDSLIDG 127
Db 102 FSSSELKVS LTNVSIISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQDITAVEG 159
QY 128 GNETVAAICIAATGKPVAHIDW-EGDL-----GEMESTTTSFPNETATIIISQYKLFPTRF 181
Db 160 --EEIEVNCCTAMASKPATTIRWFKGNTLKGKSEVEEWSDMY-----TVTSQMLMLKVHKE 212
QY 182 ARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKG--VNLKCNADAN 239
Db 213 DDGVPVICQVEHPAVTGNLQTRYLEVQYKPVQVHIQMTYPLQGLTREGDALELTCEAIGK 272
QY 240 PPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYIS 299
Db 273 POPVMVTWVRVDDDEMPQHAVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 331
QY 300 DVPF-----KQTSSIAVAGAVIGAVLALFIIAIFVT 330
Db 332 DPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTIITDSRAGEEGSIRAVDHAVIGGVAVVVFAMLC 391
QY 331 VLLTPR 336
Db 392 LIILGR 397

RESULT 8
US-09-930-803-1

; Sequence 1, Application US/09930803
; Patent No. 6596493
; GENERAL INFORMATION:
; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
; APPLICANT: REEVES, Roger
; APPLICANT: YOSHINORI, Muramaki
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS
; FILE REFERENCE: JHUI770-1
; CURRENT APPLICATION NUMBER: US/09/930,803
; CURRENT FILING DATE: 2001-08-15
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-803-1

Query Match 14.1%; Score 283; DB 4; Length 442;
Best Local Similarity 24.9%; Pred. No. 3.3e-19;
Matches 91; Conservative 70; Mismatches 147; Indels 58; Gaps 12;
QY 9 VTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKN 68
Db 52 VTVIEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YFRDRLKDSRFQLLN 101
QY 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIK-GPDSLIDG 127
Db 102 FSSSELKVS LTNVSIISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMIDIQDITAVEG 159
QY 128 GNETVAAICIAATGKPVAHIDW-EGDL-----GEMESTTTSFPNETATIIISQYKLFPTRF 181
Db 160 --EEIEVNCCTAMASKPATTIRWFKGNTLKGKSEVEEWSDMY-----TVTSQMLMLKVHKE 212
QY 182 ARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKG--VNLKCNADAN 239
Db 213 DDGVPVICQVEHPAVTGNLQTRYLEVQYKPVQVHIQMTYPLQGLTREGDALELTCEAIGK 272
QY 240 PPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYIS 299
Db 273 POPVMVTWVRVDDDEMPQHAVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 331
QY 300 DVPF-----KQTSSIAVAGAVIGAVLALFIIAIFVT 330
Db 332 DPPTTIPPPTTTTTTTTTTTTTTTTTTTTTTIITDSRAGEEGSIRAVDHAVIGGVAVVVFAMLC 391
QY 331 VLLTPR 336
Db 392 LIILGR 397

RESULT 9
US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22

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; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match      21.3%; Score 427.5; DB 4; Length 479;
Best Local Similarity 29.2%; Pred. No. 2.4e-33;
Matches 108; Conservative 64; Mismatches 151; Indels 47; Gaps 11;

QY 5 VEPHVTAVGKNVSLKCLI---EVNETITQISWEKIHGKSS-QTVAVHHPOYGFSVQGEY 60
Db 38 VLPEVRGQLGGTVLPCHELLPPVPGLYISLVTWQRPDAPANHQNVAAAFHPKMGPSFSPK 97
QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108
Db 98 PGSERLSFVSAKQSTGQDTEAELQDATLALHGLTVEDEGNYTCEFAFPKGSVRGMTWLR 157
QY 109 VLVEP-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVAAHI-----DWEGLGE 155
Db 158 VIAKPKNOAEAKVTFSDP-----TTVALCISKEGRPPARISWLSLSDWEAKETQ 208
QY 156 MESTTTSFPNETATIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVS 215
Db 209 VSGTLAG----TIVTTSRFTLVPSGRADGVTVTCKVEHESFEELIPVTLVSRYPPEVS 264
QY 216 VTGYDGNWFVGRKGVNLCNADANPPPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNY 275
Db 265 ISGYDDNWILGRDATLSCDVRNPEPTGYDWSSTSGTFTPTSAVAQGSQ-L-VIHAVDSL 323
QY 276 SGVYICKVTNSLQSRDQKVIYISDVPPFKQTSSIA--VAGAVIGAVLALFIIA--IFVT 331
Db 324 NTTFVCTVTNAVGMGRAEQVIFVRETPTRASPRDVGPLVWGAVGGTLLVLLLAGGSLAFI 383
QY 332 LLTPRKKRPS 341
Db 384 LLRVRRRKS 393
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```

RESULT 5
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62

Query Match      19.4%; Score 390; DB 4; Length 408;
Best Local Similarity 30.8%; Pred. No. 9e-30;
Matches 108; Conservative 61; Mismatches 160; Indels 22; Gaps 10;

QY 3 IIVPHVTAVGKNVSLKCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPOYGFSVQGE 59
Db 32 VLVYPNSTGVLGGSTLHCSLTSNENVTITQITWMKKDSGGSHALVAFHPKGPNIKEP 91
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QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEP--TVSL 117
Db 92 ERVKFLAAQQDLRNASLAISNLSVEDEGIYECQIATFPRGSRSTNAWLKVQARPKNATAEA 151
QY 118 IKGPDSLI--DGGNETVAAICIAATGKPVAAHIDW----EGDLGEMESTTTSFPNETATII 171
Db 152 LEPSPTLILQD-----VAKCISANGHPGRISWPSNVNGSHREMKE-PCSQPG-TTTVT 203
QY 172 SQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFVGRKGV 230
Db 204 SYLSMVPSRQADGKNITCTVEHESLQELDQLLVLSQPYPPENVSISGYDGNWYVGLTNL 263
QY 231 NLKCNADANPPPFKS--VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLG 288
Db 264 TLTCEAHSKPAPDMAGYNWSTNTGDFNSVKRQGNMLLISTVEDGLNNTVIVCEVTNALG 323
QY 289 QRSQDKVIYISDVPPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKR 339
Db 324 SGQGVHIIIVKEKPEPMQONTRLHLGVIFLIVFVLAVVIIIAALYTIRRCR 374
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RESULT 6
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match      14.1%; Score 283; DB 4; Length 440;
Best Local Similarity 24.9%; Pred. No. 3.3e-19;
Matches 91; Conservative 70; Mismatches 147; Indels 58; Gaps 12;

QY 9 VTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKN 68
Db 50 VTVEIGEVATISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLLN 99
QY 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIK-GPDSLIDG 127
Db 100 FSSSELKVSLTNVSVISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMDIQDITAVEG 157
QY 128 GNETVAAICIAATGKPVAAHIDW-EGDL-----GEMESTTTSFPNETATIISQYKLFPTRF 181
Db 158 --EEIEVNCTAMASKPATTIRWFKGNTLKGKSEVEWSDMY-----TVTSQMLKVHKE 210
QY 182 ARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKG--VNLKCNADAN 239
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Db 281 HWTTLNGSLPKGVEAQNRTLFPKGPINYSLAGTYICEATNPIGTRSGQVEVNITEKPRPQ 340
QY 306 TSSIAVAGAVIGAVLALFIILAFVTV--LLTPRKKRPSYLDKV-IDLPPTHKPPPLYEER 362
Db 341 RGLGSAARLLAGTVAVFLILVAVLTVFFLYNRQOKSPPETDGAGTDQPLSQKPEPSPSRQ 400
QY 363 SPPLPQ 368
Db 401 SSLVPE 406

RESULT 2

US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITEBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match 28.2%; Score 566.5; DB 4; Length 517;
Best Local Similarity 35.2%; Pred. No. 5.9e-47;
Matches 122; Conservative 68; Mismatches 134; Indels 23; Gaps 7;

QY 14 GKNVSLKCLIE---VNETITQISWEKHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPMSGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLELEDEGVYICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTRFARGR 185
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEABYQEIRNPNGTIVTSRYRLVPSREAHQ 222
QY 186 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLKCNADANPPPFKS 245
Db 223 SLACIVNYHM--DRFKESLTINVQYEPEVTIEGFDGNWYQLQMDVKLTCKADANPPATEY 280
QY 246 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQ 305
Db 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYTP 340
QY 306 TS-----SIAVAGAVIGAVLALFIILAFVTVLLTPRKKRPSY 342
Db 341 SPPEHGRRAGVPVTAIGGVAGSILLVIVGGIVVAL--RRRRHTF 385

RESULT 3

US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20

Query Match 27.1%; Score 544; DB 4; Length 518;
Best Local Similarity 33.4%; Pred. No. 9.6e-45;
Matches 119; Conservative 68; Mismatches 129; Indels 40; Gaps 8;

QY 14 GKNVSLKCLIE---VNETITQISWEKHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPMSGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLELEDEGVYICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWE-----GDLGEMESTTTSFPNETATIIISQYKL 176
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEARVPDGSCT-----PMAFVTVISRYRL 214
QY 177 FPTRPARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLKCN 236
Db 215 VPSREAHQQSLACIVNYHM--DRFKESLTINVQYEPEVTIEGFDGNWYQLQMDVKLTCKA 272
QY 237 DANPPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVI 296
Db 273 DANPATEYHWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332
QY 297 YISDVPEFKQTS-----SIAVAGAVIGAVLALFIILAFVTVLLTPRKKRPSY 342
Db 333 NITEFPYTPSPPEHGRRAGVPVTAIGGVAGSILLVIVGGIVVAL--RRRRHTF 386

RESULT 4

US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITEBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 12.5439 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-31_COPY_58_437
Perfect score: 2009
Sequence: 1 GPIIIEPHTAVMGKNVSLK.....ERSPPLPQKDLFQVCVHEYT 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	578	28.8	458	4	US-09-435-956A-1 Sequence 1, Appli
2	566.5	28.2	517	4	US-09-723-368-4 Sequence 4, Appli
3	544	27.1	518	4	US-09-919-172-20 Sequence 20, Appl
4	427.5	21.3	479	4	US-09-723-368-2 Sequence 2, Appli
5	390	19.4	408	4	US-09-724-864-62 Sequence 62, Appl
6	283	14.1	440	4	US-09-866-028-61 Sequence 61, Appl
7	283	14.1	442	4	US-09-778-510-20 Sequence 20, Appl
8	283	14.1	442	4	US-09-930-803-1 Sequence 1, Appli
9	279	13.9	423	4	US-09-778-510-22 Sequence 22, Appl
10	248.5	12.4	398	4	US-09-778-510-4 Sequence 4, Appli
11	238.5	11.9	398	4	US-09-778-510-6 Sequence 6, Appli
12	238.5	11.9	398	4	US-09-907-794A-84 Sequence 84, Appl
13	238.5	11.9	398	4	US-09-905-125A-84 Sequence 84, Appl
14	238.5	11.9	398	4	US-09-902-775A-84 Sequence 84, Appl
15	238.5	11.9	432	4	US-09-778-510-2 Sequence 2, Appli
16	237	11.8	421	2	US-08-659-984A-1 Sequence 1, Appli
17	237	11.8	421	3	US-08-660-531-1 Sequence 1, Appli
18	237	11.8	444	2	US-08-659-984A-5 Sequence 5, Appli
19	237	11.8	444	3	US-08-660-531-5 Sequence 5, Appli
20	190.5	9.5	227	4	US-09-205-258-947 Sequence 947, App
21	188.5	9.4	1101	3	US-08-986-485-2 Sequence 2, Appli
22	187.5	9.3	274	4	US-09-570-367C-19 Sequence 19, Appl
23	187.5	9.3	274	4	US-09-915-524-19 Sequence 19, Appl
24	170.5	8.5	387	4	US-09-175-928-2 Sequence 2, Appli
25	165.5	8.2	467	3	US-09-046-736-2 Sequence 2, Appli
26	163.5	8.1	1091	3	US-08-986-485-5 Sequence 5, Appli
27	163	8.1	365	3	US-08-928-383B-23 Sequence 23, Appl

28	163	8.1	365	3	US-08-928-383B-24	Sequence 24, Appl
29	162.5	8.1	278	4	US-09-570-367C-2	Sequence 2, Appli
30	162.5	8.1	278	4	US-09-915-524-2	Sequence 2, Appli
31	162	8.1	365	2	US-08-979-424-3	Sequence 3, Appli
32	162	8.1	365	3	US-08-928-383B-2	Sequence 2, Appli
33	162	8.1	365	3	US-09-272-496-2	Sequence 2, Appli
34	161	8.0	365	3	US-08-928-383B-26	Sequence 26, Appl
35	160.5	8.0	642	1	US-08-217-299-1	Sequence 1, Appli
36	160.5	8.0	698	2	US-08-602-725-36	Sequence 36, Appl
37	160.5	8.0	734	2	US-08-389-459A-17	Sequence 17, Appl
38	160.5	8.0	734	3	US-08-987-867A-17	Sequence 17, Appl
39	159.5	7.9	278	4	US-09-570-367C-21	Sequence 21, Appl
40	159.5	7.9	278	4	US-09-915-524-21	Sequence 21, Appl
41	154	7.7	477	2	US-08-432-016-3	Sequence 3, Appli
42	154	7.7	477	2	US-08-684-594-3	Sequence 3, Appli
43	151.5	7.5	1059	4	US-09-907-794A-290	Sequence 290, App
44	151.5	7.5	1059	4	US-09-905-125A-290	Sequence 290, App
45	151.5	7.5	1059	4	US-09-902-775A-290	Sequence 290, App

ALIGNMENTS

RESULT 1
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: Higr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 28.8%; Score 578; DB 4; Length 458;
Best Local Similarity 35.5%; Pred. No. 3.6e-48;
Matches 130; Conservative 65; Mismatches 157; Indels 14; Gaps 7;

QY	14	GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS	70
Db	44	GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS	103
QY	71	INDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLDG---	127
Db	104	FTDGTIRLSRLEDEGVYICGFATPPTGNRESQNLTVMAKPT-NWIEGTQAVLRAKKG	162
QY	128	-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLPPTRFARGR	185
Db	163	QDDKVLVATCTSANGKPPSVSWETRLKGEABYQEI RNPNGT VTVISRYRLVPSREAHQQ	222
QY	186	RITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVLNLCNADANPPPFKS	245
Db	223	SLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFGDNWYLRQMDVVKLTCKADANPPATEY	280
QY	246	VWSRLDQWPDGLLASDNTLHFVHPLTFNFYSGVYICKVTNSLQGRSDQKVIYISDVPFKQ	305

Qy

324 IIAFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLPQ 373
 ::: : |:: | | : | | : | | : | | :

Db

411 LVSVLAGIFCYRRRTFRGYFAK-----NYIPSDMKES---QIDVLQ 452

```

RESULT 12
US-09-972-268-4
; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from human
; OTHER INFORMATION: n human Nectin-3 alpha
US-09-972-268-4

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Query Match	80.3%;	Score 1612.5;	DB 10;	Length 549;
Best Local Similarity	76.5%;	Pred. No. 7e-134;		
Matches 315;	Conservative 16;	Mismatches 32;	Indels 49;	Gaps 4;

Qy	1	GPII	VEPHVTAVGKNVSLKCLIEVN	ETITQISWEKIHGKSSQTVAVHH	PQYGF	SVQGEY	60			
Db	58	GPII	VEPHVTAVGKNVSLKCLIEVN	ETITQISWEKIHGKSSQTVAVHH	PQYGF	SVQGEY	117			
Qy	61	QGRV	LFKNYSLNDA	ITILHNI	GFSDSGKYICKAVT	FPLGNAQS	TTVTVLVEPTVSLIKG	120		
Db	118	QGRV	LFKNYSLNDA	ITILHNI	GFSDSGKYICKAVT	FPLGNAQS	TTVTVLVEPTVSLIKG	177		
Qy	121	PD	SLIDGGNETVAA	ICIAATGKPV	AHIDWEGDLGEMEST	TTTSPNETAT	IIISQYKLFPTR	180		
Db	178	PD	SLIDGGNETVAA	ICIAATGKPV	AHIDWEGDLGEMEST	TTTSPNETAT	IIISQYKLFPTR	237		
Qy	181	FARG	RRITCVV	KHPALEKDIR	YSFILDIQYAPE	SVVTGYDGNWFVGR	KGVNLKCNADANP	240		
Db	238	FARG	RRITCVV	KHPALEKDIR	YSFILDIQYAPE	SVVTGYDGNWFVGR	KGVNLKCNADANP	297		
Qy	241	PP	FKSVWSRLDG	OWPDG	LLASDNTLHFVH	PLTFNYS	SGVYICKVTNSLCORS	DDQKVIYISD	300	
Db	298	PP	FKSVWSRLDG	OWPDG	LLASDNTLHFVH	PLTFNYS	SGVYICKVTNSLCORS	DDQKVIYISD	357	
Qy	301	VP	-----	-----	-----	FKQTS	STIAVAGAVIGAVL	ALF	323	
Db	358	PP	TTTTLQPT	IQWHPSTADIED	LATEPKKLPP	PLSTLATIKDD	TTATIIASVVG	GALFIV	417	
Qy	324	II	AFVTVLLTP	RKK--RPS	YLDKVIDLPP	THKPP	PPPLYEERS	PPLPQ	KDLFQ	373
Db	418	LVS	VLAGIFCYRR	RRRTFRG	YFAK-----	NYI	PPSDMOKES	----	QIDVLQ	459

RESULT 13
US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.

```

; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-972-268-6

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Query Match	80.3%	Score 1612.5;	DB 10;	Length 549;
Best Local Similarity	76.5%;	Pred. No. 7e-134;		
Matches 315: Conservative	16;	Mismatches 32;	Indels 49;	Gaps 4

QY	1	GPIIVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY	60
DB	58	GPIIVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY	117
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVS LIKG	120
DB	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVS LIKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISOYKLFPTR	180
DB	178	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISOYKLFPTR	237
QY	181	FARGRRITCVVKHPALEKDRIYSFILDIQYAPEVSVTGYDGNWFVGPKGVNLKCNADANP	240
DB	238	FARGRRITCVVKHPALEKDRIYSFILDIQYAPEVSVTGYDGNWFVGPKGVNLKCNADANP	297
QY	241	PPFKSVWSRLDGWPDDLASDNLT LHFVHPLTFENYSGVI CKVTNSLGORS DQKVIYISD	300
DB	298	PPFKSVWSRLDGWPDDLASDNLT LHFVHPLTFENYSGVI CKVTNSLGORS DQKVIYISD	357
QY	301	VP-----FXQTSSIAVAGAVIGAVLALF	323
DB	358	PPTTTTLQPTIQMHPSTADIEDLATEPKLPFLPLSTLATIKDDTIATIIASVVGGLFIV	417
QY	324	IIAIFVTVLTPRK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ	373
DB	418	LVSVLAGFCYRRRTFRGDYFAK-----NYIPPSDMOKES----OIDVLO	459

RESULT 14
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45


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; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

Query Match      81.4%; Score 1636; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 3.6e-136;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db      58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY      61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db      118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY      121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db      178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237

QY      181 FARRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db      238 FARRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297

QY      241 PPKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db      298 PPKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

QY      301 VPFKQTSS 308
Db      358 VPFKQTSS 365

RESULT 10
US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match      81.4%; Score 1636; DB 10; Length 595;
Best Local Similarity 100.0%; Pred. No. 6.5e-136;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db      58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
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QY      61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db      118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY      121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db      178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237

QY      181 FARRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db      238 FARRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297

QY      241 PPKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db      298 PPKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

QY      301 VPFKQTSS 308
Db      358 VPFKQTSS 365

RESULT 11
US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match      80.3%; Score 1612.5; DB 10; Length 542;
Best Local Similarity 76.5%; Pred. No. 6.9e-134;
Matches 315; Conservative 16; Mismatches 32; Indels 49; Gaps 4;
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QY      1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db      51 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 110

QY      61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db      111 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 170

QY      121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db      171 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 230

QY      181 FARRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db      231 FARRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 290

QY      241 PPKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db      291 PPKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 350

QY      301 VP-----
Db      351 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFLPLSTLATIKDDTIATIIASVWGALFIV 410
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Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
Qy 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
Qy 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
Qy 361 ERSPLPQKDLFQVCVH 377
Db 418 ERIPSLPQKDLGQTEH 434

RESULT 7

US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshimi TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-6

Query Match 93.6%; Score 1880; DB 10; Length 438;
Best Local Similarity 94.9%; Pred. No. 1.le-157;
Matches 352; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVEY 60
Db 58 GSIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSTQTAVVHHPQYGFSGVDY 117
Qy 61 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKG 177
Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAVCVAATGKPVQAIDWEGDLGEMESTTSPNETATIVSQYKLPFTR 237
Qy 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
Qy 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
Qy 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
Qy 361 ERSPLPQKDL 371
Db 418 ERIPSLPQKDL 428

RESULT 8

US-09-972-268-19
; Sequence 19, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 438
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-19

Query Match 93.6%; Score 1880; DB 10; Length 438;
Best Local Similarity 94.9%; Pred. No. 1.le-157;
Matches 352; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVEY 60
Db 58 GSIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSTQTAVVHHPQYGFSGVDY 117
Qy 61 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKG 177
Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAVCVAATGKPVQAIDWEGDLGEMESTTSPNETATIVSQYKLPFTR 237
Qy 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
Qy 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
Qy 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
Qy 361 ERSPLPQKDL 371
Db 418 ERIPSLPQKDL 428

RESULT 9

US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKOLFQVCVHEYT 380
Db 418 ERSPPLPQKOLFQVCVHEYT 437

RESULT 2
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

Query Match 97.9%; Score 1967; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 2.7e-165;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 52 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 111
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEPTVSLIKG 120
Db 112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEPTVSLIKG 171
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 231
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 232 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 291
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 292 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 351
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 352 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 411
QY 361 ERSPPLPQKOLFQ 373
| | | | |

Db 412 ERSPPLPQKDLFQ 424
RESULT 3
US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest ar
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10

Query Match 97.9%; Score 1967; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 2.7e-165;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKDLFQ 373
Db 418 ERSPPLPQKDLFQ 430

RESULT 4
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 31.7579 Seconds
(without alignments)
3146.189 Million cell updates/sec

Title: US-09-972-268-31_COPY_58_437
Perfect score: 2009
Sequence: 1 GPIIVEPHVTAVWGKNVSLK.....ERSPPLPKDLFQVCVHEYT 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	2009	100.0	437	10	US-09-972-268-31
2	1967	97.9	504	10	US-09-972-268-8
3	1967	97.9	510	10	US-09-972-268-10
4	1967	97.9	510	10	US-09-972-268-12
5	1881	93.6	510	10	US-09-959-845-4
6	1881	93.6	510	10	US-09-972-268-18
7	1880	93.6	438	10	US-09-959-845-6
8	1880	93.6	438	10	US-09-972-268-19
9	1636	81.4	387	10	US-09-972-268-16
10	1636	81.4	595	10	US-09-972-268-14
11	1612.5	80.3	542	10	US-09-972-268-2
12	1612.5	80.3	549	10	US-09-972-268-4
13	1612.5	80.3	549	10	US-09-972-268-6
14	1612.5	80.3	549	14	US-10-161-572-45
15	1603	79.8	634	10	US-09-972-268-13

16	1602	79.7	426	10	US-09-972-268-15	Sequence 15, Appl
17	1576	78.4	549	10	US-09-959-845-2	Sequence 2, Appl
18	1576	78.4	549	10	US-09-972-268-17	Sequence 17, Appl
19	581	28.9	458	10	US-09-972-268-21	Sequence 21, Appl
20	566.5	28.2	514	14	US-10-161-572-60	Sequence 60, Appl
21	566.5	28.2	517	10	US-09-972-268-20	Sequence 20, Appl
22	544	27.1	518	9	US-09-919-172-20	Sequence 20, Appl
23	502	25.0	479	10	US-09-766-511B-35	Sequence 35, Appl
24	502	25.0	497	10	US-09-972-268-37	Sequence 37, Appl
25	502	25.0	510	10	US-09-766-511B-33	Sequence 33, Appl
26	502	25.0	510	12	US-10-058-270A-54	Sequence 54, Appl
27	502	25.0	510	14	US-10-161-572-55	Sequence 55, Appl
28	502	25.0	510	14	US-10-241-220-94	Sequence 94, Appl
29	502	25.0	510	15	US-10-295-027-66	Sequence 66, Appl
30	502	25.0	510	15	US-10-173-999-76	Sequence 76, Appl
31	500.5	24.9	498	10	US-09-972-268-39	Sequence 39, Appl
32	500.5	24.9	511	10	US-09-972-268-34	Sequence 34, Appl
33	500	24.9	510	10	US-09-972-268-24	Sequence 24, Appl
34	500	24.9	510	14	US-10-161-572-54	Sequence 54, Appl
35	470.5	23.4	580	10	US-09-972-268-36	Sequence 36, Appl
36	469.5	23.4	314	10	US-09-766-511B-36	Sequence 36, Appl
37	459	22.8	538	10	US-09-972-268-23	Sequence 23, Appl
38	459	22.8	538	10	US-09-984-130-138	Sequence 138, App
39	459	22.8	538	10	US-09-836-353A-138	Sequence 138, App
40	459	22.8	538	14	US-10-161-572-61	Sequence 61, Appl
41	459	22.8	538	15	US-10-411-010-17	Sequence 17, Appl
42	434.5	21.6	458	12	US-10-296-115-1150	Sequence 1150, Ap
43	427.5	21.3	479	10	US-09-972-268-22	Sequence 22, Appl
44	427.5	21.3	479	14	US-10-161-572-62	Sequence 62, Appl
45	425.5	21.2	522	15	US-10-264-049-2969	Sequence 2969, Ap

ALIGNMENTS

RESULT 1
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match 100.0%; Score 2009; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.3e-169;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	60
Db	58	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	117
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTPLGNAQSSTTVTLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTPLGNAQSSTTVTLVEPTVSLIKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR	180

FT Modified-site 83 /note= "N-glycosylated"
FT Modified-site 125 /note= "N-glycosylated"
FT Modified-site 186 /note= "N-glycosylated"
FT Domain 189. .250 /note= "Extracellular Ig domain"
FT Modified-site 222 /note= "N-glycosylated"
FT Domain 287. .342 /note= "Extracellular Ig domain"
FT Modified-site 331 /note= "N-glycosylated"
FT Domain 405. .424 /note= "Transmembrane domain"
FT Domain 425. .549 /note= "C-terminal domain"
XX
PN WO200228902-A2.
XX PD 11-APR-2002.
XX PF 05-OCT-2001; 2001WO-US031392.
XX PR 05-OCT-2000; 2000US-0238557P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37442.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 89-91; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha DNA.
XX
SQ Sequence 549 AA;

Query Match 80.3%; Score 1612.5; DB 5; Length 549;
Best Local Similarity 76.5%; Pred. No. 2e-126;
Matches 315; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
DB 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
|||||

Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANP 297
QY 241 PPEKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 300
Db 298 PPEKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 357
QY 301 VP-----FKQTSSIAVAGAVIGAVLALF 323
Db 358 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKODTIATIASVVGALFIV 417
QY 324 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPLYEERSPPLPQKDLFQ 373
Db 418 LVSVLGIFCYRRRTFRGDYFAK-----NYIPPSDMOKES-----QIDVLQ 459

RESULT 13
AAE23282
ID AAE23282 standard; protein; 549 AA.
XX
AC AAE23282;
XX
DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin 3alpha fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
KW chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .7 /note= "Mouse nectin-3 protein"
FT Region 8. .549 /note= "Human nectin-3alpha protein"
FT
FT WO200228902-A2.
XX
PN 11-APR-2002.
XX
PD 05-OCT-2001; 2001WO-US031392.
XX
PF 05-OCT-2000; 2000US-0238557P.
XX
PR (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37441.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 80-82; 141pp; English.
XX

FH	Key	Location/Qualifiers	
FT	Region	1. .365	
FT		/note= "Human nectin-3alpha protein"	
FT	Region	366. .381	
FT		/note= "FLAG peptide"	
FT	Region	382. .387	
FT		/note= "PolyHis tag"	
XX			
XX			
PN	WO200228902-A2.		
XX			
XX			
PD	11-APR-2002.		
XX			
PF	05-OCT-2001; 2001WO-US031392.		
XX			
PR	05-OCT-2000; 2000US-0238557P.		
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
PI	Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;		
XX			
XX	WPI; 2002-426103/45.		
XX			
PT	Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,		
PT	useful for treating or preventing heart failure, malaria,		
PT	glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,		
PT	sepsis, stroke.		
XX			
PS	Claim 9; Page 105-107; 141pp; English.		
XX			
CC	The invention relates to a substantially purified nectin3alpha, beta,		
CC	gamma and nectin-4 polypeptides and their corresponding polynucleotides.		
CC	Nectin DNA and protein are useful for treating a disease associated with		
CC	cell adhesion activity, adherens junction formation activity, epithelial		
CC	or endothelial barrier function activity, endothelial proliferation or		
CC	migration activity, viral polypeptide binding activity. The epithelial or		
CC	endothelial barrier function disorder which is treated by the above		
CC	mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,		
CC	asthma, allergy, allograft rejection, metastasis of cancer cells,		
CC	paracellular transport disorders such as magnesium transport defects in		
CC	the kidney or inflammatory bowel disease. Nectin DNA is also useful for		
CC	inhibiting angiogenesis in a mammal and treating endothelial migration,		
CC	proliferation or angiogenic condition of a tissue or a subject, such as		
CC	ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,		
CC	stroke, restenosis, tumour growth and treating herpesvirus infection.		
CC	Nectin is also useful for modulating proliferation or migration of an		
CC	endothelial cell, an epithelial cell or a smooth muscle cell (vascular		
CC	smooth muscle cell). The present sequence is human nectin-3beta-		
CC	FLAGpolyHis fusion protein		
XX			
SQ	Sequence 387 AA;		
Query Match			
Best Local Similarity 81.4%; Score 1636; DB 5; Length 387;			
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60	
Db	58	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117	
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120	
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177	
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGMESTTTSFPNETATIIISQYKLFPTTR 180	
Db	178	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGMESTTTSFPNETATIIISQYKLFPTTR 237	
QY	181	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240	
Db	238	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297	
QY	241	PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300	

Db	298	PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357	
QY	301	VPFKQTSS 308	
Db	358	VPFKQTSS 365	
RESULT 10			
AAE23288			
ID	AAE23288	standard; protein; 595 AA.	
XX			
AC	AAE23288;		
XX			
DT	27-AUG-2002	(first entry)	
XX			
DE	Human nectin-3beta-IgG1Fc region fusion protein.		
XX			
KW	Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;		
KW	paracellular transport disorder; kidney; diabetic retinopathy; allergy;		
KW	allograft rejection; metastasis; restenosis; inflammatory bowel disease;		
KW	oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;		
KW	stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;		
KW	cancer; asthma.		
XX			
OS	Homo sapiens.		
OS	Unidentified.		
OS	Chimeric.		
XX			
PN	WO200228902-A2.		
XX			
PD	11-APR-2002.		
XX			
PF	05-OCT-2001; 2001WO-US031392.		
XX			
PR	05-OCT-2000; 2000US-0238557P.		
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
PI	Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;		
XX			
DR	WPI; 2002-426103/45.		
XX			
PT	Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,		
PT	useful for treating or preventing heart failure, malaria,		
PT	glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,		
PT	sepsis, stroke.		
XX			
PS	Claim 9; Page 102-104; 141pp; English.		
XX			
CC	The invention relates to a substantially purified nectin3alpha, beta,		
CC	gamma and nectin-4 polypeptides and their corresponding polynucleotides.		
CC	Nectin DNA and protein are useful for treating a disease associated with		
CC	cell adhesion activity, adherens junction formation activity, epithelial		
CC	or endothelial barrier function activity, endothelial proliferation or		
CC	migration activity, viral polypeptide binding activity. The epithelial or		
CC	endothelial barrier function disorder which is treated by the above		
CC	mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,		
CC	asthma, allergy, allograft rejection, metastasis of cancer cells,		
CC	paracellular transport disorders such as magnesium transport defects in		
CC	the kidney or inflammatory bowel disease. Nectin DNA is also useful for		
CC	inhibiting angiogenesis in a mammal and treating endothelial migration,		
CC	proliferation or angiogenic condition of a tissue or a subject, such as		
CC	ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,		
CC	stroke, restenosis, tumour growth and treating herpesvirus infection.		
CC	Nectin is also useful for modulating proliferation or migration of an		
CC	endothelial cell, an epithelial cell or a smooth muscle cell (vascular		
CC	smooth muscle cell). The present sequence is human nectin-3beta-		
CC	FLAGpolyHis fusion protein		
XX			
SQ	Sequence 595 AA;		
Query Match			
Best Local Similarity 81.4%; Score 1636; DB 5; Length 595;			
Best Local Similarity 100.0%; Pred. No. 2.4e-128;			

Query Match 93.6%; Score 1880; DB 4; Length 438;
Best Local Similarity 94.9%; Pred. No. 5.5e-149;
Matches 352; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSQTVAVHHPOYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSQTVAVHHPOYGFVSQGDY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPPTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPPTR 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297

QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357

QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPPVE 417

QY 361 ERSPPLPQKDL 371
Db 418 ERIPSLPQKDL 428

RESULT 8
AAE23293
ID AAE23293 standard; protein; 438 AA.
XX
AC AAE23293;
XX
DT 27-AUG-2002 (first entry)
DE Mouse nectin-3gamma protein.
XX
KW Mouse; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma.
XX
OS Mus musculus.
XX
PN WO200228902-A2.
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Disclosure; Page 111-112; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,

CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is mouse nectin-3gamma protein
XX
SQ Sequence 438 AA;

Query Match 93.6%; Score 1880; DB 5; Length 438;
Best Local Similarity 94.9%; Pred. No. 5.5e-149;
Matches 352; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSQTVAVHHPOYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSQTVAVHHPOYGFVSQGDY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPPTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPPTR 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297

QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357

QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPPVE 417

QY 361 ERSPPLPQKDL 371
Db 418 ERIPSLPQKDL 428

RESULT 9
AAE23290
ID AAE23290 standard; protein; 387 AA.
XX
AC AAE23290;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta-FLAGpolyHis fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX

XX AAE23285;
AC
XX
DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX Mouse nectin-3-human nectin-3beta fusion protein.
DE
XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
OS
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .6
FT /note= "Mouse nectin-3 pprotein"
FT Region 7. .510
FT /note= "Human nectin-3beta protein"
XX
PN WO200228902-A2.
XX
XX 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37444.
DR
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 94-95; 14lpp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 510 AA;

Query Match 97.9%; Score 1967; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 3.4e-156;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTVWGKNSVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
DB 58 GPIIIVPHVTVWGKNSVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
DB 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIIISQYKLPFTR 180
DB 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIIISQYKLPFTR 237
QY 181 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANP 240
DB 238 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANP 297
QY 241 PPFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSDQKVIYISD 300
DB 298 PPFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
DB 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPPLPQKDLFQ 373
DB 418 ERSPPPLPQKDLFQ 430

RESULT 4
ID AAE23286 standard; protein; 510 AA.
XX
AC AAE23286;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 73
FT Domain /note= "N-glycosylated"
FT 74. .152
FT /note= "Extracellular Ig domain"
FT Modified-site 83
FT /note= "N-glycosylated"
FT Modified-site 125
FT /note= "N-glycosylated"
FT Modified-site 186
FT /note= "N-glycosylated"
FT Domain 189. .250
FT /note= "Extracellular Ig domain"
FT Modified-site 222
FT /note= "N-glycosylated"
FT Domain 287. .342
FT /note= "Extracellular Ig domain"
FT Modified-site 331
FT /note= "N-glycosylated"
FT Domain 386. .510
FT /note= "Intracellular C-terminal domain"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.

CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3gamma protein.
CC Human nectin-3gamma gene is located on chromosome 3
XX
SQ Sequence 437 AA;

Query Match 100.0%; Score 2009; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 8.3e-160;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKDLFQVCVHEYT 380
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
418 ERSPPLPQKDLFQVCVHEYT 437

RESULT 2
AAE23284
ID AAE23284 standard; protein; 504 AA.
XX
AC AAE23284;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3beta protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX

PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37443.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 89-91; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX
SQ Sequence 504 AA;

Query Match 97.9%; Score 1967; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 3.3e-156;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
52 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 111
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 231
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
232 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 291
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 300
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
292 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 351
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
352 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 411
QY 361 ERSPPLPQKDLFQ 373
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
412 ERSPPLPQKDLFQ 424

RESULT 3
AAE23285
ID AAE23285 standard; protein; 510 AA.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 45.8947 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-31_COPY_58_437
Perfect score: 2009
Sequence: 1 GPIIVEPHVTAVWGNVSLK.....ERSPPLPQKDLFQVCVHEYT 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2009	100.0	437	5	AAE23299	Aae23299 Human nec
2	1967	97.9	504	5	AAE23284	Aae23284 Human del
3	1967	97.9	510	5	AAE23285	Aae23285 Mouse nec
4	1967	97.9	510	5	AAE23286	Aae23286 Human nec
5	1881	93.6	510	4	AAG63983	Aag63983 Amino aci
6	1881	93.6	510	5	AAE23292	Aae23292 Mouse nec
7	1880	93.6	438	4	AAG63984	Aag63984 Amino aci
8	1880	93.6	438	5	AAE23293	Aae23293 Mouse nec
9	1636	81.4	387	5	AAE23290	Aae23290 Human nec
10	1636	81.4	595	5	AAE23288	Aae23288 Human nec
11	1612.5	80.3	542	5	AAE23281	Aae23281 Human del
12	1612.5	80.3	549	5	AAE23283	Aae23283 Human nec
13	1612.5	80.3	549	5	AAE23282	Aae23282 Mouse nec
14	1612.5	80.3	549	6	ABJ20222	Abj20222 Human IG
15	1612.5	80.3	555	4	AAM39143	Aam39143 Human pol
16	1603	79.8	634	5	AAE23287	Aae23287 Human nec
17	1602	79.7	426	5	AAE23289	Aae23289 Human nec
18	1576	78.4	549	4	AAG63982	Aag63982 Amino aci
19	1576	78.4	549	4	AAG63985	Aag63985 Amino aci
20	1576	78.4	549	5	AAE23291	Aae23291 Mouse nec
21	1534.5	76.4	559	4	AAM40929	Aam40929 Human pol
22	1218	60.6	267	4	AAM93536	Aam93536 Human pol
23	581	28.9	458	5	AAE23295	Aae23295 Human nec
24	566.5	28.2	514	6	ABJ20237	Abj20237 Human IG
25	566.5	28.2	517	3	AAY32390	Aay32390 Herpesvir

26	566.5	28.2	517	5	AAE23294	Aae23294 Human nec
27	544	27.1	518	5	ABG77170	Abg77170 Prostate
28	502	25.0	497	5	AAE23303	Aae23303 Human nec
29	502	25.0	510	4	AAB93365	Aab93365 Human pro
30	502	25.0	510	4	AAU00471	Aau00471 Human TAN
31	502	25.0	510	5	ABJ05562	Abj05562 Breast ca
32	502	25.0	510	6	ABJ20232	Abj20232 Human IG
33	502	25.0	510	6	ABR48229	Abr48229 Human bla
34	502	25.0	510	6	ABU56613	Abu56613 Lung canc
35	502	25.0	510	6	ABP97212	Abp97212 Tumour-as
36	502	25.0	510	7	ADB80512	Adb80512 Ovarian c
37	500.5	24.9	498	5	AAE23305	Aae23305 Human nec
38	500.5	24.9	511	5	AAE23301	Aae23301 Human nec
39	500	24.9	510	5	AAE23300	Aae23300 Human nec
40	500	24.9	510	6	ABJ20231	Abj20231 Human IG
41	470.5	23.4	580	5	AAE23302	Aae23302 Human nec
42	459	22.8	538	5	AAE23297	Aae23297 Human nec
43	459	22.8	538	6	ABJ20238	Abj20238 Human IG
44	459	22.8	538	8	ADE86687	Ade86687 Human pol
45	434.5	21.6	458	4	AAM25635	Aam25635 Human pro

ALIGNMENTS

RESULT 1
AAE23299
ID AAE23299 standard; protein; 437 AA.
XX
AC AAE23299;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3gamma protein.
XX
KW Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37450.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 125-126; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

Db 40 VTIVLGGQDAKLPCFYRGDSGEVQGVAVARVDAGEGAQELALLHSKYGLHVSAPAYEGRVE 99
Qy 66 FKNYSLN--DATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPD 123
Db 100 QPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQARLRLRVLPPLSLNPGP-A 158
Qy 124 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIIISQYKLFPTREFAR 183
Db 159 LEEGQGLTLAASC-TAEGSPAPSVTWDTEVKGTSSRFKHSRAAVTSEFHLVPSRMN 217
Qy 184 GRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTYDGN--WFGVGRKGVNLKCNADANPP 241
Db 218 GQPLTCVVSHPGLLQDQRIITHLVHSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPP 277
Qy 242 PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDV 301
Db 278 PSYN-WTRLDGPLSGVRVDGDTLGF-PPLTTEHSGIYVCHVSNEFSSRDSQVTVVDVLDP 335
Qy 302 ---PFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRK 339
Db 336 QEDSGKQVDLVASVVVGVIAALLFCLLVVVVLMRSYHR 376

RESULT 14
Q9DBP8 PRELIMINARY; PRT; 483 AA.
AC Q9DBP8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 1200017F15RIK protein.
GN PVRL4 OR 1200017F15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK004821; BAB23592.1; -.
DR MGD; MGI:1918990; Pvrl4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 483 AA; 53030 MW; F8F0466C000852E8 CRC64;

Query Match 24.4%; Score 489.5; DB 11; Length 483;
Best Local Similarity 33.4%; Pred. No. 4e-33;

Matches 116; Conservative 63; Mismatches 141; Indels 27; Gaps 10;
Qy 9 VTAVWGKNVSLKCLI--EVNETITQISWEKIH-GKSSQTVAVHHPOYGFVSQGEYQGRV- 64
Db 39 VTIVLGGQDAKLPCFYRGDPDEQVGVAVARVDPNEGIRELALLHSKYGLHVNPAVEDRVE 98
Qy 65 -----LFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVS 116
Db 99 QPPPRDPL-----DGSVLLRNAVQADEGEYECRVSTFPAGSFQARMRLRLVLPPLPS 151
Qy 117 LIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIIISQYKL 176
Db 152 LNPGP-PLIEGQGLTLAASC-TAEGSPAPSVTWDTEVKGTQSSRSFTHPRSAAVTSEFHL 209
Qy 177 FPTRFARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTYDGN--WFGVGRKGVNLKC 234
Db 210 VPSRSMNGQPLTCVVSHPGLLQDRIITHLQVAFLEASVRGLEDQNLWQVREGATLKC 269
Qy 235 NADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQK 294
Db 270 LSEGQPPPP-KYNWTRLDGPLSGVRVKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQV 327
Qy 295 VIYISDV--PFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRK 339
Db 328 TVEVLDPEDPGKQVDLVASVVIIVGVIAALLFCLLVVVVLMRSYHR 374

RESULT 15
Q8R007 PRELIMINARY; PRT; 508 AA.
AC Q8R007;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Similar to poliovirus receptor-related 4 (Nectin 4).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE=21560925; PubMed=11544254;
RA Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RT "Nectin4/PRR4, a new afadin-associated member of the nectin family
that trans-interacts with nectin1/PRR1 through V domain interaction.";
RL J. Biol. Chem. 276:43205-43215(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024948; AAH24948.1; -.
DR EMBL; AF472510; AAL79833.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 508 AA; 55657 MW; 24DAEBD21F22E376 CRC64;

Query Match 24.4%; Score 489.5; DB 11; Length 508;
Best Local Similarity 33.4%; Pred. No. 4.3e-33;

Matches 116; Conservative 63; Mismatches 141; Indels 27; Gaps 10;

Qy 9 VTAVWGKNVSLKCLI--EVNETITQISWEKIH-GKSSQTVAVHHPOYGFVSQGEYQGRV- 64
Db 39 VTIVLGGQDAKLPCFYRGDPDEQVGVAVARVDPNEGIRELALLHSKYGLHVNPAVEDRVE 98

Db	178	PSSIDGGNETVAAVCVSTGKPVQIDWEGDLGEREFSTISFLNETATIVSQYELFPTR	237
QY	181	FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANP	240
Db	238	FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANP	297
QY	241	PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVNSLQSRSDQKVIYISD	300
Db	298	PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVNSLQSRSDQKVIYISD	357
QY	301	VPEFKQT-----SSIA-----VAGAVIGAVLALF	323
Db	358	PPTTTTLOPTVQWHSSPADVQDIATEHKLPPLSTLATLKDDTIGTIIASVVGGLFLV	417
QY	324	IIAIFVTVLLTPRKKR-----PSYLDKVIDLPPTHK-----PPPLYEERSPP	365
Db	418	LVSILAGVFCYRRRTFRGDYFAKNYPPSPDMQKESQIDVLHQDELDSYDPSVKKENKNP	477
QY	366	---LPQKDLFQ	373
Db	478	VNNLRKDYLE	488
RESULT 6			
Q8NC05	Q8NC05	PRELIMINARY;	PRT; 267 AA.
AC	Q8NC05;		
DT	01-OCT-2002	(TrEMBLrel. 22, Created)	
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Hypothetical protein FLJ90624.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Placenta;		
RA	Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,		
RA	Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,		
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,		
RA	Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,		
RA	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;		
RT	"NEDO human cDNA sequencing project.";		
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AK075105; BAC11404.1; --		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; Ig-like.		
DR	Pfam; PF00047; ig; 1.		
DR	SMART; SM00409; IG; 1.		
DR	PROSITE; PS50835; IG_LIKE; 2.		
KW	Hypothetical protein.		
SQ	SEQUENCE	267 AA; 29253 MW; 4F464A8A1BA0C451	CRC64;
Query Match 60.6%; Score 1218; DB 4; Length 267;			
Best Local Similarity 99.6%; Pred. No. 1.3e-95;			
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;			
QY	1	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY	60
Db	35	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY	94
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120
Db	95	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	154
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR	180
Db	155	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR	214
QY	181	FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGRKGVNLK	233

Db	215	FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFVGKGVNLK	267
RESULT 7			
Q9Y412	Q9Y412	PRELIMINARY;	PRT; 407 AA.
AC	Q9Y412;		
DT	01-NOV-1999	(TrEMBLrel. 12, Created)	
DT	01-NOV-1999	(TrEMBLrel. 12, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Hypothetical protein (Fragment).		
GN	DKFZP566B0846.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Kidney;		
RA	Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;		
RL	Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AL050071; CAB43256.1; --		
DR	PIR; T08732; T08732.		
DR	InterPro; IPR007110; Ig-like.		
DR	PROSITE; PS50835; IG_LIKE; 2.		
KW	Hypothetical protein.		
FT	NON_TER		
SQ	SEQUENCE	407 AA; 45718 MW; 4E6B6C05068D63AC	CRC64;
Query Match 57.7%; Score 1159.5; DB 4; Length 407;			
Best Local Similarity 70.3%; Pred. No. 2.3e-90;			
Matches 230; Conservative 16; Mismatches 32; Indels 49; Gaps 4;			
QY	86	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVA	145
Db	1	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVA	60
QY	146	HIDWEGDLGEMESTTTSFPNETATIISQYKLFPTFRFARGRRITCVVKKHPALEKDIRYSFI	205
Db	61	HIDWEGDLGEMESTTTSFPNETATIISQYKLFPTFRFARGRRITCVVKKHPALEKDIRYSFI	120
QY	206	LDIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANPPPKSVWSRLDGQWPDGGLASDNTL	265
Db	121	LDIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANPPPKSVWSRLDGQWPDGGLASDNTL	180
QY	266	HFVHPLTFNYSGVYICKVNSLQSRSDQKVIYISDVP-----	302
Db	181	HFVHPLTFNYSGVYICKVNSLQSRSDQKVIYISDPTTTTLOPTIQWHPSTADIEDLAT	240
QY	303	-----FKQTSIAVAGAVIGAVLALFIAIFVTVLLTPRKK--RPSYLDKV	346
Db	241	EPKKLPFPLSTLATIKDDTIATIIASVWGGALFVLVSLAGIFCYRRRTFRGDYFAK-	299
QY	347	IDLPPTHKPPPLYEERSPPLPQKDLFQ	373
Db	300	-----NYIPSPDMQKES-----QIDVLQ	317
RESULT 8			
Q9BVA9	Q9BVA9	PRELIMINARY;	PRT; 304 AA.
ID	Q9BVA9;		
AC	Q9BVA9;		
DT	01-JUN-2001	(TrEMBLrel. 17, Created)	
DT	01-JUN-2001	(TrEMBLrel. 17, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Similar to nectin 3, DKFZP566B0846 protein (Fragment).		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Cervix;		

Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357

QY 301 VP-----FKQTSSIAVAGAVIGALF 323

Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIV 417

QY 324 IIAIFVTVLLTPRK--RPSYLDKVIDLPFTHKPPPLYEERSPPLPQKDLFQ 373

Db 418 LVSVLAGIFCYRRRTFRGDYFAK-----NYIPPSDMQKES----QIDVLQ 459

RESULT 4

Q9JLB9 ID Q9JLB9 PRELIMINARY; PRT; 549 AA.

AC Q9JLB9;

DT 01-OCT-2000 (TReMBLrel. 15, Created)

DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Cell adhesion molecule nectin-3 alpha.

GN PVRL3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20209403; PubMed=10744716;

RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,

RA Tachibana K., Mizoguchi A., Takai Y.;

RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules

RT that shows homophilic and heterophilic cell-cell adhesion

RT activities.";

RL J. Biol. Chem. 275:10291-10299(2000).

DR EMBL; AF195833; AAF63685.1; --.

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005913; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;

Query Match 78.4%; Score 1576; DB 11; Length 549;

Best Local Similarity 71.9%; Pred. No. 1.1e-125;

Matches 310; Conservative 25; Mismatches 38; Indels 58; Gaps 5;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180

Db 178 PDSLIDGGNETVAAVCVAATGKPVQIDWEGDLGEMESSTTSFPNETATISQYKLFPTTR 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGNLKNADANP 240

Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGNLKNADANP 297

QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300

Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357

QY 301 VPFKQT-----SSIA-----VAGAVIGAVLALF 323

Db 358 PPTTTTLOPTVQWSSPADVQDIATEHKLPPLSTLATLKDITIGTIIASVVGALFLV 417

QY 324 IIAIFVTVLLTPRKKR-----PSYLDKVIDLPPTHK-----PPPLYEERSPP 365

Db 418 LVSILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSYDPSVKKENKNP 477

QY 366 ---LPQKDLFQ 373

Db 478 VNNLIRKDYLE 488

RESULT 5

Q9D006 ID Q9D006 PRELIMINARY; PRT; 549 AA.

AC Q9D006;

DT 01-JUN-2001 (TReMBLrel. 17, Created)

DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE 2610301B19Rik protein.

GN PVRL3 OR 2610301B19RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK011949; BAB27933.1; --.

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005913; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;

Query Match 76.3%; Score 1532; DB 11; Length 549;

Best Local Similarity 70.1%; Pred. No. 6e-122;

Matches 302; Conservative 28; Mismatches 43; Indels 58; Gaps 5;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180

Qy 1 GPIIVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
Qy 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLKCNADANP 297
Qy 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
Qy 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYE 417
Qy 361 ERSPLPQKDLFQVCVH 377
Db 418 ERIPSLPQKDLGQTEH 434

RESULT 2
Q9JLB7 PRELIMINARY; PRT; 438 AA.
AC Q9JLB7
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 gamma.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195835; AAF63687.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;

Query Match 93.6%; Score 1880; DB 11; Length 438;
Best Local Similarity 94.9%; Pred. No. 9.2e-152;
Matches 352; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
Qy 1 GPIIVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
Qy 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLKCNADANP 297
Qy 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
Qy 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYE 417
Qy 361 ERSPLPQKDL 371
Db 418 ERIPSLPQKDL 428

RESULT 3
Q9NQS3 PRELIMINARY; PRT; 549 AA.
AC Q9NQS3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Reymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;

Query Match 80.3%; Score 1612.5; DB 4; Length 549;
Best Local Similarity 76.5%; Pred. No. 8.2e-129;
Matches 315; Conservative 16; Mismatches 32; Indels 49; Gaps 4;
Qy 1 GPIIVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
Qy 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLKCNADANP 297
Qy 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 30.8619 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-31_COPY_58_437
Perfect score: 2009
Sequence: 1 GPIIIVPHVTAVWGKNVSLK.....ERSPPLPQKDLFQVCVHEYT 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1881	93.6	510	11 Q9JLB8	Q9jlb8 mus musculus
2	1880	93.6	438	11 Q9JLB7	Q9jlb7 mus musculus
3	1612.5	80.3	549	4 Q9NQS3	Q9nqs3 homo sapien
4	1576	78.4	549	11 Q9JLB9	Q9jlb9 mus musculus
5	1532	76.3	549	11 Q9D006	Q9d006 mus musculus
6	1218	60.6	267	4 Q8NC05	Q8nc05 homo sapien
7	1159.5	57.7	407	4 Q9Y412	Q9y412 homo sapien
8	630.5	31.4	304	4 Q9BVA9	Q9bva9 homo sapien
9	534.5	26.6	295	11 Q9ERF5	Q9erf5 mesocricetu
10	528	26.3	298	6 Q9GL74	Q9gl74 cercopithec
11	526.5	26.2	295	6 Q9GL75	Q9gl75 bos taurus
12	502	25.0	510	4 Q96NY8	Q96ny8 homo sapien
13	502	25.0	510	4 Q96K15	Q96k15 homo sapien
14	489.5	24.4	483	11 Q9DBP8	Q9dbp8 mus musculus
15	489.5	24.4	508	11 Q8R007	Q8r007 mus musculus
16	489.5	24.4	508	11 Q8CED8	Q8ced8 mus musculus

17	474.5	23.6	530	11 Q80XJ5	Q80xj5 mus musculu
18	446	22.2	467	11 Q91VT9	Q91vt9 mus musculu
19	446	22.2	467	11 Q8C6F2	Q8c6f2 mus musculu
20	427.5	21.3	449	4 Q9UEI6	Q9uei6 homo sapien
21	400	19.9	412	11 Q9R1E1	Q9rie1 rattus norv
22	398	19.8	417	4 Q96BJ1	Q96bj1 homo sapien
23	395	19.7	412	11 Q63611	Q63611 rattus norv
24	392	19.5	408	11 Q91WP1	Q91wp1 mus musculu
25	390	19.4	403	6 Q8HY15	Q8hy15 lemur catta
26	390	19.4	408	11 Q8K094	Q8k094 mus musculu
27	389	19.4	408	11 Q8BVF6	Q8bvf6 mus musculu
28	388.5	19.3	400	6 Q8HY16	Q8hy16 cebus apell
29	385	19.2	401	6 Q08835	Q08835 cercopithe
30	352	17.5	412	6 Q8HY14	Q8hy14 oryctolagus
31	348	17.3	415	11 Q60977	Q60977 mus musculu
32	289	14.4	417	11 Q7TNL1	Q7tnl1 mus musculu
33	286	14.2	394	13 Q7ZXX1	Q7zxx1 xenopus lae
34	282	14.0	442	4 Q9BY67	Q9by67 homo sapien
35	282	14.0	445	11 Q8K3T6	Q8k3t6 mus musculu
36	279	13.9	445	11 Q8R4L1	Q8r4l1 mus musculu
37	276.5	13.8	443	4 Q8N2F4	Q8n2f4 homo sapien
38	273.5	13.6	456	11 Q8R5M8	Q8r5m8 mus musculu
39	256.5	12.8	333	4 Q86WB8	Q86wb8 homo sapien
40	255	12.7	800	5 Q86LF9	Q86lf9 drosophila
41	255	12.7	801	5 Q86LF8	Q86lf8 drosophila
42	253.5	12.6	336	11 Q9D6E7	Q9d6e7 mus musculu
43	253.5	12.6	336	11 Q80VG4	Q80vg4 mus musculu
44	248.5	12.4	396	11 Q99N28	Q99n28 mus musculu
45	238.5	11.9	398	4 Q8N126	Q8n126 homo sapien

ALIGNMENTS

RESULT 1
Q9JLB8
ID Q9JLB8 PRELIMINARY; PRT; 510 AA.
AC Q9JLB8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 beta.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195834; AAF63686.1; --
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG-LIKE; 3.
SQ SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;

Query Match 93.6%; Score 1881; DB 11; Length 510;
Best Local Similarity 93.6%; Pred. No. 9.4e-152;
Matches 353; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

Db	191	EDEGTWVQVSLHLHFVPTREANGHRLGCCQAAPNTTLQFEGYASLDVKYPPVIVEMNSSVE	250
QY	218	GYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLL---ASDNTLHF-VHPLTF	273
Db	251	AIEGS-----HVSLLCGADSNPPPLLT-WMR-----DGMVLREAVAESLYLDLEEVP	297
QY	274	NYSGVYICKVTNSLGQSRSDQKVIYISDVPFKQT---SSIAVAGAVI	316
Db	298	AEDGIYACLAENAYGQDNRTVELSVMYAPWKPTVNGTVVAVEGETV	343

Search completed: April 12, 2004, 09:39:53
Job time : 7.07283 secs

Schachner M., Bartsch U.;
"Multiple functions of the myelin-associated glycoprotein MAG
(siglec-4a) in formation and maintenance of myelin";
Glia 29:154-165(2000).
[6]
INTERACTION WITH RTN4R.
MEDLINE=22171378; PubMed=12089450;
Liu B.P., Fournier A., GrandPre T., Strittmatter S.M.;
"Myelin-associated glycoprotein as a functional ligand for the Nogo-66
receptor";
Science 297:1190-1193(2002).
-!- FUNCTION: Adhesion molecule in postnatal neural development that
mediates sialic-acid dependent cell-cell interactions between
neuronal and myelinating cells. Preferentially binds to alpha2,3-
linked sialic acid. Isoform L-MAG is critical for the formation of
myelin in the CNS, whereas isoform S-MAG is sufficient to maintain
the integrity of myelin in PNS.
-!- SUBUNIT: Binds to RTN4R.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=L-MAG;
IsoId=P20917-1; Sequence=Displayed;
Name=S-MAG;
IsoId=P20917-2; Sequence=VSP_002527, VSP_002528;
-!- TISSUE SPECIFICITY: Expressed by myelinating glial cells in the
central and peripheral nervous system. Detected in oligodendrocyte
processes before formation of compact myelin. Restricted to the
periaxonal space after myelination. Isoform S-MAG is the
predominant isoform in CNS and PNS of the adult.
-!- DEVELOPMENTAL STAGE: In CNS isoform L-MAG is the major form
synthesized early in development, and it persists as a significant
proportion of the MAG present in the adult. In the PNS isoform L-
MAG is expressed at modest levels during development; it is absent
in the adult.
-!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
(sialic acid binding Ig-like lectin) family.
-!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

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or send an email to license@isb-sib.ch).

EMBL; M31811; AAA39487.1; -
DR EMBL; M74793; AAA91743.1; -
DR EMBL; M74783; AAA91743.1; JOINED.
DR EMBL; M74784; AAA91743.1; JOINED.
DR EMBL; M74785; AAA91743.1; JOINED.
DR EMBL; M74786; AAA91743.1; JOINED.
DR EMBL; M74787; AAA91743.1; JOINED.
DR EMBL; M74788; AAA91743.1; JOINED.
DR EMBL; M74790; AAA91743.1; JOINED.
DR EMBL; M74791; AAA91743.1; JOINED.
DR HSSP; Q62230; IQPP.
DR MGD; MGI:96912; Mag.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Palmitate; Lipoprotein;
KW Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 626 MYELIN-ASSOCIATED GLYCOPROTEIN.
FT DOMAIN 20 516 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 517 536 POTENTIAL.
FT DOMAIN 537 626 CYTOPLASMIC (POTENTIAL).

FT	DOMAIN	22	120	IG-LIKE V-TYPE.
FT	DOMAIN	139	237	IG-LIKE C2-TYPE 1.
FT	DOMAIN	241	325	IG-LIKE C2-TYPE 2.
FT	DOMAIN	327	412	IG-LIKE C2-TYPE 3.
FT	DOMAIN	413	508	IG-LIKE C2-TYPE 4.
FT	DISULFID	37	165	BY SIMILARITY.
FT	DISULFID	42	100	BY SIMILARITY.
FT	DISULFID	159	217	BY SIMILARITY.
FT	DISULFID	261	305	BY SIMILARITY.
FT	DISULFID	347	392	BY SIMILARITY.
FT	DISULFID	421	430	BY SIMILARITY.
FT	DISULFID	432	488	BY SIMILARITY.
FT	CARBOHYD	99	99	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	246	246	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	315	315	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	454	454	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	LIPID	531	531	S-palmitoyl cysteine (By similarity).
FT	VARSPLIC	574	582	EKRLGSERR -> REVSTRDCH (in isoform S-MAG).
FT				/FTId=VSP_002527.
FT	VARSPLIC	583	626	Missing (in isoform S-MAG).
FT				/FTId=VSP_002528.
SQ	SEQUENCE	626 AA; 69259 MW; 9C797BD6B52B6057 CRC64;		
	Query Match	8.8%; Score 177; DB 1; Length 626;		
	Best Local Similarity	24.6%; Pred. No. 2.4e-06;		
	Matches	85; Conservative 50; Mismatches 142; Indels 68; Gaps 18;		
QY		9 VTAVWGKNVSLKCLIEVNETITQISWEKTHGK-----SSQTVAVHPQY 52		
Db		30 ISAFEGTCVSIPCRDFDPD---ELRPVVHGVWYFNSPYPKNYPVVFKSRTQVVHE--- 83		
QY		53 GFSVQGEYQGRV-LFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLG--NAQSSTTVTV 109		
Db		84 -----SFQGRSRLLDGLRNCNTLLSTLSPGLGKYFRG---DLGGYNQYTFSEHSV 134		
QY		110 L-VEPTVSLIKGPDLSLIDGGNETVAICIAATGKPV--AHIDWEGDLGEMESTTTFPNE 166		
Db		135 LDIVNTNIVVPE--VVAGTE-VEVSCMVPDNCPELRPELSWLGHEGLGPTVLRLRE 191		
QY		167 ---TATISQYKLPPTFRFARRITCVVVKHPALEKDIRYSFILDIOYAPEV-----SVTG 218		
Db		192 DEGTWQVSLHVFPTREANGHRLGCAAFPNTTLQFEGYASLDVKYPPVIVEMNSSVEA 251		
QY		219 YDGNWFVGRKGVLKCNADANPPPKSVWSRLDQWPDGLL---ASDNTLHF-VHPLTFN 274		
Db		252 IEGS-----HVSLLCGADSNPPPLLT-WMR-----DGMVLRRAVAKSLYLDLEEVTPG 298		
QY		275 YSGVYICKVTNSLQGRSDQKVIYISDVPFKQT---SSIAVAGAVI 316		
Db		299 EDGVYACLAENAYGQDNRTVELSVMYAPWKPTVNGTVVAVEGETV 343		
	RESULT 15			
	MAG_RAT			
ID	MAG_RAT	STANDARD;	PRT;	626 AA.
AC	P07722; P02685; P07723;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-APR-1988 (Rel. 07, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Myelin-associated glycoprotein precursor (Siglec-4a) (Brain neuron cytoplasmic protein 3).			
GN	MAG.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS L-MAG AND S-MAG).			


```
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 268 278 GELSGVQKMT -> EP (in isoform 2).
FT /FTID=VSP 002613.
FT CONFLICT 11 11 S -> C (IN REF. 3).
FT CONFLICT 46 46 P -> T (IN REF. 1).
SQ SEQUENCE 278 AA; 31264 MW; 38DF327B382CC970 CRC64;

Query Match 9.3%; Score 187.5; DB 1; Length 278;
Best Local Similarity 24.8%; Pred. No. 1.2e-07;
Matches 52; Conservative 36; Mismatches 97; Indels 25; Gaps 4;

QY 18 SLKCLIEVNETITQISWEKIHGKSSQTAVVHPHQYGSVQGEYQGRVLFKNYSINDATIT 77
Db |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
48 SLKCSLQNAQEALIVTWQKKAVSPENMVTFSENHGVVIQPAYKDKINITQLGLQNSTIT 107
QY 78 LHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEPTVSL-IGKPDSLIDGGNETVAAIC 136
Db |||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
108 FWNITLEDGCGYMCLENTFPGFKISGTACLTIVYVQPIVSLHYKFSSEHNLN-----IT 159
QY 137 IAATGKPVAHIDWEGDLGEMESTTT--SFPNETATISQYKLFPTFRFARRRITCVVKHP 194
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
160 CSATARPAPMVFWKVRSGIENSTVTLSPNGTTSVLSILHIKDPKNQVGKEVICQVHL 219
QY 195 ALEKDIRYSFILDIAPEVSVTYGDCGNWF 224
Db | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
220 GTVTDFKQ-----TVNKGYNWF 235
```

RESULT 11

```
PGBM_HUMAN
ID_PGBM_HUMAN STANDARD; PRT; 4391 AA.
AC P98160; Q16287; Q9H3V5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basement membrane heparan sulfate proteoglycan core protein: a
RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Skin;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple
RT domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
RX MEDLINE=20553141; PubMed=11101850;
RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
RA Hentati F., Fontaine B.;
RT "Perlecan, the major proteoglycan of basement membranes, is altered in
RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";
RL Nat. Genet. 26:480-483(2000).

[4]
RN SEQUENCE OF 1016-1470 FROM N.A.
RP TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [5]
RP SEQUENCE OF 890-1396 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to 1p36.1--p35 and identification of
RT a BanHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [6]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
RN [7]
RP CARBOHYDRATE-LINKAGE SITE ASN-2121.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel
CC syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder
CC characterized by permanent myotonia (prolonged failure of muscle
CC relaxation) and skeletal dysplasia, resulting in reduced stature,
CC kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.
CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 3 laminin IV domains.
CC -!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; X62515; CAA44373.1; -.
CC EMBL; M85289; AAA52700.1; -.
CC EMBL; AL445795; CAC18534.1; -.
CC EMBL; M64283; AAA52699.1; -.
CC EMBL; S76436; AAB21121.2; -.
CC EMBL; L22078; -; NOT_ANNOTATED_CDS.
```



```
DR Pfam; PF00047; ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG LIKE; 5.
KW Transmembrane; Immunoglobulin domain; Glycoprotein; Signal; Repeat;
KW Cell adhesion.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 764 IRREGULAR CHIASM C-ROUGHEST PROTEIN.
FT DOMAIN 20 533 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 534 556 POTENTIAL.
FT DOMAIN 557 764 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 123 IG-LIKE C2-TYPE 1.
FT DOMAIN 117 230 IG-LIKE C2-TYPE 2.
FT DOMAIN 245 261 GLY-RICH.
FT DOMAIN 237 343 IG-LIKE C2-TYPE 3.
FT DOMAIN 346 419 IG-LIKE C2-TYPE 4.
FT DOMAIN 430 530 IG-LIKE C2-TYPE 5.
FT DOMAIN 637 660 GLN-RICH (OPA-REPEAT).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 764 AA; 82947 MW; 262225D2B2A1C181 CRC64;

Query Match 11.3%; Score 227; DB 1; Length 764;
Best Local Similarity 24.7%; Pred. No. 3.5e-10;
Matches 89; Conservative 60; Mismatches 142; Indels 70; Gaps 18;

QY 5 VEPH-VTAVMGKNSVLSKCLIEVNETITQISWEKIHGKSSQTAVVHHPPQVSGFVQGEYQGR 63
Db 32 MEPQDQTAVGARVTLPCRV-INKQT-LQWTK-----DDFGLGTSRDLGS- 75

QY 64 VLFKNYSL-----NDATITLHNIGFSDSGKYICKAVTFPLGNAQSST---VTVLVEPT 114
Db 76 --FERYAMVGSDEGDYSLDIYPVMLDDDDARVQCQVSPGEGQPAIRSTFAGLTVLVPPE 133

QY 115 VSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGDLG-----EMESTTSPNETA- 168
Db 134 APKITQGDVIYATADRKVEIECVSVGGKPAEITWIDGLGNVLTNDNIEYTVIPLDQRRF 193

QY 169 TIISQYKLFPTFFARGRRITCVVKHPALEKDIRYSFI-LDIQYAPEVSVT-----GYD 220
Db 194 TAKSVRLTLPKKEHHNTNFSCQAQNTA-DRTYRSAKIRVEVKYAPKVKVNMVMSLPGGAG 252

QY 221 GNWFVGRKG-----VNLKNADANPPFPKSVWSRLDQWPDGLLASDN 263
Db 253 GS--VGGAGGGSVHMSTGSRIVEHSQVRLECRADANPSDVRVWFIND-----EPIIGGQK 306

QY 264 TLHFVHPLTFNYSGVYI-CKVTNSLQSRDQKVYISDVP-FKQTSSIAVAGAVIGAVLA 321
Db 307 TEMVIRNVRKPFHDAIVKCEVQNSVGKSEDSSETLDISYAPSFQRQPSMEAD--VGSVVS 364

QY 322 L 322
Db 365 L 365

RESULT 9
NCM2 MOUSE
ID NCM2_MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (R4B12).
GN NCAM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
```

```
RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
RX MEDLINE=97368238; PubMed=9221781;
RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA Kagamiyama H., Mori K.;
RT "OCAM: A new member of the neural cell adhesion molecule family
RT related to zone-to-zone projection of olfactory and vomeronasal
axons.";
RL J. Neurosci. 17:5830-5842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX MEDLINE=97476194; PubMed=9334170;
RA Alenius M., Bohm S.;
RT "Identification of a novel neural cell adhesion molecule-related gene
RT with a potential role in selective axonal projection.";
RL J. Biol. Chem. 272:26083-26086(1997).
CC -!- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
CC attached to the membrane by a GPI-anchor (short isoform).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O35136-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=O35136-2; Sequence=VSP_002590;
CC -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and
CC vomeronasal neurons in a zone-specific manner.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC -----
DR EMBL; AF001287; AAB69125.1; -
DR EMBL; AF001286; AAB69124.1; -
DR EMBL; AF016619; AAC53375.1; -
DR MGD; MGI:97282; Ncam2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 837 NEURAL CELL ADHESION MOLECULE 2.
FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 698 718 POTENTIAL.
FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 108 IG-LIKE C2-TYPE 1.
FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
FT DOMAIN 482 581 FIBRONECTIN TYPE-III 1.
FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
FT DISULFID 42 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 281 PROBABLE.
FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
```


DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 417 POLIOVIRUS RECEPTOR.
FT DOMAIN 21 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 367 POTENTIAL.
FT DOMAIN 368 417 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 139 IG-LIKE V-TYPE.
FT DOMAIN 145 237 IG-LIKE C2-TYPE 1.
FT DOMAIN 244 328 IG-LIKE C2-TYPE 2.
FT DISULFID 49 123 BY SIMILARITY.
FT DISULFID 166 221 BY SIMILARITY.
FT DISULFID 266 312 BY SIMILARITY.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 386 392 EHASASA -> HHQSCHN (in isoform Delta).
FT VARSPLIC 393 417 /FTid=VSP 002622.
FT VARSPLIC 417 417 Missing (in isoform Delta).
FT SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6E1F CRC64;
SQ SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6E1F CRC64;
Query Match 20.5%; Score 411; DB 1; Length 417;
Best Local Similarity 30.4%; Pred. No. 4.6e-25;
Matches 105; Conservative 64; Mismatches 152; Indels 24; Gaps 11;
QY 1 GPIIVE--PHVTAVGKNVSLKCLIEV--NET-ITQISWEKIHGKSSQTVAVHH---PQ 51
Db 27 GDIIIVQAPTQVPGFLGDSVTLPCYLOVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGN 85
QY 52 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV 111
Db 86 YSEPKRLEFVAARL--GTELRDASLRMFGRLVEDEGNYTCLFVTFPQGSRSVDIWLRLA 143
QY 112 EP--TVSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTS--FPNET 167
Db 144 KPQNTAEVQKVLT---GKVPVVARCVSTGGRPPAHITWHSDLGMPNTSQAPFLSGT 199
QY 168 ATIIISQYKLPFTRFARGRRITCVVKHPALEKDIRYSFLDIQYAPEVSVTGYDGNMFVGR 227
Db 200 VVTISLWILVPSSQVDGKSVTKVEHESFEKPKQLLTNLTVTYYPPEVSVISGVDNNWYLSQ 259
QY 228 KGVNLKCNADANPPPKSVMSRLDGQWPDGGLASDNTLHFVPLTFNYSVGVICKVTNSL 287
Db 260 NEATLTCDARSNPEPTGYNWSTTMGPLPPFAVAQAQL-LIRPVDKPIINTTFCNVTNAL 318
QY 288 GQRSDQKVIYISDVPFKQTSSIA---VAGAVIGAVLALFIIAIFV 329
Db 319 GARQALTVQVKEGPPSPGSMSSNIIIFLILGIVILLTLGIGV 363
RESULT 7
PVR_HUMAN STANDARD; PRT; 417 AA.
ID AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168426; PubMed=2538245;
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;

RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
RT sequence, and expression of a new member of the immunoglobulin
RT superfamily.";
RL Cell 56:855-865 (1989).
RN [2]
RP REVISIONS.
RN Racaniello V.R.;
RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RL [3]
RN SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91006015; PubMed=2170108;
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RA Takeuchi K., Takegami T., Nomoto A.;
RT "The poliovirus receptor protein is produced both as membrane-bound
RT and secreted forms.";
RL EMBO J. 9:3217-3224 (1990).
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyianni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
RA Shannon M., Brower A., Olsen A.S., Smith L.M.;
RT "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger
RT gene cluster.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS.
RX MEDLINE=91239515; PubMed=1851992;
RA Koike S., Ise I., Nomoto A.;
RT "Functional domains of the poliovirus receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108 (1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N glycosylation of the virus binding domain is not essential for
RT function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373 (1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P15151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P15151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
CC VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".

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DR EMBL; M24407; AAA36461.1; -.
DR EMBL; M24406; AAA36462.1; -.
DR EMBL; X64116; CAA45478.1; -.
DR EMBL; X64117; CAA45478.1; JOINED.
DR EMBL; X64118; CAA45478.1; JOINED.
DR EMBL; X64119; CAA45478.1; JOINED.
DR EMBL; X64120; CAA45478.1; JOINED.
DR EMBL; X64121; CAA45478.1; JOINED.

CC CC WWW="http://www.ncbi.nlm.nih.gov/prov/guide/204270028_g.htm".

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DR EMBL; X80038; CAA56342.1; --.

DR EMBL; AF058448; AAC23797.1; --.

DR EMBL; BC003091; AAH03091.1; --.

DR EMBL; AF044968; AAC82348.1; --.

DR EMBL; AF044962; AAC82348.1; JOINED.

DR EMBL; AF044963; AAC82348.1; JOINED.

DR EMBL; AF044964; AAC82348.1; JOINED.

DR EMBL; AF044966; AAC82348.1; JOINED.

DR EMBL; AF044967; AAC82348.1; JOINED.

DR EMBL; AF050154; AAD02503.1; --.

DR PIR; I68093; I68093.

DR Genew; HGNC:9707; PVRL2.

DR MIM; 600798; --.

DR GO; GO:0005886; C:plasma membrane; TAS.

DR GO; GO:0015026; F:coreceptor activity; TAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003599; Ig.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;

KW Repeat; Alternative splicing.

FT SIGNAL 1 31 POTENTIAL.

FT CHAIN 32 538 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.

FT DOMAIN 32 360 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 361 381 POTENTIAL.

FT DOMAIN 382 538 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 32 156 IG-LIKE V-TYPE.

FT DOMAIN 162 256 IG-LIKE C2-TYPE 1.

FT DOMAIN 261 345 IG-LIKE C2-TYPE 2.

FT DISULFID 54 140 BY SIMILARITY.

FT DISULFID 183 238 BY SIMILARITY.

FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 324 324 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 351 479 NTAGAGATGGIIGGIIAIIATAVAATGIIICRQKQKQTL

FT QGAEEDELEGPPSYKPPTPKAKLEAQEMPSQLFTLGASEH

FT SPLKTPYFDAGASCTEQEMPRYHELPTLEERSGLHPGATS

FT LGSPIP -> RASPRDVGLVWAGVGTLVLLVLLAGGSLA

FT FILLRVRRRKSPGGAGGSGDGGFYDPKQVGLNGDPVF

FT WTPVPGMEPDGKDEEEEEEEKAEKGLMLPPPPALEDDM

FT ESQLDGSLISRAVVV (in isoform Alpha).

FT /FTId=VSP_002628.

FT Missing (in isoform Alpha).

FT /FTId=VSP_002629.

FT VARSPLIC 480 538

FT SEQUENCE 538 AA; 57742 MW; 3AE4F83E92F6F624 CRC64;

Query Match 22.8%; Score 459; DB 1; Length 538;

Best Local Similarity 28.3%; Pred. No. 1e-28;

Matches 117; Conservative 77; Mismatches 165; Indels 54; Gaps 14;

QY 5 VEPHTAVWGNVSLKCLI---EVNETITQISWEKIHGKSS-QTVAVHHPOYGFVSQGEY 60

Db VLPEVRGQLGGTVLPCHELLPPVPGLYISLVTWQRPDAPANHQNVAAPHKMGPSFPSPK 97

QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108

Db PGSERLSFVSAKQSTGQDTEAELQDATALHCLTVEDEGNYTCEFAFPKGSVRGMTWLR 157

QY 109 VLVEP-----TVSLIKGPDSLIDGNETVAACIAATKGPVAHI-----DWEGDLGE 155

Db VIAPKPNQAEAKQVTFSDQP-----TTVALCISKEGRPPARISWLSLSDWEAKETQ 208

QY 156 MESTTTSFPNETATIISQYKLFPTFPARGRRITCVVKHPALEKDIRYSFILDIOYAPEVS 215

Db VSGTLAG----TFTVTSRFTLVSGRADGVTVTCKVEHESFEPEPALIPVTLVSRYPPEVS 264

QY 216 VTGYDGNWFVGRKGNLKNADANPPPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNY 275

Db ISGYDDNWYLGRTDATLSCDVRSNPEFTGYDWTSTTSGTFTPSAVAQGSOL-VIHAVDSLF 323

QY 276 SGVYICKVTNSLQORSQDKVIYISDVFPKQTSSIAVAGAVICAVLALFI-IAIFVTVLLT 334

Db NTTFVCTVTVNAVGMGRAEQVIFVRETP--NTAGAGATGGIIGGIIAIIATAVAATGILI 381

QY 335 PRKRPSTYL-----DKVIDLPPTHKPP-PLYEERSPLPQKDLFQVCVHEYT 380

Db CRQQRKEQTLQGAEEDEDELEGPPSYKPPTPKAKLEAQEMPSQ-LFTLGASEHS 433

RESULT 6

ID_PVR_CERAE STANDARD; PRT; 417 AA.

AC P32506;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Poliovirus receptor precursor.

GN PVR OR PVS.

OS Cercopithecus aethiops (Green monkey) (Grivet).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;

OC Cercopithecinae; Cercopithecus.

OX NCBI_TaxID=9534;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).

RC TISSUE=Kidney;

RX MEDLINE=93059651; PubMed=1331508;

RA Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;

RT "A second gene for the African green monkey poliovirus receptor that

RT has no putative N-glycosylation site in the functional N-terminal

RT immunoglobulin-like domain.";

RL J. Virol. 66:7059-7066(1992).

CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the

CC cell.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).

CC Secreted (isoforms beta and gamma).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=4;

CC Name=Alpha;

CC IsoId=P32506-1; Sequence=Displayed;

CC Name=Beta;

CC IsoId=P32506-3; Sequence=Not described;

CC Name=Gamma;

CC IsoId=P32506-4; Sequence=Not described;

CC Name=Delta;

CC IsoId=P32506-2; Sequence=VSP_002622, VSP_002623;

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

CC -----

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CC -----

DR EMBL; D12611; BAA02136.1; --.

DR EMBL; D12612; BAA02137.1; --.

DR PIR; A44194; A44194.

DR PIR; B44194; B44194.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00406; IGv; 1.

FT	SIGNAL	1	30	POTENTIAL.
FT	CHAIN	31	515	POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT	DOMAIN	31	355	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	356	376	POTENTIAL.
FT	DOMAIN	377	515	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	141	IG-LIKE V-TYPE.
FT	DOMAIN	145	243	IG-LIKE C2-TYPE 1.
FT	DOMAIN	247	334	IG-LIKE C2-TYPE 2.
FT	DOMAIN	437	443	POLY-GLU.
FT	DOMAIN	444	447	POLY-GLY.
FT	DISULFID	51	124	BY SIMILARITY.
FT	DISULFID	172	226	BY SIMILARITY.
FT	DISULFID	269	316	BY SIMILARITY.
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	72	72	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	286	286	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	307	307	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	515 AA;	57047 MW;	BFAB00320DDE3785 CRC64;
Query Match				
		28.0%;		Score 563.5; DB 1; Length 515;
		Best Local Similarity		34.8%; Pred. No. 5.3e-37;
		Matches 130; Conservative		62; Mismatches 145; Indels 37; Gaps 10;
QY	14	GKNSVLKCLIE---	VNETITQISWEKIHGKSSQTVAVHHPOYGFVSQVGYQGRVLFKNYS	70
Db	44	GTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPAMGVSVLAPYRVERVEFLRPS	103	
QY	71	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEPTVSLIKGPDSDLIDG---	127	
Db	104	FTDGTIRLSRLLEDEGVYICEFATFPAGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG	162	
QY	128	-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTSPNETATIISQYKLPFTRFARGR	185	
Db	163	KDDKVLVATCTSANGKPPSVSWETHLKGEAEYQEIERNPNGTVTVISRYRLVPSREDHRQ	222	
QY	186	RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVLNKCNDANPPPFKS	245	
Db	223	SLACIVNYHM--DRFRESLTNLNVQYEPEVTIEGFDGNWYLRQMDVKLTCKADANPPATEY	280	
QY	246	VMSRLDGQWPDGLLASDNTLHFVHPLTFENYSVYICKVTNSLQORSQDKVYISDVPFKQ	305	
Db	281	HWTTLNGSLPKGVBAQNRTLFRGRPINYSMAGFYCEATNPIGTRSGQVEVNITEFPYTP	340	
QY	306	TS-----SIAVAGAVIGAV-LALFIILAFVTVLLTPR-----KKR---	342	PSY
Db	341	SPPEHGRRAGQVFTAIIGGVGSILLVLFVVGSIIVVALCRRRHTFKGDYSTKKHVGNGY	400	
QY	343	LDKVIDLPPTHKPP	356	
Db	401	SKAGI---PQHHP	411	
RESULT 4				
PVR2 MOUSE		STANDARD;		PRT; 530 AA.
ID	PVR2 MOUSE			
AC	P32507; Q62096;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Poliovirus receptor related protein 2 precursor (Murine herpesvirus entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).			
GN	PVR2 OR PVS OR PVR OR MPH.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=92219365; PubMed=1560525;			

RA	Morrison M.E., Racaniello V.R.;
RT	"Molecular cloning and expression of a murine homolog of the human poliovirus receptor gene.";
RL	J. Virol. 66:2807-2813(1992).
RN	[2]
RP	SEQUENCE FROM N.A. (ISOFORM BETA).
RC	STRAIN=C57BL/6; TISSUE=Brain;
RX	MEDLINE=94179228; PubMed=8132569;
RA	Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT	"Amino acid residues on human poliovirus receptor involved in interaction with poliovirus.";
RL	J. Biol. Chem. 269:8431-8438(1994).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM BETA).
RC	STRAIN=FVB/N; TISSUE=Colon;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshitsuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schrerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT	human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[4]
RP	CHARACTERIZATION.
RX	MEDLINE=99214397; PubMed=10196354;
RA	Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
RT	"The murine homolog (Mph) of human herpesvirus entry protein B (HvEB) mediates entry of pseudorabies virus but not herpes simplex virus types 1 and 2.";
RL	J. Virol. 73:4493-4497(1999).
CC	-!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY INTO CELLS.
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-!- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=Beta;
CC	Isoid=P32507-1; Sequence=Displayed;
CC	Name=Alpha;
CC	Isoid=P32507-2; Sequence=VSP_002630, VSP_002631;
CC	-!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and liver.
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC	-----
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CC	-----
DR	EMBL; M80206; AAA39734.1; -.
DR	EMBL; D26107; BAA05103.1; -.
DR	EMBL; BC059941; AAH59941.1; -.
DR	PIR; A38211; HLMSP3.
DR	PIR; A53437; A53437.
DR	MGI; 97822; Pvr12.
DR	InterPro; IPR007110; Ig-like.


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CC -----
DR EMBL; X76400; CAA53980.2; ALT_INIT.
DR EMBL; AF060231; AAC23798.1; -.
DR EMBL; AY029539; AAK33124.1; -.
DR EMBL; AF252867; AAG16648.1; -.
DR EMBL; AF196768; AAG16648.1; JOINED.
DR EMBL; AF196769; AAG16648.1; JOINED.
DR EMBL; AF196770; AAG16648.1; JOINED.
DR EMBL; AF196771; AAG16648.1; JOINED.
DR EMBL; AF196774; AAG16649.1; -.
DR EMBL; AF196768; AAG16649.1; JOINED.
DR EMBL; AF196769; AAG16649.1; JOINED.
DR EMBL; AF196770; AAG16649.1; JOINED.
DR EMBL; AF196771; AAG16649.1; JOINED.
DR EMBL; AF196772; AAG16649.1; JOINED.
DR EMBL; AF196773; AAG16649.1; JOINED.
DR Genew; HGNC:9706; PVRL1.
DR MIM; 600644; -.
DR MIM; 225000; -.
DR MIM; 225060; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004895; F:cell adhesion receptor activity; NAS.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 30
FT CHAIN 31 517
FT DOMAIN 31 355
FT TRANSMEM 356 376
FT DOMAIN 377 517
FT DOMAIN 31 141
FT DOMAIN 149 238
FT DOMAIN 247 334
FT DOMAIN 437 444
FT DOMAIN 445 449
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 307 307
FT CARBOHYD 332 332
FT VARSPLIC 335
FT VARSPLIC 353
FT VARSPLIC 336
FT VARSPLIC 459
FT SEQUENCE 517 AA; 57158 MW; DF34C8AEC893EE6D CRC64;
Query Match 28.2%; Score 566.5; DB 1; Length 517;
Best local Similarity 35.2%; Pred. No. 3.1e-37;
Matches 122; Conservative 68; Mismatches 134; Indels 23; Gaps 7;
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QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTQKSTNGSKQNVAIYNPSMGVSLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICEFATPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATCKPVAHIDWEGDL-GEMESTTSPNETATIISQYKLFPTFRFARGR 185
Db 163 QDDKVLVATCTSAANGKPPSVVSWETRLKGEAEYQEIRNPNGTIVISRYRLVPSREAHQQ 222
QY 186 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANPPPFKS 245
Db 223 SLACIVNYHM--DRFKESLTINVQYEPEVTIEGPDGNWYLRQMDVKLTCKADANPPATEY 280
QY 246 VMSRLDQGWPDGLLASDNTLHFVHPLTENYSGVYICKVNTSLGQRSDDQKVIYISDVPEKQ 305
Db 281 HMTTLNGSLPKGVFAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYTP 340
QY 306 TS-----SIAVAGAVIGAVLALFIATFVTVLLTPRKKRPSY 342
Db 341 SPPEHGRRAGVPVPTAIGGVAGSILLVIVGGIVVAL--RRRRHTF 385

RESULT 3
PVRL1_PIG STANDARD; PRT; 515 AA.
AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HveC) (Nectin 1).
GN PVRL1 OR PRR1 OR HVEC.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF308632; AAG30281.1; -.
DR HSSP; P06907; INEU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
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DR EMBL; AF270977; AAF76195.1; -.
DR EMBL; AF297665; AAG22808.1; -.
DR MGI; MGI:1926483; Pvr1l1.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 354
FT TRANSMEM 355 375
FT DOMAIN 376 515
FT DOMAIN 31 141
FT DOMAIN 145 243
FT DOMAIN 247 334
FT DOMAIN 436 442
FT DOMAIN 443 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 202
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 332 332
FT CONFLICT 138 138
FT CONFLICT 165 165
FT CONFLICT 342 342
FT CONFLICT 428 428
SQ SEQUENCE 515 AA; 57064 MW; FFF608EB5FFB7A0F CRC64;

Query Match 28.9%; Score 580; DB 1; Length 515;
Best Local Similarity 36.7%; Pred. No. 2.6e-38;
Matches 127; Conservative 67; Mismatches 130; Indels 22; Gaps 8;

QY 14 GKNSVLKLEIE---VNETITQISWEKIHGKSSQTVAVHHHPQYGSVQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTWQKASNGSKQNMAIYNPTMGVSVLPPEYKRVFELRPS 103

QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEVTSLIKGPDSLIDG--- 127
Db 104 FIDGTIRLSGLEDEGMYICEFATFPTGNRESQLNLTVMAKPT-NWIEGTRAVLRARKG 162

QY 128 -GNETVAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTREAGR 185
Db 163 QDNKVLVATCTSANGKPPSAVSWEIRLKGAEYQEIRNPNGTIVTISRVLVPSREAHKQ 222

QY 186 RITCVVKHPALEKDIRYSFILDIOYAPESVVTGYDGNWFVGRKGVMNLKCNADANPPPFKS 245
Db 223 SLACIVNY-HLDR-FRESLTINVQVEPEVTIEGFDGNWYLQRTDVKLTCKADANPPATEY 280

QY 246 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQBSDDQKVIYISDVPFKQ 305
Db 281 HWTTLNGSLPKGVEAQNRTLFFRGPITYSLAGTYICEATNPICRSGQVEVNITEFPYTP 340

QY 306 TSS-----IAGAVAGVAGVALFLFIAFVTVLLTPRKRPESY 342
Db 341 TPEHGRRAGQMETAIGGVAGSVLLVLIVVGGIIVAL--RRRRHTF 384

RESULT 2
PVR1_HUMAN
ID PVR1_HUMAN STANDARD; PRT; 517 AA.
AC Q15223; O75465; Q9HBE6; Q9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)
```

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DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)
DE (CD111 antigen).
GN PVRL1 OR PRRI OR HVEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102;
RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
RA Dubreuil P.;
RT "cDNA characterization and chromosomal localization of a gene related
RT to the poliovirus receptor gene.";
RL Gene 155:261-265(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=98279152; PubMed=9616127;
RA Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
RA Spear P.G.;
RT "Entry of alphaherpesviruses mediated by poliovirus receptor-related
RT protein 1 and poliovirus receptor.";
RL Science 280:1618-1620(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=21256041; PubMed=11356977;
RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
RA Campadelli-Fjume G., Dubreuil P.;
RT "Novel, soluble isoform of the herpes simplex virus (HSV) receptor
RT nectin1 (or prr1-HIGR-Hvec) modulates positively and negatively
RT susceptibility to hsv infection.";
RL J. Virol. 75:5684-5691(2001).
RN [4]
RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
RX MEDLINE=20392396; PubMed=10932188;
RA Helms J.A., Spritz R.A.;
RA Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
RT "Mutations of PVRL1, encoding a cell-cell adhesion
RT molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
RT dysplasia.";
RL Nat. Genet. 25:427-430(2000).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gpD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoform gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Delta;
CC IsoId=Q15223-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
CC Name=Gamma;
CC IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
CC -!- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
CC ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is
CC responsible for allelic forms known as Margarita island ectodermal
CC dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
CC -----
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 6.07283 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-31_COPY_58_437

Perfect score: 2009

Sequence: 1 GPIIVPHVTAVWGNVSLK.....ERSPPLPQDLFQVCVHEYT 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	580	28.9	515	1 PVR1_MOUSE	Q9jfk6 mus musculus
2	566.5	28.2	517	1 PVR1_HUMAN	Q15223 homo sapien
3	563.5	28.0	515	1 PVR1_PIG	Q9gl76 sus scrofa
4	474.5	23.6	530	1 PVR2_MOUSE	P32507 mus musculus
5	459	22.8	538	1 PVR2_HUMAN	Q92692 homo sapien
6	411	20.5	417	1 PVR_CERAE	P32506 cercopithec
7	401	20.0	417	1 PVR_HUMAN	P15151 homo sapien
8	227	11.3	764	1 ICCR_DROME	Q08180 drosophila
9	208.5	10.4	837	1 NCM2_MOUSE	Q35136 mus musculus
10	187.5	9.3	278	1 OX2G_HUMAN	P41217 homo sapien
11	187	9.3	4391	1 PGBM_HUMAN	P98160 homo sapien
12	177.5	8.8	853	1 NCA1_BOVIN	P31836 bos taurus
13	177	8.8	626	1 MAG_HUMAN	P20916 homo sapien
14	177	8.8	626	1 MAG_MOUSE	P20917 mus musculus
15	175	8.7	626	1 MAG_RAT	P07722 rattus norv
16	175	8.7	837	1 NCM2_HUMAN	O15394 homo sapien
17	174.5	8.7	2012	1 DSCA_HUMAN	O60469 homo sapien
18	167	8.3	509	1 SHS1_RAT	P97710 r protein-t
19	166	8.3	588	1 C166_CHICK	P42292 gallus gall
20	162.5	8.1	278	1 OX2G_MOUSE	O54901 mus musculus
21	162.5	8.1	278	1 OX2G_RAT	P04218 rattus norv
22	162.5	8.1	858	1 NCA1_RAT	P13596 rattus norv
23	162	8.1	353	1 CEPU_CHICK	Q90773 gallus gall
24	162	8.1	365	1 CXAR_HUMAN	P78310 homo sapien
25	162	8.1	761	1 NCA2_HUMAN	P13592 homo sapien
26	162	8.1	848	1 NCA1_HUMAN	P13591 homo sapien
27	161	8.0	365	1 CXAR_MOUSE	P97792 mus musculus
28	160.5	8.0	702	1 CEAS_HUMAN	P06731 homo sapien
29	157.5	7.8	595	1 SILL_HUMAN	Q96pq1 homo sapien
30	157	7.8	739	1 VCA1_MOUSE	P29533 mus musculus
31	157	7.8	1091	1 NCA1_CHICK	P13590 gallus gall
32	156.5	7.8	597	1 SILL_PANTR	Q951h0 pan troglod
33	156	7.8	337	1 OPCM_CHICK	Q98892 gallus gall

34	156	7.8	847	1	CD22_HUMAN	P20273 homo sapien
35	155.5	7.7	467	1	SIL7_HUMAN	Q9y286 homo sapien
36	153.5	7.6	725	1	NCA2_MOUSE	P13594 mus musculus
37	153.5	7.6	1115	1	NCA1_MOUSE	P13595 mus musculus
38	153	7.6	3707	1	PGBM_MOUSE	Q05793 mus musculus
39	150	7.5	646	1	MUI8_HUMAN	P43121 homo sapien
40	149	7.4	344	1	NTRI_MOUSE	Q99pj0 mus musculus
41	149	7.4	344	1	NTRI_RAT	Q62718 rattus norv
42	149	7.4	345	1	OPCM_BOVIN	P11834 bos taurus
43	149	7.4	1051	1	PTK7_CHICK	Q91048 gallus gall
44	148.5	7.4	467	1	SIL5_MOUSE	Q91y57 mus musculus
45	148.5	7.4	569	1	TACT_HUMAN	P40200 homo sapien

ALIGNMENTS

RESULT 1
PVR1_MOUSE
ID PVR1_MOUSE STANDARD; PRT; 515 AA.
AC Q9JKF6; Q9ERL5; Q9J117;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Hvec) (Nectin 1).
GN PVRL1 OR PRRI OR HVEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubreuil P., Campadelli-Fiume G.;
RT "The murine homolog of human nectin1 delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-lalpha to human nectin-lalpha (Hvec) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRRI), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF239762; AAF60333.1; -.

RESULT 15

Query Match	9.3%;	Score 187.5;	DB 2;	Length 274;
Best Local Similarity	24.8%;	Pred. No. 9.7e-07;		
Matches 52;	Conservative	36;	Mismatches 97;	Indels 25;
				Gaps 4;

Search completed: April 12, 2004, 09:47:08
Job time : 11.055 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 10.055 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-31_COPY_58_437
Perfect score: 2009
Sequence: 1 GPIIIEPHVTAVGKNVSLK.....ERSPLPQKDLFQVCVHEYT 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1159.5	57.7	407	2 T08732	hypothetical prote
2	544	27.1	518	2 JC4024	poliovirus recepto
3	474.5	23.6	530	2 A53437	poliovirus recepto
4	459	22.8	538	2 I68093	PRR2 delta - human
5	446	22.2	467	1 HLMSP3	poliovirus recepto
6	424	21.1	478	2 I53960	PRR2 alpha - human
7	411	20.5	392	2 B44194	poliovirus recepto
8	411	20.5	417	2 A44194	poliovirus recepto
9	398	19.8	392	1 RWHUPD	poliovirus recepto
10	398	19.8	417	1 RWHUPA	poliovirus recepto
11	315	15.7	416	2 A54017	colon carcinoma-as
12	227	11.3	764	2 A49448	irregular chiasm C
13	196.5	9.8	5175	2 T20992	hypothetical prote
14	196.5	9.8	5198	2 T43290	hemocentin precurs
15	187.5	9.3	274	2 A47639	OX-2 membrane glyc
16	187	9.3	4391	2 A38096	perlecan precursor
17	177.5	8.8	853	1 IJBONC	neural cell adhesi
18	177	8.8	626	1 A61084	myelin-associated
19	177	8.8	637	2 B33785	myelin-associated
20	175	8.7	582	1 BNRT3S	myelin-associated
21	175	8.7	626	1 BNRT3	myelin-associated
22	174.5	8.7	1896	2 T08851	Down syndrome cell
23	166.5	8.3	7962	2 I38346	elastic titin - hu
24	166	8.3	588	2 JH0506	adhesion molecule
25	166	8.3	588	2 A45254	surface glycoprote
26	165	8.2	365	2 JC7780	coxsackie- and ade
27	163.5	8.1	1091	2 A58532	glial cell membran
28	162.5	8.1	278	1 TDRTOX	OX-2 membrane glyc
29	162.5	8.1	858	1 IJRTNC	neural cell adhesi

30	162	8.1	761	1 IJHUNG	neural cell adhesi
31	161	8.0	765	2 C42632	cell adhesion mole
32	161	8.0	812	2 B42632	cell adhesion mole
33	161	8.0	932	2 A42632	cell adhesion mole
34	160.5	8.0	702	2 A36319	carcinoembryonic a
35	157	7.8	739	2 JN0581	vascular cell adhe
36	157	7.8	1091	1 IJCHNL	neural cell adhesi
37	156	7.8	847	2 JH0371	B-cell adhesion pr
38	154	7.7	587	2 JH0464	DM-GRASP precursor
39	153.5	7.6	725	1 IJMSNG	neural cell adhesi
40	153.5	7.6	1115	1 IJMSNL	neural cell adhesi
41	153	7.6	3707	2 S18252	heparan sulfate pr
42	152.5	7.6	1612	2 T30805	duffy protein - mo
43	150	7.5	646	2 I38049	cell surface glyco
44	149	7.4	344	2 I56551	neurotrophin - rat
45	149	7.4	345	2 S03199	opioid-binding pro

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08732
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732
A;Molecule type: mRNA
A;Residues: 1-407 <OTT>
A;Cross-references: EMBL:AL050071
A;Experimental source: fetal kidney; clone DKFZp566B0846
C;Genetics:
A;Note: DKFZp566B0846.1

Query Match 57.7%; Score 1159.5; DB 2; Length 407;
Best Local Similarity 70.3%; Pred. No. 1.6e-79;
Matches 230; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY	86	SGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDLSLIDGGNETVAAICIAATGKPVA	145
DB	1	SGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDLSLIDGGNETVAAICIAATGKPVA	60
QY	146	HIDWEGDLGEMESTTTSFPNETATIIISQYKLPPTFRFARRRITCVVKHPALEKDIRYSFI	205
DB	61	HIDWEGDLGEMESTTTSFPNETATIIISQYKLPPTFRFARRRITCVVKHPALEKDIRYSFI	120
QY	206	LDIQYAPEVSVTGYDGNWFGVGRKGNLKNADANPPFKSVWSRLDQWPDGLLASDNTL	265
DB	121	LDIQYAPEVSVTGYDGNWFGVGRKGNLKNADANPPFKSVWSRLDQWPDGLLASDNTL	180
QY	266	HFVHPLTFNYSYGVYICKVTNSLQGRSDQKVIYISDVP-----	302
DB	181	HFVHPLTFNYSYGVYICKVTNSLQGRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT	240
QY	303	-----FKQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPRKK--RPSYLDKV	346
DB	241	EPKKLPPLSTLATIKDDTIATIASVVGALFIVLSVLGIFCYRRRTFRGDYFAK-	299
QY	347	IDLPPTHKPPPLYEERSPPLPQKDLFQ	373
DB	300	-----NYIPPSDMQKES-----QIDVLQ	317

RESULT 2
JC4024
poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-5

Query Match 12.6%; Score 223; DB 3; Length 444;
Best Local Similarity 23.8%; Pred. No. 2.4e-13;
Matches 75; Conservative 63; Mismatches 143; Indels 34; Gaps 13;

QY 1 GPIIPEPHVTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 33 GQFPLTQNTVVEGGTAILTCTRVQNDN-TSLQWS---NPAQQTL-----YFDDKKALR 82
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVE-PTVSLIK 119
Db 83 DNRIELVRASWHELSSISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFS 142
QY 120 GPDSLIDGGNEVAAICIAATGKPAHIDW---EGDLGEMESTTTSFPN-ETATIISQYK 175
Db 143 SP--VMEG--DLMLQTKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLD 198
QY 176 LFPTRFARRITCVVVKHPALEKDIRYSP-ILDIQYAPEVSVT-----GYDGNWVFGRKG 229
Db 199 FRVDRSDDGVAVICRVDEHESLNATPQVAMQVLEIHYPSTVKIIPSTFPFQEGQPLI---- 254
QY 230 VNLKCNADANPPPKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 255 --LTCEKKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNILF-LNKTDNGTYRCEATNTI 311
QY 288 GQRSDQKVIYISDVP 302
Db 312 GQSSAEYVLIVHDVP 326

RESULT 15
US-09-778-510-6
; Sequence 6, Application US/09778510 .
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510

; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 12.1%; Score 214.5; DB 4; Length 398;
Best Local Similarity 26.1%; Pred. No. 1.4e-12;
Matches 82; Conservative 52; Mismatches 149; Indels 31; Gaps 13;

QY 10 TAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNY 69
Db 39 TVVAGGTVVLKCQVKDHED-SSLQWS---NPAQQTL-----YFGEKRALFDNRRIQLVTS 88
QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGN 129
Db 89 TPHELSSISNVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145
QY 130 ETVAACIAATGKPAHIDWEGDLGEMESTTTSF--PN-ETATIISQYKLFPTRFARGR 185
Db 146 DTATLNCQSSSGSKPAARLTWRKGDQELHGETRIQEDPNGKTFTVSSSVTFQVTRDDGA 205
QY 186 RITCVVKHPALE-KDIRYSFILDIOYAPEVSVTGYDGNWVFGRKGVNLCNADANPPPEK 244
Db 206 SIVCSVNHESLKGADRSTSQRIEVLVYTPAMIRPDPPHPREGQK-LLHCEGRGNPVPQQ 264
QY 245 SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQRSQDKVIYISD---V 301
Db 265 YLWEK-EGSVFPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYKAYYTLNVNDPSPV 322
QY 302 PFKQTSSRSQSSDY 315
Db 323 P-----SSSSTY 329

Search completed: April 12, 2004, 09:49:28
Job time : 11.8934 secs

STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-1

Query Match 12.6%; Score 223; DB 3; Length 421;
Best Local Similarity 23.8%; Pred. No. 2.2e-13;
Matches 75; Conservative 63; Mismatches 143; Indels 34; Gaps 13;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 10 GQFPLTQNVTVVEGGTAILTCRVDQNDN-TSLQWS---NPAQQTL-----YFDDKKALR 59
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVTLVE-PTVSLIK 119
Db 60 DNRIELVRASWHELSSISVSDVSLDEGQYTCSLFTMPVKTSKAYLTVLGVEKPKQISGFS 119
QY 120 GPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATIIISQYK 175
Db 120 SP--VMEG--DLMQLTCKTSGSKPAADIRWFKNDEIKDVYKYLKEEDANRKTFTVSSTLD 175
QY 176 LFPTRFARGRRITCVVKHPALEKDIRYSF-ILDIOYAPEVSVT-----GYDGNWVFVGRKG 229
Db 176 FRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKIIIPSTPPFQEGQPLI--- 231
QY 230 VNLKCNADANPPPKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 232 --LTCESKGKPLPEPVLWTKGGELPDPDRMVVSGRELNILF-LNKTDNGTYRCEATNTI 288
QY 288 GQRSDQKVYIYISDVP 302
Db 289 GQSSAEYVLIVHDVP 303

RESULT 13
US-08-659-984A-5
Sequence 5, Application US/08659984A
Patent No. 5942400
GENERAL INFORMATION:
APPLICANT: Anderson, John P.
APPLICANT: Sinha, Sukanto
APPLICANT: Jacobson-Croak, Kirsten L.
TITLE OF INVENTION: Assays for Detecting Beta-Secretase
TITLE OF INVENTION: Inhibition
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Ctr., 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 12.6%; Score 223; DB 2; Length 444;
Best Local Similarity 23.8%; Pred. No. 2.4e-13;
Matches 75; Conservative 63; Mismatches 143; Indels 34; Gaps 13;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 33 GQFPLTQNVTVVEGGTAILTCRVDQNDN-TSLQWS---NPAQQTL-----YFDDKKALR 82
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVTLVE-PTVSLIK 119
Db 83 DNRIELVRASWHELSSISVSDVSLDEGQYTCSLFTMPVKTSKAYLTVLGVEKPKQISGFS 142
QY 120 GPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATIIISQYK 175
Db 143 SP--VMEG--DLMQLTCKTSGSKPAADIRWFKNDEIKDVYKYLKEEDANRKTFTVSSTLD 198
QY 176 LFPTRFARGRRITCVVKHPALEKDIRYSF-ILDIOYAPEVSVT-----GYDGNWVFVGRKG 229
Db 199 FRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKIIIPSTPPFQEGQPLI--- 254
QY 230 VNLKCNADANPPPKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 255 --LTCESKGKPLPEPVLWTKGGELPDPDRMVVSGRELNILF-LNKTDNGTYRCEATNTI 311
QY 288 GQRSDQKVYIYISDVP 302
Db 312 GQSSAEYVLIVHDVP 326

RESULT 14
US-08-660-531-5
Sequence 5, Application US/08660531
Patent No. 6221645
GENERAL INFORMATION:
APPLICANT: Chrysler, Susanna M.S.
APPLICANT: Sinha, Sukanto
APPLICANT: Keim, Pamela S.
APPLICANT: Anderson, John P.
TITLE OF INVENTION: Beta-Secretase
NUMBER OF SEQUENCES: 21

QY 300 DVP 302
Db 314 DPP 316

RESULT 10

US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-4

Query Match 12.7%; Score 224.5; DB 4; Length 398;
Best Local Similarity 26.8%; Pred. No. 1.4e-13;
Matches 84; Conservative 52; Mismatches 147; Indels 31; Gaps 13;
QY 10 TAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEYQGRVLFKNY 69
Db 39 TVVAGGTVVLLKQVQKHED-SSLQWS---NPAQQTLD-----YFGEKRALRDNRIQLVSS 88
QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGNN 129
Db 89 TPHELSSISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145
QY 130 ETVAACIAATGKPVAHIDWEGDLGEMESTTSF---PN-ETATIIISQYKLFPTRFARGR 185
Db 146 ETATLNCQSSGSKPAAQLTWKGDQELHGDQTRIQEDPNKGTFTVSSVSFQVTRDDGA 205
QY 186 RITCVVHPALE-KDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFK 244
Db 206 NIVCSVMHESLKGADRTSQRIEVLYTPTAMIRPEPAHPREGQK-LLLHCEGRGNPVPOQ 264
QY 245 SVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD---V 301
Db 265 YVWVK-EGSEPPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYTAYFTLNVDNPPSPV 322
QY 302 PFKQTSSRSRGSSDY 315
Db 323 P-----SSSSTY 329

RESULT 11

US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 421 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-1

Query Match 12.6%; Score 223; DB 2; Length 421;
Best Local Similarity 23.8%; Pred. No. 2.2e-13;
Matches 75; Conservative 63; Mismatches 143; Indels 34; Gaps 13;
QY 1 GPIIVERHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 60
Db 10 GQFPLTONVTVEGGTAILTCRVDQNDN-TSLQWS---NPAQQTLD-----YFDDKKALR 59
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVE-PTVSLIK 119
Db 60 DNRIELVRASWHELISVSDVLSDEGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFS 119
QY 120 GPDSLIDGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATIIISQYK 175
Db 120 SP--VMEG--DLMLTCKTSGSKPAADIRWFKNDEIKDKVKLKEBDANRKTFTVSSILD 175
QY 176 LFPTRFARGRRITCVVHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWFGVRKG 229
Db 176 FRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYPSTVKIIPSTPPFQEGQPLI---- 231
QY 230 VNLKNADANPPPFKSVWSRLDQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 232 --LTCESKGGKPLPEPVLWTKDGGELPDPDRMVVSGRELNILF-LNKTDNGTYRCEATNTI 288
QY 288 GQRSDQKVIYISDVP 302
Db 289 GQSSAEYVLIVHDVP 303

RESULT 12

US-08-660-531-1
; Sequence 1, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco


```

; ORGANISM: Homo sapiens
US-09-723-368-2
Query Match      22.5%; Score 397.5; DB 4; Length 479;
Best Local Similarity 29.1%; Pred. No. 2.1e-30;
Matches 95; Conservative 57; Mismatches 132; Indels 43; Gaps 9;

QY 5 VEPHVTAVWGKNVSLKCLII---EVNETITQISWEKIHGKSS-QTVAVHHPOYGFVSQGEY 60
Db 38 VLPEVRGQLGGTVELPCHLLPPVPLGLYISLVTWQRPDAPANHQNVAAAFHPKMGSPFPSPK 97
QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108
Db 98 PGSERLSFVSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFAFPKGSVRGMTWLR 157
QY 109 VLVEP-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVAAHI-----DWEGDLGE 155
Db 158 VIAKPKNQAEAKVTFSSQDP-----TTVALCISKEGRPPPARISWLSLSDWEAKETQ 208
QY 156 MESITTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVS 215
Db 209 VSGTLAG----TVTVTSRFTLVPSGRADGVTVTCKVEHESFEELIPVTLVSRYPPEVS 264
QY 216 VTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDQWPDGGLASDNTLHFVHPLTFNY 275
Db 265 ISGYDDNWYLGRDATALSCDVRNPEPTGYDWMSTTSGTFTPSAVAQSQQL-VIHAVDSL 323
QY 276 SGVYICKVNSLQGRSDQKVIYISDVP 302
Db 324 NTTFVCTVTNAVGMGRAEQVIFVRETP 350
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```

RESULT 5
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62
Query Match      21.2%; Score 375; DB 4; Length 408;
Best Local Similarity 32.5%; Pred. No. 2.7e-28;
Matches 102; Conservative 53; Mismatches 137; Indels 22; Gaps 10;

QY 3 IIVEPHVTAVWGKNVSLKCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPOYGFVSQGE 59
Db 32 VLVPYNSTGVLGSTTLHCSLTSNENVTTITQITWMKKDSGGSHALVAVFHKPKGPNKEP 91
QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSL 117
Db 92 ERVKFLAAQQDLRNASLAISNLSEDEGIYECQIATFPRGSRSTNAWLKVQARPKNTAEA 151
QY 118 IKGPDSLI--DGNETVAAICIAATGKPVAAHIW----EGDLGEMESTTTSFPNETATII 171
Db 152 LEPSPTLILQD-----VAKCISANGHPGRISWPSNVNGSHREMKE-PGSQPG-TTIVT 203
QY 172 SQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFVGRKGV 230
Db 204 SYLSMVPSRQADGKNITCTVEHESLQELDQLLVLTLSQPYPPENVSISGYDGNWYVGLTNL 263
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QY 231 NLKCNADANPPPFKS--VMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVNTSLG 288
Db 264 TLTCEAHSKPAPDMAGYNWSTNTGDFPNSVKRQGNMILLISTVEDGLNNTIVICEVTNALG 323
QY 289 QRSQKQVIYISDVP 302
Db 324 SGQGQVHHIIVKEKP 337

RESULT 6
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumaas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61
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```

Query Match      15.0%; Score 265.5; DB 4; Length 440;
Best Local Similarity 26.4%; Pred. No. 1.6e-17;
Matches 80; Conservative 61; Mismatches 133; Indels 29; Gaps 11;

QY 9 VTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKN 68
Db 50 VTVEIEGAVATISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLLN 99
QY 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLIDG 127
Db 100 FSSSELKVSLTNVSIISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMDIQKDTAVEG 157
QY 128 GNETVAAICIAATGKPVAAHIW-EGDL-----GEMESTTTSFPNETATIIISQYKLFPTRF 181
Db 158 --EEIEVNCNTAMASKPATIRWFKNGTELKSKSEVEEWSDMY-----TVTSQMLMKVHKE 210
QY 182 ARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKG--VNLKCNADAN 239
Db 211 DDGVFPVICQVEHPAVTGNLQTRYLEVQYKPVQVHIQMTYPLQGLTREGDALELTCEAIGK 270
QY 240 PPPFKSVWSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVNTSLGQRSDQKVIYIS 299
Db 271 PQPVMVTWVRVDDDEMPQHAVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYVY 329
QY 300 DVP 302
Db 330 DPP 332
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Db 223 SLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRMVMDVKLTCKADANPPATEY 280
QY 246 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVFPKQ 305
Db 281 HWTTLNGLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYTP 340
QY 306 TSSRSRG 311
Db 341 SPPEHG 346

RESULT 2
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: HIGR and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 30.3%; Score 535.5; DB 4; Length 458;
Best Local Similarity 37.7%; Pred. No. 5.9e-44;
Matches 113; Conservative 55; Mismatches 121; Indels 11; Gaps 5;

QY 14 GKNVSLKCLIE--VNETHITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTRFARGR 185
Db 163 QDDKVLVATCTTSANGKPPSVSVSWETRLKGEAEYQEIRNPNGTVTVISRYRLVPSREAHQ 222
QY 186 RITCVVXHPALEKDIRYSFTLDIQYAPEVSVTGYDGNWVFGKGVNLCNADANPPFPKS 245
Db 223 SLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRMVMDVKLTCKADANPPATEY 280
QY 246 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVFPKQ 305
Db 281 HWTTLNGLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEKPRPQ 340

RESULT 3
US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US

; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20

Query Match 29.5%; Score 521; DB 4; Length 518;
Best Local Similarity 34.9%; Pred. No. 1.9e-42;
Matches 110; Conservative 58; Mismatches 119; Indels 28; Gaps 6;
QY 14 GKNVSLKCLIE--VNETHITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLF 176
Db 163 QDDKVLVATCTTSANGKPPSVSVSWETRLKGEARVPGDSGT-----PMAPVTVISRYRL 214
QY 177 FPFTRFARGRRITCVVXHPALEKDIRYSFTLDIQYAPEVSVTGYDGNWVFGKGVNLCNKA 236
Db 215 VPSREAHQOSLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRMVMDVKLTCKA 272
QY 237 DANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVI 296
Db 273 DANPPATEYHWTTLNGLSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332
QY 297 YISDVFPKQTSRSRG 311
Db 333 NITEFPYTPSPPEHG 347

RESULT 4
US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 10.8934 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-16_COPY_58_387

Perfect score: 1768

Sequence: 1 GPIIIEPHVTAVWGKNVSLK.....GSSDYKDDDDKGSSHHHHH 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	ID	Description
1	543.5	30.7	517	4	US-09-723-368-4
2	535.5	30.3	458	4	US-09-435-956A-1
3	521	29.5	518	4	US-09-919-172-20
4	397.5	22.5	479	4	US-09-723-368-2
5	375	21.2	408	4	US-09-724-864-62
6	265.5	15.0	440	4	US-09-866-028-61
7	265.5	15.0	442	4	US-09-778-510-20
8	265.5	15.0	442	4	US-09-930-803-1
9	262.5	14.8	423	4	US-09-778-510-22
10	224.5	12.7	398	4	US-09-778-510-4
11	223	12.6	421	2	US-08-659-984A-1
12	223	12.6	421	3	US-08-660-531-1
13	223	12.6	444	2	US-08-659-984A-5
14	223	12.6	444	3	US-08-660-531-5
15	214.5	12.1	398	4	US-09-778-510-6
16	214.5	12.1	398	4	US-09-907-794A-84
17	214.5	12.1	398	4	US-09-905-125A-84
18	214.5	12.1	398	4	US-09-902-775A-84
19	214.5	12.1	432	4	US-09-778-510-2
20	190.5	10.8	227	4	US-09-205-258-947
21	187.5	10.6	274	4	US-09-570-367C-19
22	187.5	10.6	274	4	US-09-915-524-19
23	168	9.5	642	1	US-08-217-299-1
24	168	9.5	738	2	US-08-602-725-36
25	168	9.5	694	2	US-08-389-459A-17
26	168	9.5	734	3	US-08-987-867A-17
27	162.5	9.2	278	4	US-09-570-367C-2

28	162.5	9.2	278	4	US-09-915-524-2	Sequence 2, Appli
29	162	9.2	477	2	US-08-432-016-3	Sequence 3, Appli
30	162	9.2	477	2	US-08-684-594-3	Sequence 3, Appli
31	159.5	9.0	278	4	US-09-570-367C-21	Sequence 21, Appl
32	159.5	9.0	278	4	US-09-915-524-21	Sequence 21, Appl
33	159	9.0	1101	3	US-08-986-485-2	Sequence 2, Appli
34	152.5	8.6	313	4	US-09-700-397-4	Sequence 4, Appli
35	152.5	8.6	344	4	US-09-700-397-3	Sequence 3, Appli
36	151	8.5	467	3	US-09-046-736-2	Sequence 2, Appli
37	146	8.3	1018	1	US-08-408-093-6	Sequence 6, Appli
38	146	8.3	1018	1	US-08-408-420A-6	Sequence 6, Appli
39	146	8.3	1018	1	US-08-714-901-6	Sequence 6, Appli
40	146	8.3	1018	3	US-08-040-741-6	Sequence 6, Appli
41	146	8.3	1059	4	US-09-907-794A-290	Sequence 290, App
42	146	8.3	1059	4	US-09-905-125A-290	Sequence 290, App
43	146	8.3	1059	4	US-09-902-775A-290	Sequence 290, App
44	146	8.3	1119	4	US-09-907-794A-294	Sequence 294, App
45	146	8.3	1119	4	US-09-905-125A-294	Sequence 294, App

ALIGNMENTS

RESULT 1
US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

QY	14	GKNVSLKCLIE---VNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFKNYS	70
Db	44	GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAINPSMGVSVLAPYRERVEFLRPS	103
QY	71	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIG---	127
Db	104	FTDGTIRLSRLEDEGVYICFATFPTGNRESQLNLTVMAKPT-NWIEGTQAVLRKKG	162
QY	128	-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTTFNETATIIISOYKLFPTTFARGR	185
Db	163	QDDKVLVATCTSANGKPPSVSWETRLKGEAEYQEIIRNPNGTIVTISRRLVPSREAHQQ	222
QY	186	RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGKGNLKNADANPPPFKS	245

Publication No. US20030008334A1
GENERAL INFORMATION:
APPLICANT: Yoshimi TAKAI
APPLICANT: Hiroyuki NAKANISHI
APPLICANT: Keiko SATO
APPLICANT: Kenichi TAKAHASHI
TITLE OF INVENTION: Protein Nectin-3
FILE REFERENCE: 2001-1678A/LC/00653
CURRENT APPLICATION NUMBER: US/09/959,845
CURRENT FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: PCT/JP01/01871
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: JP 2000-065595
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 510
TYPE: PRT
ORGANISM: Mouse
US-09-959-845-4

Query Match 89.5%; Score 1582; DB 10; Length 510;
Best Local Similarity 95.5%; Pred. No. 5.8e-131;
Matches 294; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY	1	GP	IIVPHV	TA	VWG	KNV	SLK	CL	IE	VN	ET	IT	Q	I	S	W	E	K	I	H	G	K	S	S	Q	T	V	A	V	H	H	P	Q	Y	G	F	S	V	Q	G	E	Y	60																			
Db	58	GS	IIVPHV	TA	VWG	KNV	SLK	CL	IE	VN	ET	IT	Q	I	S	W	E	K	I	H	G	K	S	S	Q	T	V	A	V	H	H	P	Q	Y	G	F	S	V	Q	G	E	Y	117																			
QY	61	Q	R	V	L	F	K	N	S	L	N	D	A	T	I	T	L	H	N	I	G	F	S	D	S	G	K	Y	I	C	K	A	V	T	F	P	L	G	N	A	Q	S	T	T	V	L	V	E	P	T	V	S	L	I	K	120						
Db	118	Q	R	V	L	F	K	N	S	L	N	D	A	T	I	T	L	H	N	I	G	F	S	D	S	G	K	Y	I	C	K	A	V	T	F	P	L	G	N	A	Q	S	T	T	V	L	V	E	P	T	V	S	L	I	K	177						
QY	121	P	D	S	L	I	D	G	G	N	E	T	V	A	A	I	C	I	A	A	T	G	K	P	V	A	H	I	D	W	E	G	L	G	E	M	E	S	T	T	S	F	P	N	E	T	A	I	I	S	Q	Y	K	L	F	P	T	R	180			
Db	178	P	D	S	L	I	D	G	G	N	E	T	V	A	A	I	C	I	A	A	T	G	K	P	V	A	H	I	D	W	E	G	L	G	E	M	E	S	T	T	S	F	P	N	E	T	A	I	I	S	Q	Y	K	L	F	P	T	R	237			
QY	181	F	A	R	G	R	R	I	T	C	V	V	K	H	P	A	L	E	K	D	I	R	Y	S	F	I	L	D	I	Q	Y	A	P	E	V	S	V	T	G	Y	D	G	N	W	F	V	G	R	K	G	V	N	L	K	C	N	A	D	A	N	P	240
Db	238	F	A	R	G	R	R	I	T	C	V	V	K	H	P	A	L	E	K	D	I	R	Y	S	F	I	L	D	I	Q	Y	A	P	E	V	S	V	T	G	Y	D	G	N	W	F	V	G	R	K	G	V	N	L	K	C	N	A	D	A	N	P	297
QY	241	P	P	F	K	S	V	N	S	R	L	D	G	Q	W	P	D	G	L	L	A	S	D	N	T	L	H	F	V	H	P	L	T	F	N	Y	S	G	V	Y	I	C	K	T	N	S	L	G	Q	R	S	D	Q	K	V	I	Y	I	S	D	300	
Db	298	P	P	F	K	S	V	N	S	R	L	D	G	Q	W	P	D	G	L	L	A	S	D	N	T	L	H	F	V	H	P	L	T	F	N	Y	S	G	V	Y	I	C	K	T	N	S	L	G	Q	R	S	D	Q	K	V	I	Y	I	S	D	357	
QY	301	V	P	F	K	Q	T	S	S	308																																																				
Db	358	I	P	L	T	Q	T	S	S	365																																																				

Search completed: April 12, 2004, 10:25:30
Job time : 28.5793 secs

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; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match      90.6%;   Score 1602;   DB 10;   Length 634;
Best Local Similarity 98.7%;   Pred. No. 1.3e-132;
Matches 302;   Conservative 0;   Mismatches 4;   Indels 0;   Gaps 0;

QY      1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db      58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117

QY      61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db      118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY      121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db      178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237

QY      181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db      238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297

QY      241 PPFSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 300
Db      298 PPFSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 357

QY      301 VPFKQT 306
Db      358 PPTTTT 363

RESULT 13
US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-6

Query Match      89.5%;   Score 1582;   DB 10;   Length 438;
Best Local Similarity 95.5%;   Pred. No. 4.7e-131;
Matches 294;   Conservative 9;   Mismatches 5;   Indels 0;   Gaps 0;

QY      1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db      58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGDY 117

QY      61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db      118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY      121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db      178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237

QY      181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db      238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297

QY      241 PPFSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 300
Db      298 PPFSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 357

QY      301 VPFKQT 306
Db      358 PPTTTT 363

RESULT 15
US-09-959-845-4
; Sequence 4, Application US/09959845
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QY      121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db      178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237

QY      181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db      238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297

QY      241 PPFSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 300
Db      298 PPFSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 357

QY      301 VPFKQTSS 308
Db      358 IPLTQTSS 365

RESULT 14
US-09-972-268-19
; Sequence 19, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 438
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-19

Query Match      89.5%;   Score 1582;   DB 10;   Length 438;
Best Local Similarity 95.5%;   Pred. No. 4.7e-131;
Matches 294;   Conservative 9;   Mismatches 5;   Indels 0;   Gaps 0;

QY      1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db      58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGDY 117

QY      61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db      118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY      121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db      178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237

QY      181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db      238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297

QY      241 PPFSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 300
Db      298 PPFSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQORSDDQKVIYISD 357

QY      301 VPFKQTSS 308
Db      358 IPLTQTSS 365

RESULT 15
US-09-959-845-4
; Sequence 4, Application US/09959845
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QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VPFKQT 306
Db 358 PPTTTT 363

RESULT 10

US-09-972-268-6

; Sequence 6, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 6

; LENGTH: 549

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-972-268-6

Query Match 90.6%; Score 1602; DB 10; Length 549;
Best Local Similarity 98.7%; Pred. No. 1.1e-132;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VPFKQT 306
Db 358 PPTTTT 363

RESULT 11

US-10-161-572-45

; Sequence 45, Application US/10161572

; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE P53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 90.6%; Score 1602; DB 14; Length 549;
Best Local Similarity 98.7%; Pred. No. 1.1e-132;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VPFKQT 306
Db 358 PPTTTT 363

RESULT 12

US-09-972-268-13

; Sequence 13, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

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RESULT 7
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match      92.5%; Score 1636; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.9e-136;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGEY 60
Db 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVPVLEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVPVLEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297

QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD 357

QY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365

RESULT 8
US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2

Query Match      92.5%; Score 1636; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 9.9e-136;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGEY 60
Db 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVPVLEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVPVLEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297

QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD 357

QY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365
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; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match      90.6%; Score 1602; DB 10; Length 542;
Best Local Similarity 98.7%; Pred. No. 1.1e-132;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGEY 60
Db 51 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGEY 110

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVPVLEPTVSLIKG 120
Db 111 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVPVLEPTVSLIKG 170

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 180
Db 171 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 230

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 231 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 290

QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD 300
Db 291 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD 350

QY 301 VPFKQT 306
Db 351 PPTTTT 356

RESULT 9
US-09-972-268-4
; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are fr
; OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match      90.6%; Score 1602; DB 10; Length 549;
Best Local Similarity 98.7%; Pred. No. 1.1e-132;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGEY 60
Db 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVPVLEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVPVLEPTVSLIKG 177
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; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match
Best Local Similarity 92.5%; Score 1636; DB 10; Length 437;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

QY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365

RESULT 5
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

Query Match
Best Local Similarity 92.5%; Score 1636; DB 10; Length 504;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 52 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 111

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 120
Db 112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 171

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 231

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 232 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 291

QY 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 292 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 351

QY 301 VPFKQTSS 308
Db 352 VPFKQTSS 359

RESULT 6
US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10

Query Match
Best Local Similarity 92.5%; Score 1636; DB 10; Length 510;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

QY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 VPFKQTSSRGSSDYKDDDDKGGSSHHHHH 330
Db 358 VPFKQTSSRGSSDYKDDDDKGGSSHHHHH 387
RESULT 2
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15
Query Match 96.5%; Score 1706.5; DB 10; Length 426;
Best Local Similarity 87.8%; Pred. No. 4.7e-142;
Matches 324; Conservative 2; Mismatches 4; Indels 39; Gaps 1;
QY 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 VPFKQT-----SSRGSSDYKDDDDK 321
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTTIATRSGSSDYKDDDDK 417
QY 322 GSSHHHHH 330
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Db 418 GSSHHHHH 426
RESULT 3
US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14
Query Match 93.0%; Score 1645; DB 10; Length 595;
Best Local Similarity 100.0%; Pred. No. 2e-136;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 VPFKQTSSRS 310
Db 358 VPFKQTSSRS 367
RESULT 4
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 27.5793 Seconds
(without alignments)
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Perfect score: 1768
Sequence: 1 GPIIPEPHVTAVGKNVSLK.....GSSDYKDDDDKGSSHHHHH 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
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14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1768	100.0	387	10	US-09-972-268-16
2	1706.5	96.5	426	10	US-09-972-268-15
3	1645	93.0	595	10	US-09-972-268-14
4	1636	92.5	437	10	US-09-972-268-31
5	1636	92.5	504	10	US-09-972-268-8
6	1636	92.5	510	10	US-09-972-268-10
7	1636	92.5	510	10	US-09-972-268-12
8	1602	90.6	542	10	US-09-972-268-2
9	1602	90.6	549	10	US-09-972-268-4
10	1602	90.6	549	10	US-09-972-268-6
11	1602	90.6	549	14	US-10-161-572-45
12	1602	90.6	634	10	US-09-972-268-13
13	1582	89.5	438	10	US-09-959-845-6
14	1582	89.5	438	10	US-09-972-268-19
15	1582	89.5	510	10	US-09-959-845-4

16	1582	89.5	510	10	US-09-972-268-18	Sequence 18, Appl
17	1562.5	88.4	549	10	US-09-959-845-2	Sequence 2, Appl
18	1562.5	88.4	549	10	US-09-972-268-17	Sequence 17, Appl
19	543.5	30.7	514	14	US-10-161-572-60	Sequence 60, Appl
20	543.5	30.7	517	10	US-09-972-268-20	Sequence 20, Appl
21	538.5	30.5	458	10	US-09-972-268-21	Sequence 21, Appl
22	521	29.5	518	9	US-09-919-172-20	Sequence 20, Appl
23	469.5	26.6	314	10	US-09-766-511B-36	Sequence 36, Appl
24	469.5	26.6	479	10	US-09-766-511B-35	Sequence 35, Appl
25	469.5	26.6	497	10	US-09-972-268-37	Sequence 37, Appl
26	469.5	26.6	510	10	US-09-766-511B-33	Sequence 33, Appl
27	469.5	26.6	510	12	US-10-058-270A-54	Sequence 54, Appl
28	469.5	26.6	510	14	US-10-161-572-55	Sequence 55, Appl
29	469.5	26.6	510	14	US-10-241-220-94	Sequence 94, Appl
30	469.5	26.6	510	15	US-10-295-027-66	Sequence 66, Appl
31	469.5	26.6	510	15	US-10-173-999-76	Sequence 76, Appl
32	467.5	26.4	510	10	US-09-972-268-24	Sequence 24, Appl
33	467.5	26.4	510	14	US-10-161-572-54	Sequence 54, Appl
34	465.5	26.3	498	10	US-09-972-268-39	Sequence 39, Appl
35	465.5	26.3	511	10	US-09-972-268-34	Sequence 34, Appl
36	465.5	26.3	580	10	US-09-972-268-36	Sequence 36, Appl
37	397.5	22.5	479	10	US-09-972-268-22	Sequence 22, Appl
38	397.5	22.5	479	14	US-10-161-572-62	Sequence 62, Appl
39	397.5	22.5	538	10	US-09-972-268-23	Sequence 23, Appl
40	397.5	22.5	538	10	US-09-984-130-138	Sequence 138, App
41	397.5	22.5	538	10	US-09-836-353A-138	Sequence 138, App
42	397.5	22.5	538	14	US-10-161-572-61	Sequence 61, Appl
43	397.5	22.5	538	15	US-10-411-010-17	Sequence 17, Appl
44	395.5	22.4	522	15	US-10-264-049-2969	Sequence 2969, Ap
45	387	21.9	424	12	US-10-383-201-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

Query Match 100.0%; Score 1768; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.5e-147;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	60
Db	58	GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	117
Qy	61	QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVEPTVSLIKG	177

XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
XX Claim 9; Page 100-102; 141pp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX Nectin DNA and protein are useful for treating a disease associated with
XX cell adhesion activity, adherens junction formation activity, epithelial
XX or endothelial barrier function activity, endothelial proliferation or
XX migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX asthma, allergy, allograft rejection, metastasis of cancer cells,
XX paracellular transport disorders such as magnesium transport defects in
XX the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX inhibiting angiogenesis in a mammal and treating endothelial migration,
XX proliferation or angiogenic condition of a tissue or a subject, such as
XX ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
XX stroke, restenosis, tumour growth and treating herpesvirus infection.
XX Nectin is also useful for modulating proliferation or migration of an
XX endothelial cell, an epithelial cell or a smooth muscle cell (vascular
XX smooth muscle cell). The present sequence is a fusion protein containing
XX human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region
XX SQ Sequence 634 AA;

Query Match 90.6%; Score 1602; DB 5; Length 634;
Best Local Similarity 98.7%; Pred. No. 1.3e-125;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPEKQT 306
Db 358 PPTTTT 363

RESULT 14
AAG63984
ID AAG63984 standard; protein; 438 AA.
XX AAG63984;
AC AAG63984;
XX 26-NOV-2001 (first entry)
DT
XX

DE Amino acid sequence of murine nectin-3.

XX Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
KW
XX Mus sp.

XX WO200166736-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP001871.

XX 09-MAR-2000; 2000JP-00065595.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.

XX Takahashi K, Takai Y, Nakanishi H, Sato K;

XX WPI; 2001-570771/64.

XX N-PSDB; AAH78181.

XX New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and
PT corresponding antibodies.

XX Claim 3; Page 53-55; 64pp; Japanese.

XX The present sequence represents a murine nectin-3 polypeptide. Nectin-3
CC is an immunoglobulin-like cell adhesion molecule that shows homophilic
CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
CC polynucleotides are useful for investigating the mechanisms of cell
CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
CC malignancies of various cancers, and the development of methods for the
CC treatment and prevention of cancer
XX SQ Sequence 438 AA;

Query Match 89.5%; Score 1582; DB 4; Length 438;
Best Local Similarity 95.5%; Pred. No. 3.7e-124;
Matches 294; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSS 308
Db 358 IPLTQTSS 365

RESULT 15
AAE23293
ID AAE23293 standard; protein; 438 AA.
XX
AC AAE23293;
XX

QY 61 QGRVLFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVWKHPALEKDIRYSPFILDIOYAPEVSVTGYNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVWKHPALEKDIRYSPFILDIOYAPEVSVTGYNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357
QY 301 VPFFKQT 306
Db 358 PPTTTT 363

RESULT 12
AAM39143
ID AAM39143 standard; protein; 555 AA.
XX
AC AAM39143;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2288.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-0048725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI58299.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 4; SEQ ID NO 2288; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,

CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 555 AA;
SQ
Query Match 90.6%; Score 1602; DB 4; Length 555;
Best Local Similarity 98.7%; Pred. No. 1.1e-125;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 64 GPIIPEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 123
QY 61 QGRVLFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 120
Db 124 QGRVLFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 183
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIISQYKLFPTTR 180
Db 184 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIISQYKLFPTTR 243
QY 181 FARGRRITCVWKHPALEKDIRYSPFILDIOYAPEVSVTGYNWFGVGRKGVNLKCNADANP 240
Db 244 FARGRRITCVWKHPALEKDIRYSPFILDIOYAPEVSVTGYNWFGVGRKGVNLKCNADANP 303
QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 304 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 363
QY 301 VPFFKQT 306
Db 364 PPTTTT 369

RESULT 13
AAE23287
ID AAE23287 standard; protein; 634 AA.
XX
AC AAE23287;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-IgG1Fc region fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.

FT	Key	Location/Qualifiers	
FT	Region	1..7	
FT		/note= "Mouse nectin-3 protein"	
FT	Region	8..549	
FT		/note= "Human nectin-3alpha protein"	
XX	WO200228902-A2.		
PN			
XX			
XX	11-APR-2002.		
XX			
PF	05-OCT-2001; 2001WO-US031392.		
XX			
PR	05-OCT-2000; 2000US-0238557P.		
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
PI	Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;		
XX			
DR	WPI; 2002-426103/45.		
DR	N-PSDB; AAD37441.		
XX			
PT	Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,		
PT	useful for treating or preventing heart failure, malaria,		
PT	glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,		
PT	sepsis, stroke.		
XX			
PS	Claim 1; Page 80-82; 141pp; English.		
XX			
CC	The invention relates to a substantially purified nectin3alpha, beta,		
CC	gamma and nectin-4 polypeptides and their corresponding polynucleotides.		
CC	Nectin DNA and protein are useful for treating a disease associated with		
CC	cell adhesion activity, adherens junction formation activity, epithelial		
CC	or endothelial barrier function activity, endothelial proliferation or		
CC	migration activity, viral polypeptide binding activity. The epithelial or		
CC	endothelial barrier function disorder which is treated by the above		
CC	mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,		
CC	asthma, allergy, allograft rejection, metastasis of cancer cells,		
CC	paracellular transport disorders such as magnesium transport defects in		
CC	the kidney or inflammatory bowel disease. Nectin DNA is also useful for		
CC	inhibiting angiogenesis in a mammal and treating endothelial migration,		
CC	proliferation or angiogenic condition of a tissue or a subject, such as		
CC	ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,		
CC	stroke, restenosis, tumour growth and treating herpesvirus infection.		
CC	Nectin is also useful for modulating proliferation or migration of an		
CC	endothelial cell, an epithelial cell or a smooth muscle cell (vascular		
CC	smooth muscle cell). The present sequence is a fusion protein containing		
CC	mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3		
CC	alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to		
CC	standardise OS field)		
XX			
SQ	Sequence 549 AA;		
	Query Match	90.6%; Score 1602; DB 5; Length 549;	
	Best Local Similarity	98.7%; Pred. No. 1e-125;	
	Matches 302; Conservative	0; Mismatches 4; Indels 0; Gaps 0;	
QY	1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60		
Db	58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117		
QY	61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 120		
Db	118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 177		
QY	121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPTR 180		
Db	178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPTR 237		
QY	181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFVGRKGNLKNADANP 240		
Db	238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFVGRKGNLKNADANP 297		
QY	241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300		
Db	298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357		
QY	301 VPFKQT 306		
Db	358 PPTTTT 363		
	RESULT 11		
	ABJ20222		
ID	ABJ20222 standard; protein; 549 AA.		
XX			
AC	ABJ20222;		
XX			
DT	13-AUG-2003 (first entry)		
XX			
DE	Human IG gene related protein SEQ ID No 45.		
XX			
KW	Breast cancer; p53 pathway modulating agent; IG; colon cancer;		
KW	kidney cancer; lung cancer; ovary cancer; human.		
XX			
OS	Homo sapiens.		
XX			
PN	WO200299040-A2.		
XX			
PD	12-DEC-2002.		
XX			
PF	03-JUN-2002; 2002WO-US017313.		
XX			
PR	05-JUN-2001; 2001US-0296076P.		
PR	10-CCT-2001; 2001US-0328605P.		
PR	22-CCT-2001; 2001US-0338733P.		
PR	15-FEB-2002; 2002US-0357253P.		
PR	15-FEB-2002; 2002US-0357600P.		
XX			
PA	(EXEL-) EXELIXIS INC.		
XX			
PI	Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;		
PI	Lioubin MN;		
XX			
DR	WPI; 2003-148660/14.		
XX			
PT	Identifying a candidate p53 pathway modulators that are useful as targets		
PT	for therapeutics or for diagnosing cancers associated with defective p53		
PT	function, by providing an assay system having a purified IG polypeptide		
PT	or nucleic acid.		
XX			
PS	Claim 13; Page 206-209; 248pp; English.		
XX			
CC	The invention relates to a novel method for identifying a candidate p53		
CC	pathway modulating agent. The method comprises providing an assay system		
CC	having a purified IG polypeptide or nucleic acid, or their functionally		
CC	active fragment or derivative. The method is useful for identifying		
CC	modulators of the p53 pathway, particularly for identifying agents for		
CC	treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung		
CC	cancer or cancer of the ovary) associated with defective p53 function.		
CC	The identified modulators are useful as targets for novel therapeutics.		
CC	The method is also useful for diagnosing disorders associated with		
CC	defective p53 function. The IG proteins or nucleic acids are useful as		
CC	modifiers of the p53 pathway, and as therapeutic targets for disorders		
CC	associated with defective p53 function. This sequence represents a human		
CC	protein relating to the human IG genes used in the assay for identifying		
CC	modulators of the p53 pathway of the invention		
XX			
SQ	Sequence 549 AA;		
	Query Match	90.6%; Score 1602; DB 6; Length 549;	
	Best Local Similarity	98.7%; Pred. No. 1e-125;	
	Matches 302; Conservative	0; Mismatches 4; Indels 0; Gaps 0;	
QY	1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60		
Db	58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117		

QY 241 PPFKSVWSRLDQWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQSRSDQKVIYISD 300
Db 291 PPFKSVWSRLDQWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQSRSDQKVIYISD 350
QY 301 VPFKQT 306
Db 351 PPTTTT 356

RESULT 9
ID AAE23283 standard; protein; 549 AA.

AC AAE23283;
XX 27-AUG-2002 (first entry)
XX Human nectin-3alpha protein.

KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
OS Homo sapiens.

XX Key Location/Qualifiers
FH Modified-site 73
FT Domain /note= "N-glycosylated"
FT 74. .152
FT /note= "Extracellular Ig domain"
FT 83
FT Modified-site /note= "N-glycosylated"
FT 125
FT /note= "N-glycosylated"
FT 186
FT Modified-site /note= "N-glycosylated"
FT 189. .250
FT Domain /note= "Extracellular Ig domain"
FT 222
FT Modified-site /note= "N-glycosylated"
FT 287. .342
FT Domain /note= "Extracellular Ig domain"
FT 331
FT Modified-site /note= "N-glycosylated"
FT 405. .424
FT Domain /note= "Transmembrane domain"
FT 425. .549
FT Domain /note= "C-terminal domain"

WO200228902-A2.

11-APR-2002.

05-OCT-2001; 2001WO-US031392.

05-OCT-2000; 2000US-0238557P.

(IMMV) IMMUNEX CORP.

Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

WPI; 2002-426103/45.

N-PSDB; AAD37442.

PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.

Claim 1; Page 89-91; 141pp; English.

CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha DNA.
CC Human nectin-3alpha gene is located on chromosome 3
XX

SQ Sequence 549 AA;

Query Match 90.6%; Score 1602; DB 5; Length 549;
Best Local Similarity 98.7%; Pred. No. 1e-125;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQSRSDQKVIYISD 357
QY 301 VPFKQT 306
Db 358 PPTTTT 363

RESULT 10

AAE23282

ID AAE23282 standard; protein; 549 AA.

AC AAE23282;

XX 29-AUG-2003 (revised)

DT 27-AUG-2002 (first entry)

XX Mouse nectin-3-human nectin 3alpha fusion protein.

KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
XX chromosome 3.

OS Homo sapiens.

OS Mus musculus.

XX Chimeric.

Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; stroke; tumour; cancer; herpesvirus infection; chromosome 3; asthma.

Homo sapiens.

WO200228902-A2.

11-APR-2002.

05-OCT-2001; 2001WO-US031392.

05-OCT-2000; 2000US-0238557P.

(IMMV) IMMUNEX CORP.

Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

WPI; 2002-426103/45.

N-PSDB; AAD37440.

Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, sepsis, stroke.

Claim 1; Page 76-78; 141pp; English.

The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3alpha protein containing 7 amino acids deleted from the N-terminal end. Human nectin-3 alpha gene is located on chromosome 3

Sequence 542 AA;

Query Match 90.6%; Score 1602; DB 5; Length 542;
Best Local Similarity 98.7%; Pred. No. 1e-125;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQYGFVSQGEY 60
Db 51 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQYGFVSQGEY 110
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 111 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 170
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTTR 180
Db 171 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTTR 230
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 240
Db 231 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 290

PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37445.

Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, sepsis, stroke.

Claim 1; Page 98-99; 141pp; English.

The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3beta protein. Human nectin-3beta gene is located on chromosome 3

Sequence 510 AA;

Query Match 92.5%; Score 1636; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365

RESULT 8
AAE23281
ID AAE23281 standard; protein; 542 AA.
XX AC AAE23281;
XX DT 27-AUG-2002 (first entry)
XX DE Human deleted nectin-3alpha protein.
XX

DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX Mouse nectin-3-human nectin-3beta fusion protein.
DE Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
XX paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX Key Location/Qualifiers
PH Region 1..6
FT /note= "Mouse nectin-3 pprotein"
FT Region 7..510
FT /note= "Human nectin-3beta protein"
XX WO200228902-A2.
PN 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI WPI; 2002-426103/45.
XX N-PSDB; AAD37444.
DR Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX Claim 1; Page 94-95; 14lpp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX Sequence 510 AA;
SQ
Query Match 92.5%; Score 1636; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.3e-128;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GPIIIVPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
|||||

Db 58 GPIIIVPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
OY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLTVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLTVEPTVSLIKG 177
OY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
OY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 297
OY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQSRSDQKVIYISD 357
OY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365
RESULT 7
AAE23286
ID AAE23286 standard; protein; 510 AA.
XX
AC AAE23286;
XX
DT 27-AUG-2002 (first entry)
XX Human nectin-3beta protein.
DE Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
XX paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
PH Modified-site 73
FT /note= "N-glycosylated"
FT Domain 74..152
FT /note= "Extracellular Ig domain"
FT Modified-site 83
FT /note= "N-glycosylated"
FT Modified-site 125
FT /note= "N-glycosylated"
FT Modified-site 186
FT /note= "N-glycosylated"
FT Domain 189..250
FT /note= "Extracellular Ig domain"
FT Modified-site 222
FT /note= "N-glycosylated"
FT Domain 287..342
FT /note= "Extracellular Ig domain"
FT Modified-site 331
FT /note= "N-glycosylated"
FT Domain 386..510
FT /note= "Intracellular C-terminal domain"
XX WO200228902-A2.
PN 11-APR-2002.
XX
PD 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.

XX cell adhesion activity, adherens junction formation activity, epithelial
PA or endothelial barrier function activity, endothelial proliferation or
PI migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
DR mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX asthma, allergy, allograft rejection, metastasis of cancer cells,
XX paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3gamma protein.
XX Human nectin-3gamma gene is located on chromosome 3
SQ Sequence 437 AA;
Query Match 92.5%; Score 1636; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.1e-128; Indels 0; Gaps 0;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357
QY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365
RESULT 5
AAE23284
ID AAE23284 standard; protein; 504 AA.
XX
AC AAE23284;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3beta protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.

XX (IMMV) IMMUNEX CORP.
PA Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI WPI; 2002-426103/45.
XX N-PSDB; AAD37443.
DR Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX Claim 1; Page 89-91; 141pp; English.
PS The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX
SQ Sequence 504 AA;
Query Match 92.5%; Score 1636; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.3e-128; Indels 0; Gaps 0;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 52 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 111
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 231
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db 232 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 291
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 292 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 351
QY 301 VPFKQTSS 308
Db 352 VPFKQTSS 359
RESULT 6
AAE23285
ID AAE23285 standard; protein; 510 AA.
XX
AC AAE23285;
XX

QY 301 VPFKQT-----SSRSGSDYKDDDDK 321
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPPLPLSTLATIKDDTIATRSGSDYKDDDDK 417
QY 322 GSSHHHHH 330
Db 418 GSSHHHHH 426

RESULT 3
AAE23288
ID AAE23288 standard; protein; 595 AA.
XX
AC AAE23288;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta-IgG1Fc region fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.

Claim 9; Page 102-104; 141pp; English.
XX
PS The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 595 AA;

Query Match 93.0%; Score 1645; DB 5; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.9e-129;
Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237
QY 181 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357
QY 301 VPFKQTSSRS 310
Db 358 VPFKQTSSRS 367

RESULT 4
AAE23299
ID AAE23299 standard; protein; 437 AA.
XX
AC AAE23299;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3gamma protein.
XX
KW Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37450.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 125-126; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta-
CC FLAGpolyHis fusion protein
XX

SQ Sequence 387 AA;

Query Match 100.0%; Score 1768; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 7.7e-140;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
CC |
CC |
CC |
DB 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
CC |
CC |
CC |
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
CC |
CC |
CC |
DB 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177
CC |
CC |
CC |
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 180
CC |
CC |
CC |
DB 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 237
CC |
CC |
CC |
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
CC |
CC |
CC |
DB 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
CC |
CC |
CC |
QY 241 PPKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
CC |
CC |
CC |
DB 298 PPKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
CC |
CC |
CC |
QY 301 VPFKQTSSRSGSSDYKDDDDKSSHHHHH 330
DB 358 VPFKQTSSRSGSSDYKDDDDKSSHHHHH 387
CC |
CC |
CC |

RESULT 2
AAE23289
ID AAE23289 standard; protein; 426 AA.

XX AAE23289;

DT 27-AUG-2002 (first entry)

XX Human nectin-3alpha-FLAGpolyHis fusion protein.

XX Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.

OS Homo sapiens.
OS Unidentified.
OS Chimeric.

XX Key Location/Qualifiers

FT Region 1..404
FT /note= "Human nectin-3alpha protein"
FT Region 405..420
FT /note= "FLAG peptide"
FT Region 421..426
FT /note= "PolyHis tag"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
PF
XX 05-OCT-2000; 2000US-0238557P.
PR
XX (IMMV) IMMUNEX CORP.
PA
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI WPI; 2002-426103/45.
XX
DR Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 104-105; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha-
CC FLAGpolyHis fusion protein
XX

SQ Sequence 426 AA;

Query Match 96.5%; Score 1706.5; DB 5; Length 426;
Best Local Similarity 87.8%; Pred. No. 1.3e-134;
Matches 324; Conservative 2; Mismatches 4; Indels 39; Gaps 1;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
DB |
DB |
DB |
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
DB |
DB |
DB |
DB 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177
CC |
CC |
CC |
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 180
DB |
DB |
DB |
DB 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 237
CC |
CC |
CC |
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
DB |
DB |
DB |
DB 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
CC |
CC |
CC |
QY 241 PPKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
DB |
DB |
DB |
DB 298 PPKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
CC |
CC |
CC |

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 39.8559 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-16_COPY_58_387
Perfect score: 1768
Sequence: 1 GPIIIEPHVTAVGKNVSLK.....GSSDYKDDDDKGSSHHHHH 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1768	100.0	387	5 AAE23290	Aae23290 Human nec
2	1706.5	96.5	426	5 AAE23289	Aae23289 Human nec
3	1645	93.0	595	5 AAE23288	Aae23288 Human nec
4	1636	92.5	437	5 AAE23299	Aae23299 Human nec
5	1636	92.5	504	5 AAE23284	Aae23284 Human del
6	1636	92.5	510	5 AAE23285	Aae23285 Mouse nec
7	1636	92.5	510	5 AAE23286	Aae23286 Human nec
8	1602	90.6	542	5 AAE23281	Aae23281 Human del
9	1602	90.6	549	5 AAE23283	Aae23283 Human nec
10	1602	90.6	549	5 AAE23282	Aae23282 Mouse nec
11	1602	90.6	549	6 ABJ20222	Abj20222 Human IG
12	1602	90.6	555	4 AAM39143	Aam39143 Human pol
13	1602	90.6	634	5 AAE23287	Aae23287 Human nec
14	1582	89.5	438	4 AAG63984	Aag63984 Amino aci
15	1582	89.5	438	5 AAE23293	Aae23293 Mouse nec
16	1582	89.5	510	4 AAG63983	Aag63983 Amino aci
17	1582	89.5	510	5 AAE23292	Aae23292 Mouse nec
18	1562.5	88.4	549	4 AAG63982	Aag63982 Amino aci
19	1562.5	88.4	549	4 AAG63985	Aag63985 Amino aci
20	1562.5	88.4	549	5 AAE23291	Aae23291 Mouse nec
21	1534.5	86.8	559	4 AAM40929	Aam40929 Human pol
22	1218	68.9	267	4 AAM93536	Aam93536 Human pol
23	543.5	30.7	514	6 ABJ20237	Abj20237 Human IG
24	543.5	30.7	517	3 AAY32390	Aay32390 Herpesvir
25	543.5	30.7	517	5 AAE23294	Aae23294 Human nec

26	538.5	30.5	458	5 AAE23295	Aae23295 Human nec
27	521	29.5	518	5 ABG77170	Abg77170 Prostate
28	469.5	26.6	497	5 AAE23303	Aae23303 Human nec
29	469.5	26.6	510	4 AAB93365	Aab93365 Human pro
30	469.5	26.6	510	4 AAU00471	Aau00471 Human TAN
31	469.5	26.6	510	5 ABJ05562	Abj05562 Breast Ca
32	469.5	26.6	510	6 ABJ20232	Abj20232 Human IG
33	469.5	26.6	510	6 ABR48229	Abu48229 Human bla
34	469.5	26.6	510	6 ABU56613	Abu56613 Lung canc
35	469.5	26.6	510	6 ABP97212	Abp97212 Tumour-as
36	469.5	26.6	510	7 ADB80512	Adb80512 Ovarian C
37	457.5	26.4	510	5 AAE23300	Aae23300 Human nec
38	457.5	26.4	510	6 ABJ20231	Abj20231 Human IG
39	465.5	26.3	498	5 AAE23305	Aae23305 Human nec
40	465.5	26.3	511	5 AAE23301	Aae23301 Human nec
41	465.5	26.3	580	5 AAE23302	Aae23302 Human nec
42	397.5	22.5	479	3 AAY32389	Aay32389 Herpesvir
43	397.5	22.5	479	5 AAE23296	Aae23296 Human nec
44	397.5	22.5	479	6 ABJ20239	Abj20239 Human IG
45	397.5	22.5	538	5 AAE23297	Aae23297 Human nec

ALIGNMENTS

RESULT 1
AAE23290
ID AAE23290 standard; protein; 387 AA.
XX
AC AAE23290;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta-FLAGpolyHis fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..365
FT /note= "Human nectin-3alpha protein"
FT Region 366..381
FT /note= "FLAG peptide"
FT Region 382..387
FT /note= "PolyHis tag"
XX
PD WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 105-107; 141pp; English.

RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308634; AAG30283.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 295
SQ SEQUENCE 295 AA; 33112 MW; 03E5C4DCB5032E7F CRC64;

Query Match 30.2%; Score 534.5; DB 11; Length 295;
Best Local Similarity 38.3%; Pred. No. 5.6e-38;
Matches 113; Conservative 58; Mismatches 113; Indels 11; Gaps 6;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYS 70
Db 3 GTDVVLHCSFANPLPSVKITQVTWQKATNGSKQNMAIYNPTMGVSVLPPEYKRVFLRPS 62

QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG--- 127
Db 63 FIDGTIRLSHLEDEGMVYCEFAFTPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRARKG 121

QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSPNETATIISQYKLFPTRFARGR 185
Db 122 QDDKVVVATCTTSANGKPPSVSVSWETRLKGEAEYQEIIRNPNGTIVTISRRLVPSREAHQ 181

QY 186 RITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVLNLCNADANPPPFKS 245
Db 182 SLACIVNY-HLDR-FRESLTNLNVQYEPEVTIEGFDGNWYLQRTDVKLTCADANPPATEY 239

QY 246 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 300
Db 240 HWTTLNGSLPKGVEAQNRITLFFRGPIINYSLAGTYICEATNPIGTRSGQVEVNITE 294

RESULT 10
Q9GL74 PRELIMINARY; PRT; 298 AA.
AC Q9GL74;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308635; AAG30284.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 298
SQ SEQUENCE 298 AA; 33309 MW; AEAD41842B8CA200 CRC64;

Query Match 29.9%; Score 528; DB 6; Length 298;
Best Local Similarity 37.6%; Pred. No. 2.1e-37;
Matches 112; Conservative 57; Mismatches 115; Indels 14; Gaps 6;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGSSQTVAVHHHPQYGFSGVQGEYQGRVLFK 67
Db 3 GTDVVLHCSFANPLPSVKITQVTWQKATNGSKQNVAIYNPMSGVSVLAPYRVERVEFL 62

QY 68 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG 127
Db 63 RPSFTDGTIRLSRLEDEGVVYCEFAFTPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRA 121

QY 128 ---GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSPNETATIISQYKLFPTRFA 182
Db 122 KKGQDDKVLVATCTTSANGKPPSVSVSWETRLKGEAEYQEIIRNPNGTIVTISRRLVPSREA 181

QY 183 RGRITCVVXHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVLNLCNADANPPP 242
Db 182 HQQSLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRMVMDVLTCKADANPPA 239

QY 243 FKSVMVSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 300
Db 240 TEVHTTLNGSLPKGVEAQNRITLFFKGPIISYLAGTYICEATNPIGTRSGQVEVNITE 297

RESULT 11
Q9GL75 PRELIMINARY; PRT; 295 AA.
AC Q9GL75;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308633; AAG30282.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 295
SQ SEQUENCE 295 AA; 33082 MW; 7C35D64022146AFA CRC64;

Query Match 29.8%; Score 526.5; DB 6; Length 295;
Best Local Similarity 38.7%; Pred. No. 2.8e-37;
Matches 115; Conservative 54; Mismatches 113; Indels 15; Gaps 8;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYS 70
Db 3 GTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPAMGVSVLAPYRVERVEFLRPS 62

QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSLI---DG 127
Db 63 FTDGTIRLSRLEDEGVYCEFAFTFPAGNRESQNLNLTVMAKPT-NWIEGTHAVLRARKG 121

QY 128 GNETV-AAICIAATGKPVAHIDWEGDL-GEMESTTTSPNETATIISQYKLFPTRFARGR 185
Db 122 QDEKVLVATCTTSANGKPPSVSVSWETRLKGEAEYQEIIRNPNGTIVTISRRLVPSREAHQ 181

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DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AK075105; BAC11404.1; -.
DR InterPro; IPR003599; Ig-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;

Query Match 68.9%; Score 1218; DB 4; Length 267;
Best Local Similarity 99.6%; Pred. No. 3.3e-97;
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db |||||
QY 61 QGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
QY 95 QGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 154
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPT 180
Db |||||
QY 155 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPT 214
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLK 233
Db |||||
QY 215 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLK 267

RESULT 7
QY412 PRELIMINARY; PRT; 407 AA.
AC QY412;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP566B0846.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;
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Query Match 65.0%; Score 1149; DB 4; Length 407;
Best Local Similarity 98.2%; Pred. No. 5.6e-91;
Matches 217; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 86 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPV 145
Db |||||
QY 146 HIDWEGDLGEMESTTTSFPNETATIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFI 205
Db |||||
QY 61 HIDWEGDLGEMESTTTSFPNETATIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFI 120
QY 206 LDIQYAPEVSVTYDGNWFWGKGVNLKCNADANPPPFKSVWSRLDQGWPDGGLASDNTL 265
Db |||||
QY 121 LDIQYAPEVSVTYDGNWFWGKGVNLKCNADANPPPFKSVWSRLDQGWPDGGLASDNTL 180
QY 266 HFVHPLTFNYSYGVYICKVTNSLQORSDDQKVIYISDVPEKQT 306
Db |||||
QY 181 HFVHPLTFNYSYGVYICKVTNSLQORSDDQKVIYISDVPEKQT 221

RESULT 8
Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to nectin 3, DKFZP566B0846 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 35.1%; Score 620; DB 4; Length 304;
Best Local Similarity 96.6%; Pred. No. 2.3e-45;
Matches 114; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 189 CVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLKCNADANPPPFKSVWS 248
Db |||||
QY 249 RLDGQWPDGGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQORSDDQKVIYISDVPEKQT 306
Db |||||

RESULT 9
Q9ERF5 PRELIMINARY; PRT; 295 AA.
AC Q9ERF5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
```


Q9JLB9 Q9JLB9 PRELIMINARY; PRT; 549 AA.
AC Q9JLB9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Sato-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299 (2000).
RL EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;

Query Match 88.4%; Score 1562.5; DB 11; Length 549;
Best Local Similarity 91.3%; Pred. No. 1.4e-126;
Matches 294; Conservative 10; Mismatches 13; Indels 5; Gaps 1;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAVCVATGKPVQAIDWEGDLGEMESTTSPNETATIVSQYKLPFTR 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 357

QY 301 VPFKQTSS-----RSGSSDYKD 317
Db 358 PPTTTTLQPTVQWHSSPADVQD 379

RESULT 5
Q9D006 PRELIMINARY; PRT; 549 AA.
ID Q9D006;
AC Q9D006;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2610301B19RIK protein.
GN PVRL3 OR 2610301B19RIK.
OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690 (2001).
DR EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:000515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;

Query Match 85.9%; Score 1518.5; DB 11; Length 549;
Best Local Similarity 88.8%; Pred. No. 8.8e-123;
Matches 286; Conservative 13; Mismatches 18; Indels 5; Gaps 1;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAVCVSTGKPVQAIDWEGDLGEMESTTSPNETATIVSQYELFPTTR 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 357

QY 301 VPFKQTSS-----RSGSSDYKD 317
Db 358 PPTTTTLQPTVQWHSSPADVQD 379

RESULT 6
Q8NC05 PRELIMINARY; PRT; 267 AA.
ID Q8NC05
AC Q8NC05;

QY	121	PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR	180
Dd	178	PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR	237
QY	181	FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGKGVNLKCNDANP	240
Dd	238	FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGKGVNLKCNDANP	297
QY	241	PPFKSVWSRLDGOWPDGLLASDNLTILHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIIYISD	300
Dd	298	PPFKSVWSRLDGOWPDGLLASDNLTILHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIIYISD	357
QY	301	VPFKQT	306
Dd	358	PPTTTT	363

RESULT	2
Q9JLB7	
ID	Q9JLB7 PRELIMINARY; PRT; 438 AA.
AC	Q9JLB7;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Cell adhesion molecule nectin-3 gamma.
GN	PVRL3.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheraia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20209403; PubMed=10744716;
RA	Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA	Tachibana K., Mizoguchi A., Takai Y.;
RT	"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT	that shows homophilic and heterophilic cell-cell adhesion
RT	activities.";
RL	J. Biol. Chem. 275:10291-10299(2000).
DR	EMBL; AF195835; AAF63687.1; --.
DR	MGD; MGI:1930171; Pvrl3.
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR	GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR	GO; GO:0005515; F:protein binding; IPI.
DR	GO; GO:0007155; P:cell adhesion; IDA.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	Pfam; PF00047; ig; 2.
DR	SMART; SM00409; IG; 1.
DR	PROSITE; PS50835; IG LIKE; 3.
SQ	SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;

	Query Match	89.5%;	Score 1582;	DB 11;	Length 438;
	Best Local Similarity	95.5%;	Pred. No. 2e-128;		
	Matches 294;	Conservative	9;	Mismatches 5;	Indels 0; Gaps 0;
QY	1	GPIIVEPHVTAVGKNSLKLCLIEVNETITQISWEKIHGSSQTQAVVHHPQYGFVSQGEY	60		
Db	58	GSIIVEPHVTAVGKNSLKLCLIEVNETITQISWEKIHGSKTQTAVVHHPQYGFVSQGDY	117		
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK	120		
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK	177		
QY	121	PDSLIDGGNETVAAICIAATGKPPVAHIDWEGDLGEMESSTTSPNETATIIISQYKLFPTTR	180		
Db	178	PDSLIDGGNETVAAVCVAATGKPPVAQIDWEGDLGEMESSTTSPNETATIVSQYKLFPTTR	237		
QY	181	FARGRRITCVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGWNLKCNDANP	240		
Db	238	FARGRRITCVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGWNLKCNDANP	297		
QY	241	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD	300		

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||||| 298 PPFKSVWSRLDQWFDGLLASDNTLHFVHPLTVNYSGVYVCKVSNLQORSDDQKVIYISD 357
|||||
Db 301 VPFKQTSS 308
QY : ||||
Db 358 IPLTQTSS 365

RESULT 3
Q9JLB8 ID Q9JLB8 PRELIMINARY; PRT; 510 AA.
AC Q9JLB8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 beta.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195834; AAF63686.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;

```

RESULT 4

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 26.8012 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-16_COPY_58_387
Perfect score: 1768
Sequence: 1 GPIIVEPHVTAVWGKNVSLK.....GSSDYKDDDDKGSSHHHHH 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1602	90.6	549	4 Q9NQS3	Q9nqs3 homo sapien
2	1582	89.5	438	11 Q9JLB7	Q9jlb7 mus musculu
3	1582	89.5	510	11 Q9JLB8	Q9jlb8 mus musculu
4	1562.5	88.4	549	11 Q9JLB9	Q9jlb9 mus musculu
5	1518.5	85.9	549	11 Q9D006	Q9d006 mus musculu
6	1218	68.9	267	4 Q8NC05	Q8nc05 homo sapien
7	1149	65.0	407	4 Q9Y412	Q9y412 homo sapien
8	620	35.1	304	4 Q9BVA9	Q9bva9 homo sapien
9	534.5	30.2	295	11 Q9ERF5	Q9erf5 mesocricetu
10	528	29.9	298	6 Q9GL74	Q9gl74 cercopithec
11	526.5	29.8	295	6 Q9GL75	Q9gl75 bos taurus
12	469.5	26.6	510	4 Q96NY8	Q96ny8 homo sapien
13	469.5	26.6	510	4 Q96K15	Q96k15 homo sapien
14	454.5	25.7	483	11 Q9DBP8	Q9dbp8 mus musculu
15	454.5	25.7	508	11 Q8R007	Q8r007 mus musculu
16	454.5	25.7	508	11 Q8CED8	Q8ced8 mus musculu

17	419	23.7	467	11	Q91VT9	Q91vt9 mus musculu
18	419	23.7	467	11	Q8C6F2	Q8c6f2 mus musculu
19	414	23.4	530	11	Q80XJ5	Q80xj5 mus musculu
20	397.5	22.5	449	4	Q9UEI6	Q9uei6 homo sapien
21	390	22.1	403	6	Q8HY15	Q8hy15 lemur catta
22	388.5	22.0	412	11	Q9R1E1	Q9rie1 rattus norv
23	387	21.9	417	4	Q96BJ1	Q96bj1 homo sapien
24	383.5	21.7	400	6	Q8HY16	Q8hy16 cebus apell
25	383.5	21.7	412	11	Q63611	Q63611 rattus norv
26	377	21.3	408	11	Q91WP1	Q91wp1 mus musculu
27	375.5	21.2	401	6	Q08835	Q08835 cercopithec
28	375	21.2	408	11	Q8K094	Q8k094 mus musculu
29	374	21.2	408	11	Q8BVF6	Q8bvf6 mus musculu
30	339.5	19.2	412	6	Q8HY14	Q8hy14 oryctolagus
31	333	18.8	415	11	Q60977	Q60977 mus musculu
32	264.5	15.0	442	4	Q9BY67	Q9by67 homo sapien
33	262.5	14.8	443	4	Q8N2F4	Q8n2f4 homo sapien
34	262.5	14.8	445	11	Q8K3T6	Q8k3t6 mus musculu
35	262.5	14.8	445	11	Q8R4L1	Q8r4l1 mus musculu
36	262.5	14.8	456	11	Q8R5M8	Q8r5m8 mus musculu
37	260	14.7	417	11	Q7TNL1	Q7tnl1 mus musculu
38	257.5	14.6	394	13	Q7ZXX1	Q7zxx1 xenopus lae
39	256.5	14.5	333	4	Q86WB8	Q86wb8 homo sapien
40	253.5	14.3	336	11	Q9D6E7	Q9d6e7 mus musculu
41	253.5	14.3	336	11	Q80VG4	Q80vg4 mus musculu
42	252	14.3	800	5	Q86LF9	Q86lf9 drosophila
43	252	14.3	801	5	Q86LF8	Q86lf8 drosophila
44	229	13.0	551	5	Q8MSN7	Q8msn7 drosophila
45	229	13.0	956	5	Q9W4T9	Q9w4t9 drosophila

ALIGNMENTS

RESULT 1

Q9NQS3					
ID	Q9NQS3	PRELIMINARY;	PRT;	549	AA.
AC	Q9NQS3;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Nectin 3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Reymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,				
RA	Dubreuil P., Lopez M.;				
RT	"Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that				
RT	interacts with afadin.";				
RL	Gene 0:0-0(2000).				
DR	EMBL; AF282874; AAF97597.1; -.				
DR	InterPro; IPR003599; IG.				
DR	InterPro; IPR007110; IG-like.				
DR	Pfam; PF00047; ig; 2.				
DR	SMART; SM00409; IG; 1.				
DR	PROSITE; PS50835; IG LIKE; 3.				
SQ	SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;				

Query Match 90.6%; Score 1602; DB 4; Length 549;
Best Local Similarity 98.7%; Pred. No. 5.2e-130;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	1	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHPQYGFVSQGEY	60
Db	58	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHPQYGFVSQGEY	117
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVLVEPTVSLIKG	177

DR	Pfam; PF00047; ig; 5.	
DR	SMART; SM00060; FN3; 2.	
DR	SMART; SM00408; IGC2; 5.	
DR	PROSITE; PS50835; IG-LIKE; 5.	
KW	Cell adhesion; Glycoprotein; Transmembrane; Repeat;	
KW	Immunoglobulin domain; Alternative splicing; Signal.	
FT	SIGNAL	1 19
FT	CHAIN	20 853
FT	DOMAIN	20 719
FT	TRANSMEM	720 737
FT	DOMAIN	738 853
FT	DOMAIN	20 111
FT	DOMAIN	116 205
FT	DOMAIN	212 300
FT	DOMAIN	307 412
FT	DOMAIN	415 500
FT	DOMAIN	527 604
FT	DOMAIN	633 700
FT	DOMAIN	152 156
FT	DOMAIN	161 165
FT	DISULFID	41 96
FT	DISULFID	139 189
FT	DISULFID	235 286
FT	DISULFID	328 394
FT	DISULFID	435 488
FT	CARBOHYD	222 222
FT	CARBOHYD	314 314
FT	CARBOHYD	346 346
FT	CARBOHYD	432 432
FT	CARBOHYD	458 458
FT	CARBOHYD	487 487
SQ	SEQUENCE	853 AA; 93893 MW; E12FD49231A7A368 CRC64;
Query Match		
Best Local Similarity 10.1%; Score 178.5; DB 1; Length 853;		
Matches 80; Conservative 22.9%; Pred. No. le-06;		
Matches 80; Conservative 60; Mismatches 139; Indels 71; Gaps 17;		
QY	8 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFVSQGEYQGRVLEK	67
Db	222 NATANLGQSVTLVCNAEGFPEPT-VSWTK-----DGEIENEDEKYLFS	265
QY	68 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSLDG	127
Db	266 D---DSSELTIRKVDKNDKDEAEYVCIAEN-KAGEQDASIHKLKVFAPKPKITYVENQTAM--E	319
QY	128 GNETVAAICIAATGKPVAHIDWE---GDLGEMESTTSPNETATI-----ISQ	173
Db	320 LEEQVTLTC-EASGDPIPSITWRTSTRNISSEKASWTRPEKQETLDGHMVVRSHARVSS	378
QY	174 YKLFPTRFARGRRITCVWKHPALEKDIRYSFILDQYAPE---VSVTGYDGNWVFGKRG	229
Db	379 LTLKSIQYTDAGEYVCTASN-TIGQDSQ-SMYLEVQYAPKLGQPVAVYTWEGN-----Q	430
QY	230 VNLKCNADANPPFPKSVWSRLDQGWPDGLASDNTLHF-----VHPLTFNYSYG	277
Db	431 VNITCEVFAYPSATIS-WFR-DGQ---LLPSSNYSNIKIYNTPSASYLEVTPDSENDFG	484
QY	278 VYICKVTNSLQGRSDQKVIYISDVP---FKQTSRSRSGSSDYKDDDKGS	323
Db	485 NYNCTAVNRIGQESLEFVLVQADTPSSPSIDQVEPYSSTAQVQFDEPEAT	534
RESULT 14		
DSCA_HUMAN		
ID	DSCA_HUMAN	STANDARD; PRT; 2012 AA.
AC	O60469; O60468;	
DT	16-OCT-2001 (Rel. 40, Created)	
DT	16-OCT-2001 (Rel. 40, Last sequence update)	
DT	10-OCT-2003 (Rel. 42, Last annotation update)	
DE	Down syndrome cell adhesion molecule precursor (CHD2).	
GN	DSCAM.	
OS	Homo sapiens (Human).	

OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.	
RC	TISSUE=Brain;	
RX	MEDLINE=98087574; PubMed=9426258;	
RA	Yamakawa K., Huot Y.-K., Haendelt M.A., Hubert R., Chen X.-N.,	
RA	Lyons G.B., Korenberg J.R.;	
RT	"DSCAM: a novel member of the immunoglobulin superfamily maps in a	
RT	Down syndrome region and is involved in the development of the	
RT	nervous system.";	
RL	Hum. Mol. Genet. 7:227-237(1998).	
RN	[2]	
RP	SEQUENCE FROM N.A., AND FUNCTION.	
RX	MEDLINE=20384934; PubMed=10925149;	
RA	Agarwala K.L., Nakamura S., Tsutsumi Y., Yanakawa K.;	
RT	"Down syndrome cell adhesion molecule DSCAM mediates homophilic	
RT	intercellular adhesion.";	
RL	Brain Res. Mol. Brain Res. 79:118-126(2000).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20289799; PubMed=10830953;	
RA	Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T.,	
RA	Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Groner Y.,	
RA	Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K.,	
RA	Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,	
RA	Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W.,	
RA	Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S.,	
RA	Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,	
RA	Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P.,	
RA	Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H.,	
RA	Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,	
RA	Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,	
RA	Lehrach H., Reinhardt R., Yaspo M.-L.;	
RT	"The DNA sequence of human chromosome 21.";	
RL	Nature 405:311-319(2000).	
CC	-!- FUNCTION: CELL ADHESION MOLECULE THAT CAN MEDIATE CATION-	
CC	INDEPENDENT HOMOPHILIC BINDING ACTIVITY. COULD BE INVOLVED IN	
CC	NERVOUS SYSTEM DEVELOPMENT.	
CC	-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE). THE	
CC	SHORT ISOFORM MAY BE SECRETED.	
CC	-!- ALTERNATIVE PRODUCTS:	
CC	Event=Alternative splicing; Named isoforms=2;	
CC	Name=Long; Synonyms=CHD2-52;	
CC	Isold=O60469-1; Sequence=Displayed;	
CC	Name=Short; Synonyms=CHD2-42;	
CC	Isold=O60469-2; Sequence=VSP_002502, VSP_002503;	
CC	-!- TISSUE SPECIFICITY: Primarily expressed in brain.	
CC	-!- SIMILARITY: Contains 10 immunoglobulin-like C2-type domains.	
CC	-!- SIMILARITY: Contains 6 fibronectin type III domains.	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	
CC	the European Bioinformatics Institute. There are no restrictions on its	
CC	use by non-profit institutions as long as its content is in no way	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/	
CC	or send an email to license@isb-sib.ch).	
CC	-----	
CC	EMBL; AF023450; AAC17967.1; --	
DR	EMBL; AF023449; AAC17966.1; --	
DR	EMBL; AF217525; AAF27525.1; --	
DR	EMBL; AL163283; CAB90464.1; --	
DR	EMBL; AL163282; CAB90436.1; --	
DR	EMBL; AL163281; CAB90444.1; --	
DR	Genew; HGNC:3039; DSCAM.	
DR	MIM; 602523; --	
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.	
DR	GO; GO:0005624; C:membrane fraction; TAS.	
DR	GO; GO:0007155; P:cell adhesion; TAS.	
DR	GO; GO:0007399; P:neurogenesis; TAS.	
DR	InterPro; IPR008957; FN_III-like.	

DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR002049; Laminin_EGF.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00047; ig; 22.
DR Pfam; PF00052; laminin_B; 3.
DR Pfam; PF00053; laminin_EGF; 7.
DR Pfam; PF00054; laminin_G; 3.
DR Pfam; PF00057; ldl_recept_a; 4.
DR Pfam; PF01390; SEA; 1.
DR PRINTS; PR00261; LDLRECEPTOR.
DR ProDom; PD003031; Laminin_B; 3.
DR SMART; SM00181; EGF; 15.
DR SMART; SM00180; EGF_Lam; 12.
DR SMART; SM00409; IG; 22.
DR SMART; SM00406; IGC2; 21.
DR SMART; SM00406; IGV; 7.
DR SMART; SM00281; LamB; 3.
DR SMART; SM00282; LamG; 3.
DR SMART; SM00192; LDLa; 4.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 4.
DR PROSITE; PS50835; IG_LIKE; 22.
DR PROSITE; PS50025; LAM_G DOMAIN; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
DR PROSITE; PS01209; LDLRA_1; 4.
DR PROSITE; PS50068; LDLRA_2; 4.
DR PROSITE; PS50024; SEA; 1.
KW Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; Laminin EGF-like domain; Disease mutation.
FT SIGNAL 1 21
FT CHAIN 22 4391
FT 80 194
FT DOMAIN 198 235
FT DOMAIN 284 320
FT DOMAIN 324 360
FT DOMAIN 367 404
FT DOMAIN 405 504
FT DOMAIN 521 530
FT DOMAIN 531 730
FT DOMAIN 731 763
FT DOMAIN 764 813
FT DOMAIN 814 871
FT DOMAIN 879 923
FT DOMAIN 924 933
FT DOMAIN 934 1125
FT DOMAIN 1126 1158
FT DOMAIN 1159 1208
FT DOMAIN 1209 1265
FT DOMAIN 1275 1324
FT DOMAIN 1325 1334
FT DOMAIN 1335 1529
FT DOMAIN 1530 1562
FT DOMAIN 1563 1612
FT DOMAIN 1613 1670
FT DOMAIN 1677 1771
FT DOMAIN 1772 1865
FT DOMAIN 1866 1955
FT DOMAIN 1956 2051
FT DOMAIN 2052 2151
FT DOMAIN 2152 2244
FT DOMAIN 2245 2340
FT DOMAIN 2341 2436
FT DOMAIN 2437 2533
FT DOMAIN 2534 2629

FT DOMAIN 2630 2726 IG-LIKE C2-TYPE 12.
Query Match 10.6%; Score 187; DB 1; Length 4391;
Best Local Similarity 24.1%; Pred. No. 1.8e-06;
Matches 76; Conservative 50; Mismatches 132; Indels 58; Gaps 15;
QY 2 PIIVE---PHVTAVMGKNSLKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFVSQV 58
Db 2926 PIYIEASSSHVTE--GQTLNLNCVVP-GQAHAQVTTYKRG-----SLPARHQTHG----- 2973
QY 59 EYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVV----- 109
Db 2974 -----SQLRLHLVSPADSGEYVCRASGPGPEQEAFTVTVPPEGSSYR 3018
QY 110 LVEPTVSLIKGPDLSLIDGGNETVAAICIAATKPVAHIDWEGDLGEMESTTTSFPNETAT 169
Db 3019 LRSPVIS-IDPPSSTVQQGD-ASPKCLIHDAAPISLEWKTRNQELEDNVHISP-----GS 3074
QY 170 IISQYKLFPTFRFARRRITCVVVKHPALEKDIRYSFI-LDIOYAPEVSVTYDGNWVFVGRK 228
Db 3075 IIT---IVGTRPSNHGTYRCVASN---AYGVAQSVVNLVHGPTVSVLPEGPVWVKVGK 3128
QY 229 GYNLKCNDADANPPFKSVMSRLDG-----QWPDGLLASDNTLHVFHPLTFNYSGVYICK 282
Db 3129 AVTLEC-VSAGEPRSSARWTRISSTPAKLEQRTYGLMDSHAVLQ-ISSAKPSDAGTYVCL 3186
QY 283 VTNSLQGRSDQKVIYI 298
Db 3187 AQNALGTAQKQVEVIV 3202
RESULT 12
NCM2 HUMAN
ID_NCM2 HUMAN STANDARD; PRT; 837 AA.
AC O15394;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2).
GN NCAM2 OR NCAM21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369930; PubMed=9226371;
RA Paoloni-Giacobino A., Chen H., Antonarakis S.E.;
RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2) that maps to chromosome region 21q21 and is potentially involved in Down syndrome.";
RT Genomics 43:43-51(1997).
RN [2]
RP CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: May play important roles in selective fasciculation and zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal brain.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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QY      18 SLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSINDATIT 77
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db      48 SLKCSLQNAQEAALIVTQKKKAVSPENMVTFSENHGVIQPAYKKKINITQLGLQNSTIT 107
QY      78 LHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSL-IGPDSLIDGNETVAAIC 136
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db      108 FWNITLEDEGCMCLPNTFGFGKISGTACLTVVVQPIVSLHYKFSEDHLN-----IT 159
QY      137 IAATGKPVAHIDWEGDLGEMESTTT--SFPNETATIIISQYKLFPTFRFARGRRITCVVKHP 194
      ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db      160 CSATARPAPMVFVKVPRSGIENSTVTLSPNGTTSVLSILHIKDPKNOVGKEVICQVLHL 219
QY      195 ALEKDIRYSFILDIAPEVSVTGYDGNWF 224
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db      220 GTVTDFKQ-----TVNKGWYF 235

RESULT 11
PGBM_HUMAN
ID_PGBM_HUMAN STANDARD; PRT; 4391 AA.
AC P98160; Q16287; Q9H3V5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basement membrane heparan sulfate proteoglycan core protein: a
RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Skin;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple
RT domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
RX MEDLINE=20553141; PubMed=11101850;
RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
RA Hentati F., Fontaine B.;
RT "perlecan, the major proteoglycan of basement membranes, is altered in
RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";
RL Nat. Genet. 26:480-483(2000).
RN [4]
RP SEQUENCE OF 1016-1470 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [5]
RP SEQUENCE OF 890-1396 FROM N.A.
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RC
RX TISSUE=Fibrosarcoma;
RA MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to 1p36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [6]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
RN [7]
RP CARBOHYDRATE-LINKAGE SITE ASN-2121.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel
CC syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder
CC characterized by permanent myotonia (prolonged failure of muscle
CC relaxation) and skeletal dysplasia, resulting in reduced stature,
CC kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.
CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 3 laminin IV domains.
CC -!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X62515; CAA44373.1; -.
CC EMBL; M85289; AAA52700.1; -.
CC EMBL; AL445795; CAC18534.1; -.
CC EMBL; M64283; AAA52699.1; -.
CC EMBL; S76436; AAB21121.2; -.
CC EMBL; L22078; -; NOT_ANNOTATED_CDS.
CC PIR; A38096; A38096.
CC HSSP; P00740; 1EDM.
CC Siena-2DPAGE; P98160; -.
CC Genew; HGNC:5273; HSPG2.
CC MIM; 142461; -.
CC MIM; 255800; -.
CC InterPro; IPR008985; ConA_like_lec_gl.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
```


Matches		91; Conservative	52; Mismatches	126; Indels	112; Gaps	19;
QY	2	PIIVPEP-----HVTAVGKQVSLKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFVSQ	57			
Db	209	PAIMPMQKSFNATAERGEEMTLTKKASGSPDT-ISWFR-----	246			
QY	58	GEYQGRVLPKN--YSL--NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEP	113			
Db	247	---NGKLIENEKYLKGSNTELTIVRNINKDGGSYVCKA-TNKAGEDQKQAFLOVFVQP	302			
QY	114	TVSLIKGPDSLIDGGNET-----VAAICIAATGKPVAHIDWEGDL-GEMESTTTSPNE	166			
Db	303	HILQLK-----NETTSENGHVTLVC-EAEGEPVPEITWKRAIDGVMESEGDKSPDG	352			
QY	167	TATIISQYKLPFTRFARGRRITCVVKHPALEKDIRY-----SFILDIQYAP-	212			
Db	353	RIEVKGQH-----GRSSLHIRDVKLSDSGRYDCEAASRIGGHQKQSMHLLDIEYAPK	402			
QY	213	---EVSVTGYDGNWVGRKGVNLKCNADANPPFKSV-WSRLDGGWPDGLLASDNTLHF	267			
Db	403	FVSNQTMYYSEGN-----PINISCDVTANPP--ASIHWR-----EKLKLPKANTTHL	449			
QY	268	-----VHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVPEK-----QTSS	308			
Db	450	KTHSVGRKMILEIAPTSNDNDFGRYNCTATNIGTRFQEIYLELADVPSPPHGVKIIELSQ	509			
QY	309	RSGSSDYKDDDDKSSHHHHH	329			
Db	510	TTAKISFNKPESHGGVPIHHY	530			

RESULT 10
OX2G HUMAN
ID_OX2G HUMAN STANDARD; PRT; 278 AA.
AC P41217; Q8TB85; Q9H3J3;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE OX-2 membrane glycoprotein precursor (CD200 antigen) (My033 protein).
GN MOX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 5-278 FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=87192943; PubMed=3032785;
RA McCaughan G.W., Clark M.J., Barclay A.N.;
RT "Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein."
RL Immunogenetics 25:329-335(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal brain;
RA Mao Y.M., Xie Y., Zheng Z.H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Costimulate T cell proliferation. May regulate myeloid cell activity in a variety of tissues.
CC -!- SUBUNIT: Interacts with OX2R.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P41217-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P41217-2; Sequence=VSP 002613;
CC Note=No experimental confirmation available;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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CC -----
CC EMBL; X05323; CAA28943.1; -;
CC EMBL; X05324; CAA28943.1; JOINED.
CC EMBL; X05325; CAA28943.1; JOINED.
CC EMBL; X05326; CAA28943.1; JOINED.
CC EMBL; AF063591; AAG43150.1; -;
CC EMBL; BC022522; AAH22522.1; -;
CC PIR; A47639; A47639.
CC Genew; HGNC:7203; MOX2.
CC MIM; 155970; -;
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; IG; 1.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS50835; IG LIKE; 1.
KW Antigen; Neurone; T-cell; Signal; Transmembrane;
KW Immunoglobulin domain; Glycoprotein; Alternative splicing.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 278 OX-2 MEMBRANE GLYCOPROTEIN.
FT DOMAIN 31 232 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 233 259 POTENTIAL.
FT DOMAIN 260 278 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 142 232 IG-LIKE C2-TYPE.
FT DISULFID 51 121 POTENTIAL.
FT DISULFID 160 214 POTENTIAL.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 110 110 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARSPLIC 268 278 GELSQQGVQKWT -> EP (in isoform 2).
FT /FTId=VSP 002613.
FT CONFLICT 11 11 S -> C (IN REF. 3).
FT CONFLICT 46 46 P -> T (IN REF. 1).
FT SEQUENCE 278 AA; 31264 MW; 38DF327B382CC970 CRC64;
SQ
Query Match 10.6%; Score 187.5; DB 1; Length 278;
Best local similarity 24.8%; Pred. No. 4.2e-08;
Matches 52; Conservative 36; Mismatches 97; Indels 25; Gaps 4;

FT DOMAIN 245 261 GLY-RICH.
FT DOMAIN 237 343 IG-LIKE C2-TYPE 3.
FT DOMAIN 346 419 IG-LIKE C2-TYPE 4.
FT DOMAIN 430 530 IG-LIKE C2-TYPE 5.
FT DOMAIN 637 660 GLN-RICH (OPA-REPEAT).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 764 AA; 82947 MW; 262225D2B2A1C181 CRC64;

Query Match 12.6%; Score 222; DB 1; Length 764;
Best Local Similarity 24.7%; Pred. No. 2.5e-10;
Matches 85; Conservative 56; Mismatches 135; Indels 68; Gaps 17;

QY 5 VEPH-VTAVWGKNSVLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGR 63
Db 32 MEPQDQTAVVGARVTLPCRV-INKQGT-LQWTK-----DDFGLGTSRDLGG- 75

QY 64 VLFKNYSL-----NDATITLHNIQFSDSGKYICKAVTFPLGNAQSSTT---VTVLVEPT 114
Db 76 --FERYAMVGSDEEGDYSLDIYFVMLDDDDARYQCQVSPGPEGQPAIRSTFAGLTVLVPPE 133

QY 115 VSLIKGPDSLIDGNETVAALICIAATGKPVAHIDWEGDLG-----EMESTTTSFPNETA- 168
Db 134 APKITQGDVIYATADRKVEIECVSGGKPAAEITWIDGLGNVLTNDNIEYTVIPLPDQRRF 193

QY 169 TIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFI-LDIQYAPEVSVT-----GYD 220
Db 194 TAKSVLRLTPKKEHNTNFSCQAQNTA-DRTYRSAKIRVEVKYAPKVKVNVWMSLPGGAG 252

QY 221 GNWVGRKG-----VNLKCNADANPPPFKSVMSRLDGQWPDGGLLASDN 263
Db 253 GS--VGGAGGSGVHMSTGSRIVEHSQVRLECRADANPSDVRVWFIND----EPIIGGQK 306

QY 264 TLHFVHPLTFNYSGVI-CKVNSLQGRSDQKVIYISDVP-FKQ 305
Db 307 TEMVIRNVTRKFHDAIVKCEVQNSVGKSESETLDSIYAPSPRQ 350

RESULT 9

NCM2_MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell adhesion molecule) (R4B12).
GN NCAM2 OR NCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
RX MEDLINE=97368238; PubMed=9221781;
RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA Kagamiyama H., Mori K.;
RT "OCAM: A new member of the neural cell adhesion molecule family related to zone-to-zone projection of olfactory and vomeronasal axons.";
RT J. Neurosci. 17:5830-5842 (1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX MEDLINE=97476194; PubMed=9334170;
RA Alenius M., Bohm S.;
RT "Identification of a novel neural cell adhesion molecule-related gene with a potential role in selective axonal projection.";
RT J. Biol. Chem. 272:26083-26086 (1997).

CC -!- FUNCTION: May play important roles in selective fasciculation and zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and attached to the membrane by a GPI-anchor (short isoform).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O35136-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=O35136-2; Sequence=VSP 002590;
CC -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and vomeronasal neurons in a zone-specific manner.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC -----
CC EMBL; AF001287; AAB69125.1; -.
DR EMBL; AF001286; AAB69124.1; -.
DR EMBL; AF016619; AAC53375.1; -.
DR MGD; MGI:97282; Ncam2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 837 NEURAL CELL ADHESION MOLECULE 2.
FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 698 718 POTENTIAL.
FT DOMAIN 719 837 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 108 IG-LIKE C2-TYPE 1.
FT DOMAIN 113 202 IG-LIKE C2-TYPE 2.
FT DOMAIN 208 297 IG-LIKE C2-TYPE 3.
FT DOMAIN 302 396 IG-LIKE C2-TYPE 4.
FT DOMAIN 401 491 IG-LIKE C2-TYPE 5.
FT DOMAIN 482 581 FIBRONECTIN TYPE-III 1.
FT DOMAIN 594 678 FIBRONECTIN TYPE-III 2.
FT DISULFID 42 93 PROBABLE.
FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 281 PROBABLE.
FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 694 837 TLFNGLGLGAIIGLGVAAALLILVTDVSCFFIRQCGLLMC
FT ITRMCGKSGSGSKSEEGKAAAYLKDGSKKEPVMWTE
FT DERITNHEDGSPVNEPNETPLTEPEKLPLKEENGKEVLNA
FT ETIEIKVSDNIIQSKEDDIKA -> NCCEANKGSGQSWH
FT LNAVFTFVITMSLSCLF (in isoform Short).
FT /FTid=VSP 002590.
SQ SEQUENCE 837 AA; 93203 MW; 70473B053A2D65A5 CRC64;

Query Match 12.2%; Score 215; DB 1; Length 837;
Best Local Similarity 23.9%; Pred. No. 1e-09;

Db 27 GDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESSMAVFHQTOGPN 85
 QY 52 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV 111
 Db 86 YSEPKRLEFFVAARL--GTELDRASLMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143
 QY 112 EP--TVSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTS--FPNET 167
 Db 144 KPQNTAEVQKVQLT----GKVPVVARCVSTGGRPPAHITWHSDLGMPNTSQAPGFLSGT 199
 QY 168 ATIIISQYKLFPTREARRRITCVVXKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227
 Db 200 VTVTSLWILVPSQVDGKSVTCKVEHESFEKPKQLLTVNLTVYYPPEVSIISGYDNNWYLSQ 259
 QY 228 KGVNLKCNADANPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSL 287
 Db 260 NEATLTCDARSNPEPTGYNWSTTMGPLPPFAVAQGAQL-LIRPVDKPINTFTICNVTNAL 318
 QY 288 GQRSDQKVIYISDVFPFKQTSSRSGS 312
 Db 319 GARQAELTVQKEGPPSEPSSGSSN 343

RESULT 6

PVR2_HUMAN STANDARD; PRT; 538 AA.
 AC Q92692; O75455; Q96J29;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Poliovirus receptor related protein 2 precursor (Herpes virus entry mediator B) (HvB) (Nectin 2) (CD112 antigen).
 GN PVR2 OR PRR2 OR HVB.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM DELTA).
 RX MEDLINE=95347610; PubMed=7622062;
 RA Eberle F., Dubreuil P., Mattei M.-G., Devilard E., Lopez M.;
 RT "The human PRR2 gene, related to the human poliovirus receptor gene (pvr), is the true homolog of the murine MPH gene.";
 RL Gene 159:267-272(1995).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RX MEDLINE=98321161; PubMed=9657005;
 RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
 RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
 RT "A cell surface protein with herpesvirus entry activity (HvB) confers susceptibility to infection by mutants of herpes simplex virus type 1, herpes simplex virus type 2, and pseudorabies virus.";
 RL Virology 246:179-189(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [4]
 RP SEQUENCE OF 31-538 FROM N.A.
 RA Yoshiura K., Murray J.C.;
 RT "A transcriptional map in the region of 19ql3 derived using direct sequencing and exon trapping.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE OF 449-538 FROM N.A.
 RX MEDLINE=99449047; PubMed=10520737;
 RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
 RA Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;
 RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene: PEREC1.";
 RL DNA Seq. 9:89-101(1998).
 CC -!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Delta;
 CC IsoId=Q92692-1; Sequence=Displayed;
 CC Name=Alpha;
 CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;
 CC -!- TISSUE SPECIFICITY: Ubiquitous.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:74-77(2000);
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/204270028_g.htm".
 CC -----
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 CC -----
 DR EMBL; X80038; CAA56342.1; -.
 DR EMBL; AF058448; AAC23797.1; -.
 DR EMBL; BC003091; AAH03091.1; -.
 DR EMBL; AF044968; AAC82348.1; -.
 DR EMBL; AF044962; AAC82348.1; JOINED.
 DR EMBL; AF044963; AAC82348.1; JOINED.
 DR EMBL; AF044964; AAC82348.1; JOINED.
 DR EMBL; AF044966; AAC82348.1; JOINED.
 DR EMBL; AF044967; AAC82348.1; JOINED.
 DR EMBL; AF050154; AAD02503.1; -.
 DR PIR; I68093; I68093.
 DR Genew; HGNC:9707; PVR2.
 DR MIM; 600798; -.
 DR GO; GO:0005886; C:plasma membrane; TAS.
 DR GO; GO:0015026; F:coreceptor activity; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003599; Ig.
 DR Pfam; PF00047; ig; 2.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 3.
 KW Immuglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
 KW Repeat; Alternative splicing.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 538 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.
 FT DOMAIN 32 360 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 361 381 POTENTIAL.
 FT DOMAIN 382 538 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 32 156 IG-LIKE V-TYPE.
 FT DOMAIN 162 256 IG-LIKE C2-TYPE 1.
 FT DOMAIN 261 345 IG-LIKE C2-TYPE 2.
 FT DISULFID 54 140 BY SIMILARITY.
 FT DISULFID 183 238 BY SIMILARITY.

KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
FT SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 530 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.
FT DOMAIN 32 351 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 352 372 POTENTIAL.
FT DOMAIN 373 530 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 147 IG-LIKE V-TYPE.
FT DOMAIN 153 247 IG-LIKE C2-TYPE 1.
FT DOMAIN 252 337 IG-LIKE C2-TYPE 2.
FT DISULFID 54 131 BY SIMILARITY.
FT DISULFID 174 229 BY SIMILARITY.
FT DISULFID 274 320 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 339 467 ESPSTAGAGATGGIIGGIIAIIATAVAGTGILICQQRKE
FT QRLQAADDEEELEGPPSYKPTPKAKLEPEMPSQLTIGA
FT SEHSPVKTPYFDAGVSCADQEMPRYHELPTLEERSGLLIG
FT ATGLGP -> DTPOASRDVGLVWGAVGTTLLVLLAGGFL
FT ALILLGRRRRKSPGGGNDGRGSDPKTQVFGNGCPVFW
FT RSASPEPMRPDGRDEDEEEEMKAEGLMLPPHESPKDDM
FT ESHLDGSLISRRVYV (in isoform Alpha).
FT /FTId=VSP 002630.
FT Missing (in isoform Alpha).
FT /FTId=VSP 002631.
FT SEQUENCE 530 AA; 57317 MW; 0ED71BFÄ2B231BBE CRC64;
SQ
Query Match 23.4%; Score 414; DB 1; Length 530;
Best Local Similarity 31.1%; Pred. No. 3.6e-26;
Matches 101; Conservative 51; Mismatches 143; Indels 30; Gaps 9;
QY 5 VEPHVTAVWGKNVSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVQGEY-- 60
Db 38 VLPEVRGRGLGTVLPCHLLPPTTERVSVQVTWQRLDG---TVVAAFHPSFGVDFPN SQFS 94
QY 61 QGRVLF-----KNYSINDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEP- 113
Db 95 KDRLSFVRARPETNADLRDATLAFRLGRVEDEGNYTCEFAFPNGTRRGVTWLRVIAQPE 154
QY 114 ----TVSLIKGPDSLIDGNETVAAICIAATKPVAHIDWEGDLGEMESTTTSFPN---E 166
Db 155 NHAEAQEVITGPQSV-----AVARCVSTGRRPPARITWISSLGG-EAKDTQEPGIQAG 206
QY 167 TATISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFPVG 226
Db 207 TWTIISRYSLVPVGRADGVKVTCTRVEHESFEPIILLPTLSVRYPPPEVSIISGYDDNWIYG 266
QY 227 RKGYNLKCNDANPPPKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNS 286
Db 267 RSEAILTCVRSNPEPTDYDNWSTSGVFPASAVAQGSQ-LVHSVDRMVNTTTFICTATNA 325
QY 287 LGQRSDQKVIYISDVFPKQTSRSRG 311
Db 326 VGTGRAEQVILVRESPSTAGAGATG 350
RESULT 5
PVR CERAE STANDARD; PRT; 417 AA.
AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
GN PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RX MEDLINE=93059651; PubMed=1331508;
RA Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
RT has no putative N-glycosylation site in the functional N-terminal
RT immunoglobulin-like domain.";
RL J. Virol. 66:7059-7066(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-2; Sequence=VSP 002622, VSP 002623;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL; D12611; BAA02136.1; -.
CC EMBL; D12612; BAA02137.1; -.
CC PIR; A44194; A44194.
CC PIR; B44194; B44194.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; ig; 3.
CC SMART; SMO0406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 3.
CC Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
KW SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 417 POLIOVIRUS RECEPTOR.
FT DOMAIN 21 343 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 344 367 POTENTIAL.
FT DOMAIN 368 417 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 24 139 IG-LIKE V-TYPE.
FT DOMAIN 145 237 IG-LIKE C2-TYPE 1.
FT DOMAIN 244 328 IG-LIKE C2-TYPE 2.
FT DISULFID 49 123 BY SIMILARITY.
FT DISULFID 166 221 BY SIMILARITY.
FT DISULFID 266 312 BY SIMILARITY.
FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 386 392 EHASASA -> HHQSCHN (in isoform Delta).
FT /FTId=VSP 002622.
FT Missing (in isoform Delta).
FT /FTId=VSP 002623.
SQ SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6E1F CRC64;
Query Match 22.7%; Score 400.5; DB 1; Length 417;
Best Local Similarity 31.1%; Pred. No. 3.3e-25;
Matches 101; Conservative 57; Mismatches 146; Indels 21; Gaps 10;
QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51
RN [1]
RP

FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 376 POTENTIAL.
FT DOMAIN 377 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 437 443 POLY-GLU.
FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;

Query Match 30.5%; Score 539.5; DB 1; Length 515;
Best local similarity 36.9%; Pred. No. 2.1e-36;
Matches 113; Conservative 56; Mismatches 126; Indels 11; Gaps 5;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPAMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICEFATFPAGNRESQNLITVMAKPT-NWIEGTQAVLRKKG 162
QY 128 -GNETVAAICIAATKPVVAHIDWEGDL-GEMESTTSPNETATIIISQYKLFPTFRFAGR 185
Db 163 KDDKVLVATCTSANGKPPSVSVSWETHLKGAEYQETRNPNGTVTVISRYLVPSREDHRQ 222
QY 186 RITCVVGHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKS 245
Db 223 SLACIVNYHM--DRFRESLTNVQYEPEVTIEGFGNWLQRMVDVCLKTKADANPPATEY 280
QY 246 VWSRLDGQWPDGLLASDNLHVFHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVPFKQ 305
Db 281 HWTTLNGSLPKGVEAQNRLFFRGPINYSMAGTYICEATNPITGRSQVQEVNITEFPYTP 340
QY 306 TSSRSQ 311
Db 341 SPPEHG 346

RESULT 4
PVR2_MOUSE STANDARD; PRT; 530 AA.
ID PVR2_MOUSE
AC P32507; Q62096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE poliovirus receptor related protein 2 precursor (Murine herpesvirus entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).
GN PVRL2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human poliovirus receptor gene."
RL J. Virol. 66:2807-2813(1992).

RN RP
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in interaction with poliovirus."
RL J. Biol. Chem. 269:8431-8438(1994).
RN RP
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RN CHARACTERIZATION.
RP MEDLINE=99214397; PubMed=10196354;
RX Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB) mediates entry of pseudorabies virus but not herpes simplex virus types 1 and 2."
RL J. Virol. 73:4493-4497(1999).
CC -!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P32507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P32507-2; Sequence=VSP 002630, VSP 002631;
CC -!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and liver.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC -----
CC EMBL; M80206; AAA39734.1; -.
CC EMBL; D26107; BAA05103.1; -.
CC EMBL; BC059941; AAH59941.1; -.
CC PIR; A38211; HLMSP3.
CC PIR; A53437; A53437.
CC MGD; MGI:97822; Pvrl2.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; ig; 3.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS50835; IG_LIKE; 3.
CC DR

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 5.27378 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-16_COPY_58_387

Perfect score: 1768

Sequence: 1 GPIIIEPHVTAWGKNVSLK.....GSSDYKDDDDKSSHHHHH 330

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	552.5	31.2	515	1	PVR1_MOUSE	Q9jfk6 mus musculus
2	543.5	30.7	517	1	PVR1_HUMAN	Q15223 homo sapien
3	539.5	30.5	515	1	PVR1_PIG	Q9gl76 sus scrofa
4	414	23.4	530	1	PVR2_MOUSE	P32507 mus musculus
5	400.5	22.7	417	1	PVR_CERAE	P32506 cercopithec
6	397.5	22.5	538	1	PVR2_HUMAN	Q92692 homo sapien
7	386	21.8	417	1	PVR_HUMAN	P15151 homo sapien
8	222	12.6	764	1	ICCR_DROME	Q08180 drosophila
9	215	12.2	837	1	NCM2_MOUSE	O35136 mus musculus
10	187.5	10.6	278	1	OX2G_HUMAN	P41217 homo sapien
11	187	10.6	4391	1	PGBM_HUMAN	P98160 homo sapien
12	185.5	10.5	837	1	NCM2_HUMAN	O15394 homo sapien
13	178.5	10.1	853	1	NCA1_BOVIN	P31836 bos taurus
14	174.5	9.9	2012	1	DSCA_HUMAN	O60469 homo sapien
15	174	9.8	588	1	C166_CHICK	P42292 gallus gall
16	171.5	9.7	626	1	MAG_MOUSE	P20917 mus musculus
17	170.5	9.6	626	1	MAG_HUMAN	P20916 homo sapien
18	169.5	9.6	626	1	MAG_RAT	P07722 rattus norv
19	168	9.5	702	1	CEA5_HUMAN	P06731 homo sapien
20	163.5	9.2	858	1	NCA1_RAT	P13596 rattus norv
21	163	9.2	761	1	NCA2_HUMAN	P13592 homo sapien
22	163	9.2	848	1	NCA1_HUMAN	P13591 homo sapien
23	162.5	9.2	278	1	OX2G_MOUSE	O54901 mus musculus
24	162.5	9.2	278	1	OX2G_RAT	P04218 rattus norv
25	162	9.2	353	1	CEPU_CHICK	Q90773 gallus gall
26	159.5	9.0	509	1	SHS1_RAT	P97710 r protein-t
27	158.5	9.0	3707	1	PGBM_MOUSE	Q05793 mus musculus
28	158	8.9	739	1	VCA1_MOUSE	P29533 mus musculus
29	158	8.9	1091	1	NCA1_CHICK	P13590 gallus gall
30	154.5	8.7	344	1	NTRI_MOUSE	Q99pj0 mus musculus
31	154.5	8.7	344	1	NTRI_RAT	Q62718 rattus norv
32	154.5	8.7	725	1	NCA2_MOUSE	P13594 mus musculus
33	154.5	8.7	1115	1	NCA1_MOUSE	P13595 mus musculus

34	152.5	8.6	344	1	NTRI_HUMAN	Q9pl21 homo sapien
35	152	8.6	337	1	OPCM_CHICK	Q98892 gallus gall
36	150	8.5	646	1	MU18_HUMAN	P43121 homo sapien
37	147.5	8.3	1088	1	NCA1_XENLA	P16170 xenopus lae
38	147	8.3	1709	1	SN_HUMAN	Q9bz22 homo sapien
39	146.5	8.3	345	1	OPCM_BOVIN	P11834 bos taurus
40	146	8.3	847	1	CD22_HUMAN	P20273 homo sapien
41	146	8.3	1018	1	CONT_HUMAN	Q12860 homo sapien
42	145	8.2	330	1	CD22_PONPY	Q9nie3 pongo pygma
43	144	8.1	359	1	LACH_DROME	Q24372 drosophila
44	143.5	8.1	1092	1	NCA2_XENLA	P36335 xenopus lae
45	142.5	8.1	332	1	CD22_PANPA	Q9nie5 pan paniscu

ALIGNMENTS

RESULT 1
PVR1_MOUSE
ID_PVR1_MOUSE STANDARD; PRT; 515 AA.
AC Q9JFK6; Q9ERL5; Q9JIL7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Hvec) (Nectin 1).
GN PVR1 OR PRR1 OR HVEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubreuil P., Campadelli-Fiume G.;
RT "The murine homolog of human nectin delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to GD.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
SEQUENCE FROM N.A.
RP MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-1alpha to human nectin-1alpha (Hvec) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781(2000).
RN [3]
SEQUENCE FROM N.A.
RP STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC EMBL; AF239762; AAF60333.1; -.

A:Accession: A47639

A:Molecule type: DNA

A; Cross-references: GB:X05323; NID:g34742; PIDN:CAA28943

C; Superfamily: MRC OX-2 antigen; immunoglobulin homology

F;40-119/Domain: immunoglobulin homology <

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Query Match 10.6%; Score 187.5; DB 2; Length 274;

Matches	52;	Conservative	36;	Mismatches	97
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QY 18 SLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDATIT 77

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Db 44 SLKCSLQNAQEALIVTWQKKKAVSPENMVTFSENHGVVIQPAYKDKINITQLGLQNSTIT 103

QY 78 LHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSL- IKGPDSLIDGGNETVAAIC 136

[illegible]

Db 104 FWNITLEDGCMCLFNTFFGFGKISGTACTVTVVQPIVSLHYKFSEDLN-----IT 155

1947

QY 137 IAATGKPVAHIDWEGDLGEMESTT--SFPNETATLISQYKLFPTRFARGRRITCVVRRHF 194

[illegible]

DB 156 CSATARFAPMVFKNVPRSGIENSVILSHFNGIISVISTLHINDEFNQQVGREVICQVLEHD 213

017 195 ALEKDTVPYSETI.DIOVAPREVSVTGYDGNWE 224

QY
193 ADEKTIKIBTIDDTYHFEVAVIGDGNNT 227

| :
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216 GTVTDKQ-----TVNKGWFE 231

[illegible]

Search completed: April 12, 2004, 09:47:07

Job time : 8.73199 secs

Db 253 GS--VGGAGGGSVHMTGSRIVEHSQVRLECRADANPSDVRWRFINDEPIIGGQK 306

QY 264 TLHFVHPLTFNYSGVYI-CKVTNSLQGRSDQKVYIISDVP-FKQ 305

Db 307 TEMVIRNVTRKFHDAIVKCEVQNSVGKSEDSSETLDISYAPSRQ 350

RESULT 13

T20992

hypothetical protein F15G9.4a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T20992; T24733

R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20992

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: DNA

A;Residues: 1-5175 <W1>

A;Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone F15G9

R;Kershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24733

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: DNA

A;Residues: 1-5175 <W12>

A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: CESP:F15G9.4a

A;Map position: X

A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1

Query Match 11.1%; Score 196.5; DB 2; Length 5175;

Best Local Similarity 26.4%; Pred. No. 4.3e-06;

Matches 88; Conservative 42; Mismatches 138; Indels 65; Gaps 19;

QY 2 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGE 59

Db 793 PTIIESPHTVRVNIERQVTLOCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG- 847

QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSL 117

Db 848 -----NLLITDAQI-----EDQGQFTCIARN-TYQQQSOSTILMTVGLVSPVLGH 891

QY 118 IKGPDLSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIISQYKLF 177

Db 892 VPPEEQLEGGDLTSL--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSL 943

QY 178 PTRFARGR---RITCVVKHPALEKDIRYSFIL----DIQYAPE-----VSVTYDGNW- 223

Db 944 RLRGGNPKDEGKYTCIAVSPAGNSTLHINVQLIKKPEFVYKPEGGIVFKPTISGMDEKHV 1003

QY 224 -----FVGRKGVNLKCNADANPPFPKSVWSRLDGQWP-----DGLLASDNTLHFVH 269

Db 1004 AVVNSTHDVLDGEGFAIPCVVSGTTPPI-ITW-YLDGR-PITPNSRDFTVTADNTL-IVR 1059

QY 270 PLTFNYSGVYICKVTNSLQGRSDQKVYIISDVP 302

Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTP 1092

RESULT 14

T43290

hemikentin precursor - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000

C;Accession: T43290; T20993; T24734

R;Vogel, B.E.; Hedgecock, E.M.

submitted to the EMBL Data Library, June 1998

A;Description: Hemikentin is required for hemidesmosome mediated cell adhesion and germ

A;Reference number: Z22396

A;Accession: T43290

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-5198 <VOG>

A;Cross-references: EMBL:AF074901; PIDN:AAC26792.1

R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20993

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: DNA

A;Residues: 1-5198 <W1>

A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

A;Experimental source: clone F15G9

R;Kershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24734

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: DNA

A;Residues: 1-5198 <W12>

A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: him-4; F15G9.4b

A;Map position: X

A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100

Query Match 11.1%; Score 196.5; DB 2; Length 5198;

Best Local Similarity 26.4%; Pred. No. 4.3e-06;

Matches 88; Conservative 42; Mismatches 138; Indels 65; Gaps 19;

QY 2 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGE 59

Db 793 PTIIESPHTVRVNIERQVTLOCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG- 847

QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSL 117

Db 848 -----NLLITDAQI-----EDQGQFTCIARN-TYQQQSOSTILMTVGLVSPVLGH 891

QY 118 IKGPDLSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIISQYKLF 177

Db 892 VPPEEQLEGGDLTSL--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSL 943

QY 178 PTRFARGR---RITCVVKHPALEKDIRYSFIL----DIQYAPE-----VSVTYDGNW- 223

Db 944 RLRGGNPKDEGKYTCIAVSPAGNSTLHINVQLIKKPEFVYKPEGGIVFKPTISGMDEKHV 1003

QY 224 -----FVGRKGVNLKCNADANPPFPKSVWSRLDGQWP-----DGLLASDNTLHFVH 269

Db 1004 AVVNSTHDVLDGEGFAIPCVVSGTTPPI-ITW-YLDGR-PITPNSRDFTVTADNTL-IVR 1059

QY 270 PLTFNYSGVYICKVTNSLQGRSDQKVYIISDVP 302

Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTP 1092

RESULT 15

A47639

OX-2 membrane glycoprotein precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000

C;Accession: A47639

R;McCaughan, G.W.; Clark, M.J.; Barclay, A.N.

Immunogenetics 25, 329-335, 1987

A;Title: Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein

A;Reference number: A47639; MUID:87192943; PMID:3032785

A;Gene: GDB:PVR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-417/Product: poliovirus receptor alpha #status predicted <PVRA>
F;21-343/Domain: extracellular #status predicted <EXT>
F;21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRB>
F;42-125/Domain: immunoglobulin homology <IMM1>
F;159-223/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM3>
F;344-367/Domain: transmembrane #status predicted <TMN>
F;368-417/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 21.9%; Score 387; DB 1; Length 417;
Best Local Similarity 30.4%; Pred. No. 4.7e-22;
Matches 99; Conservative 56; Mismatches 147; Indels 24; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNSVLKCLIEVNET---ITQISWEKIHGKSSQTVAVHH--PQ 51
Db 27 GDVVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQLTWTR-HGESGSMAYFHTQGPS 85

QY 52 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLV 111
Db 86 YSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLFVTFPGSRSVDIWLRLVA 143

QY 112 EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTT--TSFPNET 167
Db 144 KPQNTAEVQKVQLT---GEPVPMARCVSTGGRPPAQITWHSDDLGMPTNSQVPGFLSGT 199

QY 168 ATIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGR 227
Db 200 VTVTSWLILVPSQVGDGKNTCKVEHSEFEKPOLLTVNLTVYYPPEVSIISGYDNNWYLGQ 259

QY 228 KGVNLKCNADANPPPKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 260 NEATLTCDARSNPEPTGYNWSTMGPLPPFAVAQQAQL-LIRPVDKPINTTLCNVINAL 318

QY 288 GQRSDQKVIYISDVFPKQTSRSSGSS 313
Db 319 GARQAELTVQVKEGP---PSEHSGMS 341

RESULT 11
A54017
colon carcinoma-associated antigen pE4 precursor - rat
N;Alternate names: pE4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 01-Dec-1995
C;Accession: A54017; A61206
R;Chadaneau, C.; LeMoullac, B.; Denis, M.G.
J. Biol. Chem. 269, 15601-15605, 1994
A;Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinoma
A;Reference number: A54017; MUID:94253144; PMID:8195207
A;Accession: A54017
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <CHA>
A;Cross-references: GB:L12025
R;Chadaneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K.
Int. J. Cancer 47, 903-908, 1991
A;Title: Characterization, isolation and amino terminal sequencing of a rat colon carcinoma
A;Reference number: A61206; MUID:91184910; PMID:2010233
A;Accession: A61206
A;Molecule type: protein
A;Residues: 34-41, 'X', 43-53 <CH2>
A;Note: the residue at position 9 is suggested to be glycosylated asparagine
C;Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma cell
C;Keywords: glycoprotein; membrane protein

Query Match 17.8%; Score 314.5; DB 2; Length 416;
Best Local Similarity 29.1%; Pred. No. 1.7e-16;
Matches 91; Conservative 49; Mismatches 154; Indels 19; Gaps 9;

QY 1 GPIIVE--PHVTAVWGKNSVLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVS 56
Db 33 GEIAVQVLSNSTGLGGSTVLHCSLASKDNVTITQLTWKRDGSPFRACLPQEGPSI 92

QY 57 QGEYQGRVLF-KNY-SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVLEP- 113
Db 93 SDPERVKFLVAKVYEDLRNASLAISNLRVEDEGIYECQIATFPTGSKSANVWLKVFAFPK 152

QY 114 -TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPNETA 168
Db 153 NTAEALEPSPITLMPQD---VAKCISADGHPGPRITWSSNVNGSYREMKETGSSRAPPL 208

QY 169 TIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRK 228
Db 209 SATSPWCILLARQWARTSPAQWNMK--ASRSRTSRPLILSLPYPPEVSIISGYGNWYIGLT 266

QY 229 GVNLCNADANPPPKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSG-VYICKVTNSL 287
Db 267 NVNLTCEARSKPPTNYSWSTATGPLPNSTHFEQENGSHLLISTVDDLNNTIFVCKAINAL 326

QY 288 GQRSDQKVIYISD 300
Db 327 GSGQGQVTVLVKE 339

RESULT 12
A49448
irregular chiasm C-roughest precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: irreC-roughest protein
C;Species: Drosophila melanogaster
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 07-May-1999
C;Accession: A49448; S34129
R;Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brands
Genes Dev. 7, 2533-2547, 1993
A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal proj
A;Reference number: A49448; MUID:94102535; PMID:7503814
A;Accession: A49448
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-764 <RAM>
A;Cross-references: GB:L11040; NID:g304790; PID:g304791; EMBL:Z21641; NID:g312985; PID:
C;Genetics:
A;Gene: FlyBase:rst
A;Cross-references: FlyBase:FBgn0003285
C;Keywords: transmembrane protein

Query Match 12.6%; Score 222; DB 2; Length 764;
Best Local Similarity 24.7%; Pred. No. 4.3e-09;
Matches 85; Conservative 56; Mismatches 135; Indels 68; Gaps 17;

QY 5 VEPH-VTAVWGKNSVLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGR 63
Db 32 MEPQDQTAVVGARVTLPCR-V-INKQGT-LQWTK-----DDFGLGTSRDLSG- 75

QY 64 VLFKNYSL-----NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT---VTVLVEPT 114
Db 76 --FERYAMVGSDEEGYSLDIYPMVLDLDDARYQQVSPGPEGQPAIRSTFAGTLVLPPE 133

QY 115 VSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLG-----EMESTTTSFPNETA- 168
Db 134 APKITQGDVIYATADRKVEIECVSVGGKPAAEITWIDGLGNVLTNDNIEYTVIPLDQRRF 193

QY 169 TIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFI-LDIQYAPEVSVT-----GYD 220
Db 194 TAKSVLRLTPKKEHNTNFSCQAQNTA-DRYRSAKIRVEVKYAPKVKVNVNMSLPGGAG 252

QY 221 GNWVFGVRKG-----VNLKCNADANPPPKSVWSRLDGQWPDGGLASDN 263
Db 221 GNWVFGVRKG-----VNLKCNADANPPPKSVWSRLDGQWPDGGLASDN 263

B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: GB:S48817
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;259-314/Domain: immunoglobulin homology <IMM>

Query Match 22.7%; Score 400.5; DB 2; Length 392;
Best Local Similarity 31.1%; Pred. No. 4e-23;
Matches 101; Conservative 57; Mismatches 146; Indels 21; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQISWEKIHGKSSQTAVVH---PQ 51
Db 27 GDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGN 85

QY 52 YGFSVQGEYQGRVLFKKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV 111
Db 86 YSEPKRLEFVAARL--GTELRDASLRMFLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVLA 143

QY 112 EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTS--FPNET 167
Db 144 KPONTAEVQKVQLT----GKPVVARCVSTGGRRPPAHITWHSIDLGMPTNSQAPGFLSGT 199

QY 168 ATIIISQYKLFPTFRFARRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227
Db 200 VVTSLWILVPSQVDGKSVTCCKVEHSEFEKPQLLTVNLTVVYYPPEVSIISGYDNNWYLSQ 259

QY 228 KGVNLKCNADANPPPKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 260 NEATLTCDARSNPEPTGYNWSVTMGPLPPFAVAQGAQL-LIRPVDKPINTTFCNVTNAL 318

QY 288 QQRSDQKVIYISDVPFKQTSSRSQS 312
Db 319 GARQAELTVQVKEGPPSEPSGMSSN 343

Query Match 22.7%; Score 400.5; DB 2; Length 417;
Best Local Similarity 31.1%; Pred. No. 4.4e-23;
Matches 101; Conservative 57; Mismatches 146; Indels 21; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQISWEKIHGKSSQTAVVH---PQ 51
Db 27 GDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGN 85

QY 52 YGFSVQGEYQGRVLFKKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV 111
Db 86 YSEPKRLEFVAARL--GTELRDASLRMFLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVLA 143

QY 112 EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTS--FPNET 167
Db 144 KPONTAEVQKVQLT----GKPVVARCVSTGGRRPPAHITWHSIDLGMPTNSQAPGFLSGT 199

QY 168 ATIIISQYKLFPTFRFARRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227
Db 200 VVTSLWILVPSQVDGKSVTCCKVEHSEFEKPQLLTVNLTVVYYPPEVSIISGYDNNWYLSQ 259

QY 228 KGVNLKCNADANPPPKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 260 NEATLTCDARSNPEPTGYNWSVTMGPLPPFAVAQGAQL-LIRPVDKPINTTFCNVTNAL 318

QY 288 QQRSDQKVIYISDVPFKQTSSRSQS 312
Db 319 GARQAELTVQVKEGPPSEPSGMSSN 343

RESULT 7
I53960
PRR2 alpha - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I53960
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is t
A;Reference number: I53960; MUID:95347610; PMID:7622062
A;Accession: I53960
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-478 <RES>
A;Cross-references: GB:S79171; NID:gl042202; PID:gl042203
C;Genetics:
A;Gene: PRR2alpha
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 22.5%; Score 397.5; DB 2; Length 478;
Best Local Similarity 29.1%; Pred. No. 8.8e-23;
Matches 95; Conservative 57; Mismatches 132; Indels 43; Gaps 9;

QY 5 VEPHVTAVWGKNVSLKCLI---EVNETITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEY 60
Db 38 VLPEVRGQLGGTVLPCHELLPPVPGLYISLVTQWRPDAPANHQNVAFAHPKMGSPSPSPK 97

QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108
Db 98 PGERLSFVSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFATFPKGSVRGMTWLR 157

QY 109 VLVEP-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHI-----DWEGDLGE 155
Db 158 VIAPKNQAEAKVTFSDP-----TTVALCISKEGRPPARISWLSSLDWEAKETQ 208

QY 156 MESTTTSFPNETATIIISQYKLFPTFRFARRITCVVKHPALEKDIRYSFILDIOYAPEVS 215
Db 209 VSGTLAG---TVVTISRFTLVPSGRADGVTVTICKVEHSEFEERALIPVLSVRYYPEVS 264

QY 216 VTGYDGNWFVGRKGVNLKCNADANPPPKSVMSRLDQWPDGLLASDNTLHFVHPLTFNY 275
Db 265 ISGYDDNNWYLGRTDNLSCDVRNPEPTGYDWSSTSGTFTPTSAVAQGSQQL-VIHAVDSLF 323

QY 276 SGVYICKVTNSLQQRSDQKVIYISDVP 302
Db 324 NTFVCTVTNVAVGMRAGEQVIFVRETP 350

RESULT 8
I68093
PRR2 delta - human

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 8.73199 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-16_COPY_58_387
Perfect score: 1768
Sequence: 1 GPIIIEPHVTAVMGKNVSLK.....GSSDYKDDDDKGSSHHHHH 330

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:.*
1: pir1:.*
2: pir2:.*
3: pir3:.*
4: pir4:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1149	65.0	407	2 T08732	hypothetical prote
2	521	29.5	518	2 JC4024	poliovirus recepto
3	419	23.7	467	1 HLMSP3	poliovirus recepto
4	414	23.4	530	2 A53437	poliovirus recepto
5	400.5	22.7	392	2 B44194	poliovirus recepto
6	400.5	22.7	417	2 A44194	poliovirus recepto
7	397.5	22.5	478	2 I53960	PRR2 alpha - human
8	397.5	22.5	538	2 I68093	PRR2 delta - human
9	387	21.9	392	1 RWHUPD	poliovirus recepto
10	387	21.9	417	1 RWHUPA	poliovirus recepto
11	314.5	17.8	416	2 A54017	colon carcinoma-as
12	222	12.6	764	2 A49448	irregular chiasm C
13	196.5	11.1	5175	2 T20992	hypothetical prote
14	196.5	11.1	5198	2 T43290	hemacentrin precurs
15	187.5	10.6	274	2 A47639	OX-2 membrane glyc
16	187	10.6	4391	2 A38096	perlecan precursor
17	178.5	10.1	853	1 IJBONC	neural cell adhesi
18	174.5	9.9	1896	2 T08851	Down syndrome cell
19	174	9.8	588	2 JH0506	adhesion molecule
20	174	9.8	588	2 A45254	surface glycoprote
21	171.5	9.7	637	2 B33785	myelin-associated
22	170.5	9.6	626	1 A61084	myelin-associated
23	169.5	9.6	582	1 BNRT3S	myelin-associated
24	169.5	9.6	626	1 BNRT3	myelin-associated
25	168	9.5	702	2 A36319	carcinoembryonic a
26	165	9.3	7962	2 I38346	elastic titin - hu
27	163.5	9.2	858	1 IJRTNC	neural cell adhesi
28	163	9.2	761	1 IJHUNG	neural cell adhesi
29	162.5	9.2	278	1 TDRTOX	OX-2 membrane glyc

30	162	9.2	587	2 JH0464	DM-GRASP precursor
31	161	9.1	765	2 C42632	cell adhesion mole
32	161	9.1	812	2 B42632	cell adhesion mole
33	161	9.1	932	2 A42632	cell adhesion mole
34	158.5	9.0	3707	2 S18252	heparan sulfate pr
35	158	8.9	739	2 JN0581	vascular cell adhe
36	158	8.9	1091	1 IJCHNL	neural cell adhesi
37	154.5	8.7	344	2 I56551	neurotrophin - rat
38	154.5	8.7	725	1 IJMSNG	neural cell adhesi
39	154.5	8.7	1115	1 IJMSNL	neural cell adhesi
40	150	8.5	646	2 I38049	cell surface glyco
41	147.5	8.3	725	2 JE0099	neural cell adhesi
42	147.5	8.3	1088	1 IJXLNL	neural cell adhesi
43	146.5	8.3	345	2 S03199	opioid-binding pro
44	146.5	8.3	1651	2 T14160	transmembrane rece
45	146	8.3	847	2 JH0371	B-cell adhesion pr

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08732
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732
A;Molecule type: mRNA
A;Residues: 1-407 <OTT>
A;Cross-references: EMBL:AL050071
A;Experimental source: fetal kidney; clone DKFZp566B0846
C;Genetics:
A;Note: DKFZp566B0846.1

Query Match 65.0%; Score 1149; DB 2; Length 407;
Best Local Similarity 98.2%; Pred. No. 2.3e-80;
Matches 217; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	86	SGKYICKAVTFPLGNAQSSSTTVLVEPTVSLIKGPDLSLDGGNETVAAICIAATGKPVA	145
Db	1	SGKYICKAVTFPLGNAQSSSTTVLVEPTVSLIKGPDLSLDGGNETVAAICIAATGKPVA	60
Qy	146	HIDWEGDLGEMESTTTSPFNETATIIISQYKLFPTFRAGRRITCVVKHPALEKDIRYSFI	205
Db	61	HIDWEGDLGEMESTTTSPFNETATIIISQYKLFPTFRAGRRITCVVKHPALEKDIRYSFI	120
Qy	206	LDIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANPPFPKSVWSRLDGQWPDGLASDNTL	265
Db	121	LDIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANPPFPKSVWSRLDGQWPDGLASDNTL	180
Qy	266	HFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPEKQT	306
Db	181	HFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDPPTTTT	221

RESULT 2
JC4024
poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, C.; Dubi
Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene
A;Reference number: JC4024; MUID:95237621; PMID:7721102
A;Accession: JC4024
A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796

QY	61	QGRVLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVE-PTVSLIK	119
Db	83	DNRIELVRASWHELSSISVSDVLSLDEGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFS	142
QY	120	GPDSLIDGGNETVAAICIAATGKPFVAHIDW---EGDLGEMESTTTSFPN-ETATILISQYK	175
Db	143	SP--VMEG--DLMLTCKTSGSKPAADIRWFKNDEIKDVKYLKEEDANRKTFTVSSTLD	198
QY	176	LFPTRFARGRRITCVVKKHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWFVGRKG	229
Db	199	FRVDRSDGVAVICRVDHESLNATPQVAMQVLEIHYPSPVKIIPSTPFPQEGQPLI----	254
QY	230	VNLKCNADANPPFKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL	287
Db	255	--LTCESKGKPLPEPVLWTKDGGELPDPRMVS GRELNILF-LNKTDNGYRCEATNTI	311
QY	288	QQRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKKLPFLSTLTIKD-D	343
Db	312	QOSSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVA-ITTSPT-----TSATTSSIRDPN	366
QY	344	TIATRSRG	350
Db	367	ALAGONG	373

RESULT 14

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US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: prt
; ORGANISM: Mus musculus
US-09-778-510-4

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Query Match	11.5%;	Score	227.5;	DB 4;	Length	398;			
Best Local Similarity	26.6%;	Pred. No.	5.8e-14;						
Matches	79;	Conservative	52;	Mismatches	145;	Indels	21;	Gaps	11;

QY	10	TAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNY	69
Db	39	TVVAGGTIVLKCOVKDHED--SSLQWS---NPAQQTL-----YFGEKRALRDNRIQLVSS	88
QY	70	SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGN	129
Db	89	TPHELISISNVALADEGEYTCSIFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK	145
QY	130	ETVAAICIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLPFTRFARGR	185
Db	146	ETATLNCQSSGSKPAAQLTWKRGDQELHGDQTRIQEDPNGKTFTVSSSVSFQVTRDDGA	205
QY	186	RITCVVKHPALE-KDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFK	244
Db	206	NIVCSVNHESLKGADRSTSQRIEVLTYPTAMIRPEPAHPREGOK-LLLHCEGRGNPVPQQ	264
QY	245	SVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVYISDP	301
Db	265	YVWVK-EGSEPPKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYTAYFTLNVDP	319

RESULT 15

US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

	Query Match	11.0%;	Score 217.5;	DB 4;	Length 398;
	Best Local Similarity	25.9%;	Pred. No. 5.7e-13;		
	Matches	77;	Conservative	52;	Mismatches 147;
				Indels	21;
				Gaps	11;
QY	10	TAVWGNVSLKCLIEVNETITQISWEKIHGSSQTVAVHHPOYGFVSQGEYQGRVLFFKNY	69		
Db	39	TVVAGGTVVLKQCKDHED--SSLQWS---NPAQQTLL-----YFCEKRALRDNRIOQLVTS	88		
QY	70	SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGN	129		
Db	89	TPHELSTISNVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK	145		
QY	130	ETVAAICIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTTRFARGR	185		
Db	146	DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIOEDPNCKTFTVSSSVTFQVTRDDGA	205		
QY	186	RITCVVKHPALE-KDIRYSFILDIOYAPEVSVTGYDGNWFVRKGVNLCNADANPPPFK	244		
Db	206	SIVCSWNHESLKGADRSTSORIEVLYTPTAMIRDPDPHPREGQK-LLLHCEGRGNVPVQQ	264		
QY	245	SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISDP	301		
Db	265	YLWEK-EGSVPPKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYKAYTYTLNVNDP	319		

Search completed: April 12, 2004, 09:49:27
Job time : 13.1808 secs

QY 230 VNLKCNADANPPPFKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSVGVICKVTNSL 287
Db 232 --LTCESKGKPLPEPVLWTKDGGELPDPRMVVSGRELNILF-LNKTDNGTYRCEATNTI 288
QY 288 GQRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKLPPFLSLTIATIKD-D 343
Db 289 QGSSAEYVLIVHDVNPNTLLPTTIIPSLTTATVTTVA-ITTSPT-----TSATTSSIRDPN 343
QY 344 TIATRSR 350
Db 344 ALAQNG 350
RESULT 12
US-08-659-984A-5
; Sequence 5, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-984A-5

Query Match 12.0%; Score 236.5; DB 2; Length 444;
Best Local Similarity 23.4%; Pred. No. 8.9e-15;
Matches 86; Conservative 76; Mismatches 162; Indels 43; Gaps 17;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 33 GQFPLTQNTVVEGGTALTICRVDQNDN-TSLQWS---NPAQQL-----YFDDKKALR 82
QY 61 QGRVLEKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVE-PTVSLIK 119
Db 83 DNRIELVRASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPKQISGFS 142
QY 120 GPDSLDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTSPN-ETATIIISOYK 175

Db 143 SP--VMEG--DLMQLTCKTSGSKPAADIRWPKNDKEIKDVKYLKEEDANRKTFTVSSILD 198
QY 176 LFPTRFARGRITCVVKKHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWFVGRKG 229
Db 199 FRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHHTPSVKIIPSTPFQEGQPLI----- 254
QY 230 VNLKCNADANPPPFKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSVGVICKVTNSL 287
Db 255 --LTCESKGKPLPEPVLWTKDGGELPDPRMVVSGRELNILF-LNKTDNGTYRCEATNTI 311
QY 288 GQRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKLPPFLSLTIATIKD-D 343
Db 312 QGSSAEYVLIVHDVNPNTLLPTTIIPSLTTATVTTVA-ITTSPT-----TSATTSSIRDPN 366
QY 344 TIATRSR 350
Db 367 ALAQNG 373
RESULT 13
US-08-660-531-5
; Sequence 5, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-531-5

Query Match 12.0%; Score 236.5; DB 3; Length 444;
Best Local Similarity 23.4%; Pred. No. 8.9e-15;
Matches 86; Conservative 76; Mismatches 162; Indels 43; Gaps 17;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 33 GQFPLTQNTVVEGGTALTICRVDQNDN-TSLQWS---NPAQQL-----YFDDKKALR 82

RESULT 10
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-659-984A-1

Query Match	12.0%	Score	236.5;	DB 2;	Length	421;
Best Local Similarity	23.4%	Pred.	No. 8.le-15;			
Matches	86;	Conservative	76;	Mismatches	162;	Indels
						43; Gaps
						17;
QY	1	GPIIVEPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVEY	60			
Db	10	GQFPLTQNVTVVEGGTAILTCRVDQNDN-TSLQWS---NPAQOTL-----YFDDKKALR	59			
QY	61	QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVE-PTVSLIK	119			
Db	60	DNRIELVRASWHELSISVDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFS	119			
QY	120	GPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATISQYK	175			
Db	120	SP--VMEG--DLMLQCTKTSGSKPAADIRWFKNDKXIKDVLYKEEDANRKTFTVSSILD	175			
QY	176	LPTTRFARRITCVVKKHPALEKDIRYSF-ILDIQVAPEVSVT-----GYDGNWVFGKRG	229			
Db	176	FRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKIIPSTFPFQEGPLI----	231			
QY	230	VNLKCNADANPPFKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL	287			
Db	232	--LTCESKGXPDPVLTWKDGGELPDPDRMVVSGRELNILF-LNKTDNGTVRCEATNTI	288			
QY	288	QGRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKLPPLSLTIATIKD-D	343			

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Db      289  GOSSAEYVLIVHDPNTLLPTTIIPSLTTATVTTVA-ITTSPT----TSATTSIRDEN 344
Qy      344  TIATRSQ 350
       :||:|
Db      344  ALAQONG 350

RESULT 11
US-08-660-531-1
; Sequence 1, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-660-531-1

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	Query Match	12.0%;	Score 236.5;	DB 3;	Length 421;
	Best Local Similarity	23.4%;	Pred. No. 8.1e-15;		
	Matches 86;	Conservative 76;	Mismatches 162;	Indels 43;	Gaps 17;
QY	1	GPIIVEPHVTA	VWGNVSLKCLIEVN	ETITQLSWEKIHGKSSQTAVHH	PQYGFSVQGEY 60
Dd	10	GQFPLTQNVT	VEGGTAILTCRVDQDN-TSLQWS---NPAQQTL-----YFDDKKALR 59		
QY	61	QGRVLFKNYSLNDA	TITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVE-PTVS	LIK 119	
Dd	60	DNRIELVRASWHELSIS	VSVDVLSDEGYTCSLTMPVKTSKAYLTVLGVPEKPQISGFS 119		
QY	120	GPDSLIDCGNETVAACIAATGKPVAHIDW--- <td></td> <td></td> <td></td>			
Dd	120	SP--VMEG--DLMOLTCKTSGSKPAADIRWFKNKDKEIKDV	KYLKEEDANRKFTTVS	TLD 175	
QY	176	LFPTRFARGRRITCVV	KHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWFVGRKG 229		
Dd	176	FRVDRSDDGVAVICRV	DHESLNATQVAMQVLEIHYYTPSVKIIIPSTFPFGQGQPLI-----231		

Db 223 SLACIVNYHM--DRFKESLTNLVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEY 280
QY 246 VWSRLDGQWPDGILLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVYIISDPPTT 304
Db 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYT 339

RESULT 2

US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: H1gr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 27.1%; Score 535.5; DB 4; Length 458;
Best Local Similarity 37.7%; Pred. No. 2.3e-44;
Matches 112; Conservative 55; Mismatches 119; Indels 11; Gaps 5;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTSPNETATIIISQYKLFPTRFARGR 185
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGEAYQBIIRPNNGTIVTISRVLVPSREAHQQ 222
QY 186 RITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKCNDADANPPPFKS 245
Db 223 SLACIVNYHM--DRFKESLTNLVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEY 280
QY 246 VWSRLDGQWPDGILLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVYISDPP 302
Db 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEKP 337

RESULT 3

US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CDI
US-09-919-172-20

Query Match 26.1%; Score 516; DB 4; Length 518;
Best Local Similarity 35.7%; Pred. No. 2.4e-42;
Matches 110; Conservative 56; Mismatches 114; Indels 28; Gaps 6;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWE-----GDLGEMESTTSPNETATIIISQYKL 176
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGEARVPGDSGT-----PMAPVTVISRYRL 214
QY 177 FPTRFARGRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKCNA 236
Db 215 VPSREAHQOSLACIVNYHM--DRFKESLTNLVQYEPEVTIEGFDGNWYLQRMVDVKLTCKA 272
QY 237 DANPPPFKSVMSRLDGQWPDGILLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVI 296
Db 273 DANPPATEYHWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332
QY 297 YISDPPTT 304
Db 333 NITEFPYT 340

RESULT 4

US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match 20.1%; Score 396.5; DB 4; Length 479;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 12.1808 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-15_COPY_58_426
Perfect score: 1976
Sequence: 1 GPIIIEPHVTAVGKNVSLK.....GSSDYKDDDDKGSSHHHHH 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.5	27.3	517	4 US-09-723-368-4	Sequence 4, Appli
2	535.5	27.1	458	4 US-09-435-956A-1	Sequence 1, Appli
3	516	26.1	518	4 US-09-919-172-20	Sequence 20, Appli
4	396.5	20.1	479	4 US-09-723-368-2	Sequence 2, Appli
5	376	19.0	408	4 US-09-724-864-62	Sequence 62, Appli
6	295	14.9	440	4 US-09-866-028-61	Sequence 61, Appli
7	295	14.9	442	4 US-09-778-510-20	Sequence 20, Appli
8	295	14.9	442	4 US-09-930-803-1	Sequence 1, Appli
9	289	14.6	423	4 US-09-778-510-22	Sequence 22, Appli
10	236.5	12.0	421	2 US-08-659-984A-1	Sequence 1, Appli
11	236.5	12.0	421	3 US-08-660-531-1	Sequence 1, Appli
12	236.5	12.0	444	2 US-08-659-984A-5	Sequence 5, Appli
13	236.5	12.0	444	3 US-08-660-531-5	Sequence 5, Appli
14	227.5	11.5	398	4 US-09-778-510-4	Sequence 4, Appli
15	217.5	11.0	398	4 US-09-778-510-6	Sequence 6, Appli
16	217.5	11.0	398	4 US-09-907-794A-84	Sequence 84, Appli
17	217.5	11.0	398	4 US-09-905-125A-84	Sequence 84, Appli
18	217.5	11.0	398	4 US-09-902-775A-84	Sequence 84, Appli
19	217.5	11.0	432	4 US-09-778-510-2	Sequence 2, Appli
20	190.5	9.6	227	4 US-09-205-258-947	Sequence 947, App
21	187.5	9.5	274	4 US-09-570-367C-19	Sequence 19, Appli
22	187.5	9.5	274	4 US-09-915-524-19	Sequence 19, Appli
23	163	8.2	477	2 US-08-432-016-3	Sequence 3, Appli
24	163	8.2	477	2 US-08-684-594-3	Sequence 3, Appli
25	162.5	8.2	278	4 US-09-570-367C-2	Sequence 2, Appli
26	162.5	8.2	278	4 US-09-915-524-2	Sequence 2, Appli
27	159.5	8.1	278	4 US-09-570-367C-21	Sequence 21, Appli

28	159.5	8.1	278	4	US-09-915-524-21	Sequence 21, Appli
29	159.5	8.1	1101	3	US-08-986-485-2	Sequence 2, Appli
30	158	8.0	642	1	US-08-217-299-1	Sequence 1, Appli
31	158	8.0	698	2	US-08-602-725-36	Sequence 36, Appli
32	158	8.0	734	2	US-08-389-459A-17	Sequence 17, Appli
33	158	8.0	734	3	US-08-987-867A-17	Sequence 17, Appli
34	154.5	7.8	1018	1	US-08-408-093-6	Sequence 6, Appli
35	154.5	7.8	1018	1	US-08-408-420A-6	Sequence 6, Appli
36	154.5	7.8	1018	1	US-08-714-901-6	Sequence 6, Appli
37	154.5	7.8	1018	3	US-08-040-741-6	Sequence 6, Appli
38	151	7.6	467	3	US-09-046-736-2	Sequence 2, Appli
39	148	7.5	583	2	US-08-432-016-2	Sequence 2, Appli
40	148	7.5	583	2	US-08-684-594-2	Sequence 2, Appli
41	147.5	7.5	1059	4	US-09-907-794A-290	Sequence 290, App
42	147.5	7.5	1059	4	US-09-905-125A-290	Sequence 290, App
43	147.5	7.5	1059	4	US-09-902-775A-290	Sequence 290, App
44	147.5	7.5	1119	4	US-09-907-794A-294	Sequence 294, App
45	147.5	7.5	1119	4	US-09-905-125A-294	Sequence 294, App

ALIGNMENTS

RESULT 1
US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITECK, Charles J.
; APPLICANT: KRUMMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match	27.3%	Score	538.5	DB	4	Length	517
Best Local Similarity	37.8%	Pred. No.	1.4e-44				
Matches	113	Conservative	56	Mismatches	119	Indels	11
Gaps	5						
Qy	14	GKNVSLKCLIE---VNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEYQGRVLFKNYS	70				
Db	44	GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS	103				
Qy	71	LNDATITLHNIGFSDSGKXICKAVTFPLGNAQSSTTTVTVLVEPTVSLIKGPDSLIDG---	127				
Db	104	FTDGTIRLSRLEDEGVYCEFAFTPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG	162				
Qy	128	-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTTSPNETATIIISQYKLFPTFRFAGR	185				
Db	163	QDDKVLVATCTSANGKPPSVSVSWETRLKGEAEYQEIKNNGTIVTISRVLVPSREAHQQ	222				
Qy	186	RITCVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNFVGRKGNLKNADANPPPFKS	245				

QY	1	GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY	60
D6	58	GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY	117
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTIVTLVEPTVS LIKG	120
D6	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTIVTLVEPTVS LIKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPTR	180
D6	178	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPTR	237
QY	181	FARGRRITCVWKHPALEKDRIYSFILDIQYAPEVS VTGYDGNWFVGKGVNLKC NADANP	240
D6	238	FARGRRITCVWKHPALEKDRIYSFILDIQYAPEVS VTGYDGNWFVGKGVNLKC NADANP	297
QY	241	PPFKSVWSRLDGOWPDGLLASDN TLHFVHPLTFNYSGVYICKVTNSLGQRSDQKV IYISD	300
D6	298	PPFKSVWSRLDGOWPDGLLASDN TLHFVHPLTFNYSGVYICKVTNSLGQRSDQKV IYISD	357
QY	301	PPTTTT 306	
D6	358	VPFKQT 363	

RESULT 15

```

US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US2003008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshimi TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-6

```

Query Match 79.3%; Score 1567; DB 10; Length 438;
Best Local Similarity 95.4%; Pred. No. 2.5e-126;
Matches 292; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY	1	GPII	VEPHV	TAVG	KNVSL	KLIE	VNET	ITQIS	WEKIH	GKSSQ	TVA	VHHP	QYGF	SVQGEY	60		
Db	58	GSII	VEPHV	TAVG	KNVSL	KLIE	VNET	ITQIS	WEKIH	GKSTQ	TVA	VHHP	QYGF	SVQGDY	117		
QY	61	QGRV	LFKNY	SLND	ATI	TLHN	IGFSD	SGKYI	CKAV	TPLG	NAQS	TTVT	VLVE	PTVSLIKG	120		
Db	118	QGRV	LFKNY	SLND	ATI	TLHN	IGFSD	SGKYI	CKAV	TPLG	NAQS	TTVT	VLVE	PTVSLIKG	177		
QY	121	PD	SLIDG	NETV	AAIC	AATG	KPVA	HIDW	EGDL	GEMES	TTTS	FPNET	ATIIS	QYKLF	FPTR	180	
Db	178	PD	SLIDG	NETV	AAIC	AATG	KPVA	QIDW	EGDL	GEMES	TTTS	FPNET	ATIIS	QYKLF	FPTR	237	
QY	181	FARG	RRITC	VWKH	PALE	KDIR	YSFI	LDIQ	YAPE	VS	VTGY	DGNW	FVGR	KGVNL	KCNADANP	240	
Db	238	FARG	RRITC	VWKH	PALE	KDIR	YSFI	LDIQ	YAPE	VS	VTGY	DGNW	FVGR	KGVNL	KCNADANP	297	
QY	241	PP	FKSV	WSRL	DG	QWPD	GLLAS	NTLH	FVHP	PLTF	NYSG	VYICK	VTNS	LSLGR	SDQKVI	YISD	300
Db	298	PP	FKSV	WSRL	DG	QWPD	GLLAS	NTLH	FVHP	PLTF	NYSG	VYICK	VTNS	LSLGR	SDQKVI	YISD	357


```
RESULT 12
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match      81.2%; Score 1604; DB 10; Length 510;
Best Local Similarity 73.1%; Pred. No. 2e-129;
Matches 323; Conservative 10; Mismatches 33; Indels 76; Gaps 7;

QY 1 GPIIPEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFFVGRKGNLKCNDANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFFVGRKGNLKCNDANP 297

QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

QY 301 PP-----TTLTLOPTIQWHPSTAD-IEDLATEPKKLP-- 331
Db 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPR-KKRPSYLDKVIDLPPTHKPPPLY 416

QY 332 -----FPLSTLTIKDDTIAT-----RSGSSDYKDD----- 358
Db 417 EERSPPLPQKDLFQBEHLPLQT--QFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQ 474

QY 359 -----DKGSSHHHHH 369
Db 475 MYPLYNQMCYQDRSPGKHQNN 496

RESULT 13
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
```

```
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match      81.1%; Score 1602; DB 10; Length 437;
Best Local Similarity 98.7%; Pred. No. 2.4e-129;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFFVGRKGNLKCNDANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFFVGRKGNLKCNDANP 297

QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

QY 301 PPTTTT 306
Db 358 VPFKQT 363

RESULT 14
US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match      81.1%; Score 1602; DB 10; Length 595;
Best Local Similarity 98.7%; Pred. No. 3.6e-129;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237

QY 181 FARGRRITCVVHKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVHKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300

Db 298 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357

QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPPPLSTLATIKDDTIATRSGSSDYKDDDDK 360

Db 358 VPFXQT-----SSRSGSSDYKDDDDK 378

QY 361 GSSHHHHH 369

Db 379 GSSHHHHH 387

RESULT 10

US-09-972-268-8

; Sequence 8, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; PRIOR FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 504

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-972-268-8

Query Match 81.2%; Score 1604; DB 10; Length 504;

Best Local Similarity 73.1%; Pred. No. 1.9e-129;

Matches 323; Conservative 10; Mismatches 33; Indels 76; Gaps 7;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 52 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 111

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180

Db 172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 231

QY 181 FARGRRITCVVHKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240

Db 232 FARGRRITCVVHKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 291

QY 241 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300

Db 292 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 351

QY 301 PP-----TTTTLOPTIQWHPSTAD-IEDLATEPKKLP-- 331

Db 352 VPFKQTSSIAVAGAVIGAVLALFIAIFVTVLLTPR-KKRPSYLDKVIDLPPTHKPPPLY 410

QY 332 -----FPLSTLATIKDDTIAT-----RSGSSDYKDDD----- 358

Db 411 EERSPPLPKDLFQPEHLPLOT--QFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQ 468

QY 359 -----DKGSSHHHHH 369

Db 469 MYPLYNQMCYQDRSPGKHQNN 490

RESULT 11

US-09-972-268-10

; Sequence 10, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 10

; LENGTH: 510

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest ar

; OTHER INFORMATION: from human Nectin-3 beta

US-09-972-268-10

Query Match 81.2%; Score 1604; DB 10; Length 510;

Best Local Similarity 73.1%; Pred. No. 2e-129;

Matches 323; Conservative 10; Mismatches 33; Indels 76; Gaps 7;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237

QY 181 FARGRRITCVVHKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVHKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300

Db 298 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357

QY 301 PP-----TTTTLOPTIQWHPSTAD-IEDLATEPKKLP-- 331

Db 358 VPFKQTSSIAVAGAVIGAVLALFIAIFVTVLLTPR-KKRPSYLDKVIDLPPTHKPPPLY 416

QY 332 -----FPLSTLATIKDDTIAT-----RSGSSDYKDDD----- 358

Db 417 EERSPPLPKDLFQPEHLPLOT--QFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQ 474

QY 359 -----DKGSSHHHHH 369

Db 475 MYPLYNQMCYQDRSPGKHQNN 496

SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 549
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from human Nectin-3 alpha
OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match 93.3%; Score 1844; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 4.7e-150;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 237
QY 181 FARRRITCVVKHPEALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPEALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPKSVWSRLDGOQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLGORSQDKVIYISD 300
Db 298 PPKSVWSRLDGOQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLGORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 404

RESULT 5
US-09-972-268-6
Sequence 6, Application US/09972268
Publication No. US20030044893A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 549
TYPE: PRT
ORGANISM: homo sapiens
US-09-972-268-6

Query Match 93.3%; Score 1844; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 4.7e-150;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 237
QY 181 FARRRITCVVKHPEALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPEALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPKSVWSRLDGOQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLGORSQDKVIYISD 300
Db 298 PPKSVWSRLDGOQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLGORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 404

RESULT 6
US-10-161-572-45
Sequence 45, Application US/10161572
Publication No. US20030087266A1
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-097C-PC
CURRENT APPLICATION NUMBER: US/10/161,572
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 549
TYPE: PRT
ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 93.3%; Score 1844; DB 14; Length 549;
Best Local Similarity 100.0%; Pred. No. 4.7e-150;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 237
QY 181 FARRRITCVVKHPEALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPEALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPKSVWSRLDGOQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLGORSQDKVIYISD 300
Db 298 PPKSVWSRLDGOQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLGORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 347

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATRSQSSDYKDDDDK 360
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATRSQSSDYKDDDDK 417
QY 361 GSSHHHHH 369
Db 418 GSSHHHHH 426

RESULT 2
US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match 93.8%; Score 1853; DB 10; Length 634;
Best Local Similarity 100.0%; Pred. No. 9.7e-151;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIVEPHVTA VVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVA VHHPOYGF SVQGEY 60
Db 58 GPIIIVEPHVTA VVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVA VHHPOYGF SVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATRS 349

Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATRS 406

RESULT 3
US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match 93.3%; Score 1844; DB 10; Length 542;
Best Local Similarity 100.0%; Pred. No. 4.7e-150;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIVEPHVTA VVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVA VHHPOYGF SVQGEY 60
Db 51 GPIIIVEPHVTA VVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVA VHHPOYGF SVQGEY 110
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 111 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 170
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 171 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 230
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db 231 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 290
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 291 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 350
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 347
Db 351 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 397

RESULT 4
US-09-972-268-4
; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 30.8386 Seconds
(without alignments)
3146.189 Million cell updates/sec

Title: US-09-972-268-15_COPY_58_426
Perfect score: 1976
Sequence: 1 GPIIIEPHVTAVWGKNVSLK.....GSSDYKDDDDKGSSHHHHH 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues
Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1976	100.0	426	10	US-09-972-268-15 Sequence 15, Appl
2	1853	93.8	634	10	US-09-972-268-13 Sequence 13, Appl
3	1844	93.3	542	10	US-09-972-268-2 Sequence 2, Appli
4	1844	93.3	549	10	US-09-972-268-4 Sequence 4, Appli
5	1844	93.3	549	10	US-09-972-268-6 Sequence 6, Appli
6	1844	93.3	549	14	US-10-161-572-45 Sequence 45, Appl
7	1767	89.4	549	10	US-09-959-845-2 Sequence 2, Appli
8	1767	89.4	549	10	US-09-972-268-17 Sequence 17, Appl
9	1706.5	86.4	387	10	US-09-972-268-16 Sequence 16, Appl
10	1604	81.2	504	10	US-09-972-268-8 Sequence 8, Appli
11	1604	81.2	510	10	US-09-972-268-10 Sequence 10, Appl
12	1604	81.2	510	10	US-09-972-268-12 Sequence 12, Appl
13	1602	81.1	437	10	US-09-972-268-31 Sequence 31, Appl
14	1602	81.1	595	10	US-09-972-268-14 Sequence 14, Appl
15	1567	79.3	438	10	US-09-959-845-6 Sequence 6, Appli

16	1567	79.3	438	10	US-09-972-268-19	Sequence 19, Appl
17	1567	79.3	510	10	US-09-959-845-4	Sequence 4, Appli
18	1567	79.3	510	10	US-09-972-268-18	Sequence 18, Appl
19	594	30.1	258	15	US-10-264-237-2626	Sequence 2626, Ap
20	538.5	27.3	458	10	US-09-972-268-21	Sequence 21, Appl
21	538.5	27.3	514	14	US-10-161-572-60	Sequence 60, Appl
22	538.5	27.3	517	10	US-09-972-268-20	Sequence 20, Appl
23	516	26.1	518	9	US-09-919-172-20	Sequence 20, Appl
24	492	24.9	497	10	US-09-972-268-37	Sequence 37, Appl
25	485.5	24.6	498	10	US-09-972-268-39	Sequence 39, Appl
26	480.5	24.3	479	10	US-09-766-511B-35	Sequence 35, Appl
27	480.5	24.3	510	10	US-09-766-511B-33	Sequence 33, Appl
28	480.5	24.3	510	12	US-10-058-270A-54	Sequence 54, Appl
29	480.5	24.3	510	14	US-10-161-572-55	Sequence 55, Appl
30	480.5	24.3	510	14	US-10-241-220-94	Sequence 94, Appl
31	480.5	24.3	510	15	US-10-295-027-66	Sequence 66, Appl
32	480.5	24.3	510	15	US-10-173-999-76	Sequence 76, Appl
33	478.5	24.2	510	10	US-09-972-268-24	Sequence 24, Appl
34	478.5	24.2	510	14	US-10-161-572-54	Sequence 54, Appl
35	476.5	24.1	314	10	US-09-766-511B-36	Sequence 36, Appl
36	474	24.0	511	10	US-09-972-268-34	Sequence 34, Appl
37	470	23.8	580	10	US-09-972-268-36	Sequence 36, Appl
38	401.5	20.3	538	10	US-09-972-268-23	Sequence 23, Appl
39	401.5	20.3	538	10	US-09-984-130-138	Sequence 138, App
40	401.5	20.3	538	10	US-09-836-353A-138	Sequence 138, App
41	401.5	20.3	538	14	US-10-161-572-61	Sequence 61, Appl
42	401.5	20.3	538	15	US-10-411-010-17	Sequence 17, Appl
43	396.5	20.1	479	10	US-09-972-268-22	Sequence 22, Appl
44	396.5	20.1	479	14	US-10-161-572-62	Sequence 62, Appl
45	394.5	20.0	522	15	US-10-264-049-2969	Sequence 2969, Ap

ALIGNMENTS

RESULT 1
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

Query Match 100.0%; Score 1976; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.5e-161;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSVOGEY	60
Db	58	GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSVOGEY	117
Qy	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNASSTTVTLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNASSTTVTLVEPTVSLIKG	177

FT Modified-site 73 /note= "N-glycosylated"
FT Domain 74..152
FT /note= "Extracellular Ig domain"
FT Modified-site 83 /note= "N-glycosylated"
FT Modified-site 125 /note= "N-glycosylated"
FT Modified-site 186 /note= "N-glycosylated"
FT Domain 189..250 /note= "Extracellular Ig domain"
FT Modified-site 222 /note= "N-glycosylated"
FT Domain 287..342 /note= "Extracellular Ig domain"
FT Modified-site 331 /note= "N-glycosylated"
FT Domain 386..510 /note= "Intracellular C-terminal domain"
FT
XX
PN W0200228902-A2.
XX
PD 11-APR-2002.
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37445.
XX

Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, sepsis, stroke.

Claim 1; Page 98-99; 141pp; English.

The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is human nectin-3beta protein. Human nectin-3beta gene is located on chromosome 3

Sequence 510 AA;

Query Match 81.2%; Score 1604; DB 5; Length 510;
Best Local Similarity 73.1%; Pred. No. 3e-123;
Matches 323; Conservative 10; Mismatches 33; Indels 76; Gaps 7;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db
58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db
118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISOYKLPFPT 180
Db
178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISOYKLPFPT 237
QY 181 FARRRITCVVHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 240
Db
238 FARRRITCVVHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 297
QY 241 PPFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db
298 PPFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 PP-----TTTTLQPTIQWHPSTAD-IEDLATEPKKLP-- 331
Db
358 VPFKQTSSIAVAGAVIGAVLAFIIAIFVTVLLTPR-KKRPSYLDKVIDLPPTHKPPPLY 416
QY 332 -----FPLSTLATIKDDTIAT-----RSGSSDYKDDD----- 358
Db
417 EERSPPLPQKDLFQPEHLPLQT--QFKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQQ 474
QY 359 -----DKGSSHHHHH 369
Db
475 MYPLYNQMCYQDRSPGKHQNN 496

Search completed: April 12, 2004, 09:38:37
Job time : 45.5662 secs

241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 300
292 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 351
301 PP-----TTTTLQPTIQWHPSTAD-IEDLATEPKKLP-- 331
352 VPFKQTSSIAVAGAVIGAVLALFIAIFVTVLLTPR-KKRPSYLDKVIDLPPTHKPPPLY 410
332 -----FPLSTLATIKDDTIAT-----RSGSSDYKDDD----- 358
411 EERSPPLPQKDLFQPEHLPLQT--QFKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQQ 468
359 -----DKGSSHHHHH 369
469 MYPLYNQMCYQDRSPGKHQNN 490

RESULT 14
AAE23285
ID AAE23285 standard; protein; 510 AA.
XX AAE23285;
AC
XX
29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
XX Mouse nectin-3-human nectin-3beta fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
XX
Key Location/Qualifiers
FH Region 1..6
FT /note= "Mouse nectin-3 pprotein"
FT 7..510
FT /note= "Human nectin-3beta protein"
XX
PN WO200228902-A2.
XX
XX 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37444.
DR
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
XX Claim 1; Page 94-95; 141pp; English.
PS
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above

mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
asthma, allergy, allograft rejection, metastasis of cancer cells,
paracellular transport disorders such as magnesium transport defects in
the kidney or inflammatory bowel disease. Nectin DNA is also useful for
inhibiting angiogenesis in a mammal and treating endothelial migration,
proliferation or angiogenic condition of a tissue or a subject, such as
ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
stroke, restenosis, tumour growth and treating herpesvirus infection.
Nectin is also useful for modulating proliferation or migration of an
endothelial cell, an epithelial cell or a smooth muscle cell (vascular
smooth muscle cell). The present sequence is a fusion protein encoding 6
amino acids from mouse nectin-3 protein and the rest form human nectin-
3beta protein. Human nectin-3beta gene is located on chromosome 3.
(Updated on 29-AUG-2003 to standardise OS field)

XX
SQ Sequence 510 AA;

Query Match 81.2%; Score 1604; DB 5; Length 510;
Best Local Similarity 73.1%; Pred. No. 3e-123;
Matches 323; Conservative 10; Mismatches 33; Indels 76; Gaps 7;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNTGFSGSKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNTGFSGSKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 237
QY 181 FARGRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 240
Db 238 FARGRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 357
QY 301 PP-----TTTTLQPTIQWHPSTAD-IEDLATEPKKLP-- 331
Db 358 VPFKQTSSIAVAGAVIGAVLALFIAIFVTVLLTPR-KKRPSYLDKVIDLPPTHKPPPLY 416
QY 332 -----FPLSTLATIKDDTIAT-----RSGSSDYKDDD----- 358
Db 417 EERSPPLPQKDLFQPEHLPLQT--QFKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQQ 474
QY 359 -----DKGSSHHHHH 369
Db 475 MYPLYNQMCYQDRSPGKHQNN 496

RESULT 15
AAE23286
ID AAE23286 standard; protein; 510 AA.
XX
XX AAE23286;
AC
XX 27-AUG-2002 (first entry)
DT
XX Humar nectin-3beta protein.
DE
XX
KW Humar; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
XX stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
OS Homo sapiens.
XX
FH Key Location/Qualifiers

PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI60085.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

XX Example 2; SEQ ID NO 5860; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX Sequence 559 AA;

Query Match 81.8%; Score 1615.5; DB 4; Length 559;
Best Local Similarity 88.4%; Pred. No. 3.8e-124;
Matches 321; Conservative 3; Mismatches 26; Indels 13; Gaps 6;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db |||||
57 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 116
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
117 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 176
QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db |||||
177 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 236
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 240
Db |||||
237 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 296
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS-DQKVIYIS 299
Db |||||
297 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSPGSKEVTQKVHPTF 356
QY 300 DPPTTTTLP-----TIQW-HPSTADI-EDLATEPKKL-PFPLSTLATIKDDT-----IAT 347
Db |||||
357 QDPSLPTYPLPALQFQWASPSTAXTSRDLATEPXKIAPSPSLTLATIKGWTQLPTIIAX 416
QY 348 RSG 350
Db ||
417 CSG 419

RESULT 13
AAE23284

ID AAE23284 standard; protein; 504 AA.

XX

AC AAE23284;

XX

DT 27-AUG-2002 (first entry)

XX Human deleted nectin-3beta protein.

DE

KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.

XX WO200228902-A2.

PN

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMV) IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

XX N-PSD3; AAD37443.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.

XX Claim 1; Page 89-91; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3

XX Sequence 504 AA;

Query Match 81.2%; Score 1604; DB 5; Length 504;
Best Local Similarity 73.1%; Pred. No. 2.9e-123;
Matches 323; Conservative 10; Mismatches 33; Indels 76; Gaps 7;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db |||||
52 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 111
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171
QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db |||||
172 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 231
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 240
Db |||||
232 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 291

XX WO200166736-A1.
PN 13-SEP-2001.
XX 09-MAR-2001; 2001WO-JP001871.
PF 09-MAR-2000; 2000JP-00065595.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.
XX Takahashi K, Takai Y, Nakanishi H, Sato K;
XX WPI; 2001-570771/64.
DR N-PSDB; AAH78182.
XX New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and
PT corresponding antibodies.
XX Disclosure; Page 56-61; 64pp; Japanese.
XX The present sequence represents a murine nectin-3 polypeptide. Nectin-3
CC is an immunoglobulin-like cell adhesion molecule that shows homophilic
CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
CC polynucleotides are useful for investigating the mechanisms of cell
CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
CC malignancies of various cancers, and the development of methods for the
CC treatment and prevention of cancer
XX
SQ Sequence 549 AA;
Query Match 89.4%; Score 1767; DB 4; Length 549;
Best Local Similarity 94.2%; Pred. No. 1.3e-136;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 PPTTTTLQPTQVHSSPADVQDIATEHKLPFPLSLTLATLKDDTIGT 347
Db 358 PPTTTTLQPTQVHSSPADVQDIATEHKLPFPLSLTLATLKDDTIGT 404
RESULT 10
AAE23291
ID AAE23291 standard; protein; 549 AA.
XX
AC AAE23291;
XX
DT 27-AUG-2002 (first entry)
XX Mouse nectin-3alpha protein.
DE
XX Mouse; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma.
XX
OS Mus musculus.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Disclosure; Page 107-109; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is mouse nectin-3alpha protein
XX
SQ Sequence 549 AA;
Query Match 89.4%; Score 1767; DB 5; Length 549;
Best Local Similarity 94.2%; Pred. No. 1.3e-136;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI58299.

Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries.

Example 4; SEQ ID NO 228; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with neurotropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification

Sequence 555.AA;

```
Query Match          93.3%; Score 1844; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 6e-143;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY	1	GPIIIVPHVTVAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGYY	60
Dd	64	GPIIIVPHVTVAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGYY	123
QY	61	QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTIVTLVEPTVSLIKG	120
Dd	124	QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTIVTLVEPTVSLIKG	183
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISOYKLPFTR	180
Dd	184	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISOYKLPFTR	243
QY	181	FARGRRITCVVKHPALEKDRIYSFILDIIQYAPEVSVTYGDGNWFVGKGVNLKCNDANP	240
Dd	244	FARGRRITCVVKHPALEKDRIYSFILDIIQYAPEVSVTYGDGNWFVGKGVNLKCNDANP	303
QY	241	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVYISD	300
Dd	304	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVYISD	363
QY	301	PPTTTTLOPTIOHWPSTADIEDLATEPKLPFPPLSTLATIKODDTIAT	347
Dd	364	PPTTTTLOPTIOHWPSTADIEDLATEPKLPFPPLSTLATIKODDTIAT	410

RESULT 8

AAG63982
ID AAG63982 standard; protein; 549 AA.

AA
AC AAG63982;

26-NOV-2001 (first entry)

Amino acid sequence of murine nectin-3.

Nectin-3: cell adhesion: cell infiltration: cancer metastasis: cancer.

MUS SP.

WO200166736-A1

13-SEP-2001.
09-MAR-2001; 2001WO-JP001871.
09-MAR-2000; 2000JP-00065595.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(TAKA/) TAKAHASHI K.
Takahashi K, Takai Y, Nakanishi H, Sato K;
WPI; 2001-570771/64.
N-PSDB; AAH78179.
New protein family for diagnosing and treating tumor infiltration and metastasis comprises the mouse nectin-3 protein families and corresponding antibodies.
Claim 1; Page 37-40; 64pp; Japanese.
The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer

Query Match 89.4%; Score 1767; DB 4; Length 549;
Best Local Similarity 94.2%; Pred. No. 1.3e-136;
Matches 327; Conservative 13; Mismatches 7; Indels

QY	1	GPII	VEPHVTA	VWGNK	VSCLKCLIE	VNETITQISWEKI	HGKSQTVA	VHHHPQYGFSVQGEY	60
Dd	58	GSI	IPEPHVTA	VWGNK	VSCLKCLIE	VNETITQISWEKI	HGKSQTVA	VHHHPQYGFSVQGDY	117
QY	61	QGRVLFKNYS	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG	120					
Dd	118	QGRVLFKNYS	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG	177					
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTR	180						
Dd	178	PDSLIDGGNETVAAVCVAATGKPPAQIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTR	237						
QY	181	FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGVDGNWFVGKGVNLKCYNADANP	240						
Dd	238	FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGVDGNWFVGKGVNLKCYNADANP	297						
QY	241	PFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGSQRSDQKVVIYISD	300						
Dd	298	PFKSVWSRLDGOWPDGLLASDNTLHFVHPLTVNYSGVYCKVSNLSLGSQRSDQKVVIYISD	357						
QY	301	PPTTTTLQPTIO	NHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT	347					
Dd	358	PPTTTTLQPTIO	VQHSSPADYQDIATEHKLPFPLSTLATLKDDTI	GT 404					

RESULT 9

AAG63985
ID AAG63985 standard; protein; 549 AA.

AC AAG63985;

26-NOV-2001 (first entry)

DE Amino acid sequence of murine nectin-3.

XX
Nectin-3: cell adhesion; cell infiltration; cancer metastasis; cancer.

XX 50 Mus sp.

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 404

RESULT 6

ABJ20222
ID ABJ20222 standard; protein; 549 AA.

AC ABJ20222;

XX 13-AUG-2003 (first entry)

DT Human IG gene related protein SEQ ID No 45.

DE Breast cancer; p53 pathway modulating agent; IG; colon cancer;

XX kidney cancer; lung cancer; ovary cancer; human.

OS Homo sapiens.

XX WO200299040-A2.

PN 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US017313.

PR 05-JUN-2001; 2001US-0296076P.

PR 10-OCT-2001; 2001US-0328605P.

PR 22-OCT-2001; 2001US-0338733P.

PR 15-FEB-2002; 2002US-0357253P.

PR 15-FEB-2002; 2002US-0357600P.

XX (EXEL-) EXELIXIS INC.

XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

PI Lioubin MN;

XX WPI; 2003-148660/14.

XX Identifying a candidate p53 pathway modulators that are useful as targets

PT for therapeutics or for diagnosing cancers associated with defective p53

PT function, by providing an assay system having a purified IG polypeptide

PT or nucleic acid.

XX Claim 13; Page 206-209; 248pp; English.

XX The invention relates to a novel method for identifying a candidate p53

CC pathway modulating agent. The method comprises providing an assay system

CC having a purified IG polypeptide or nucleic acid, or their functionally

CC active fragment or derivative. The method is useful for identifying

CC associated with defective p53 function. This sequence represents a human

CC protein relating to the human IG genes used in the assay for identifying

CC modulators of the p53 pathway of the invention

XX Sequence 549 AA;

Query Match 93.3%; Score 1844; DB 6; Length 549;

Best Local Similarity 100.0%; Pred. No. 5.9e-143;

Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 237

QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357

QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347

Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 404

RESULT 7

AAM39143
ID AAM39143 standard; protein; 555 AA.

XX AAM39143;

XX 22-OCT-2001 (first entry)

DT Human polypeptide SEQ ID NO 2288.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;

XX peripheral nervous system; neuropathy; central nervous system; CNS;

XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

XX leukaemia.

OS Homo sapiens.

XX WO200153312-A1.

PN 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-0052317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI WPI; 2002-426103/45.
DR N-PSDB; AAD37442.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX Claim 1; Page 89-91; 141pp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha DNA.
XX Human nectin-3alpha gene is located on chromosome 3
SQ Sequence 549 AA;
Query Match 93.3%; Score 1844; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 5.9e-143;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 237
QY 181 FARRRITCVVKKHPPALEKDIRYSFILDIOYAPEVSVTGDNWFGVGRKGVNLCNADANP 240
Db 238 FARRRITCVVKKHPPALEKDIRYSFILDIOYAPEVSVTGDNWFGVGRKGVNLCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQSRSDQKVIYISD 357
QY 301 PPTTTTLOPTIOHWPSTADIEDLATEPKLPFLPSTLTIKDDTIAT 347
Db 358 PPTTTTLOPTIOHWPSTADIEDLATEPKLPFLPSTLTIKDDTIAT 404

RESULT 5
AAE23282
ID AAE23282 standard; protein; 549 AA.
XX
AC AAE23282;
XX
DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX

DE Mouse nectin-3-human nectin 3alpha fusion protein.
XX Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
KW chromosome 3.
XX Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX Key Location/Qualifiers
FH Region 1..7
FT /note= "Mouse nectin-3 protein"
FT Region 8..549
FT /note= "Human nectin-3alpha protein"
XX WO200228902-A2.
XX 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI WPI; 2002-426103/45.
DR N-PSDB; AAD37441.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX Claim 1; Page 80-82; 141pp; English.
PS The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
CC alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX Sequence 549 AA;
Query Match 93.3%; Score 1844; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 5.9e-143;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117

Db 358 PPTTTTQQTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATRS 406

RESULT 3

AAE23281

ID AAE23281 standard; protein; 542 AA.

XX

AC AAE23281;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human deleted nectin-3alpha protein.

XX

KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;

KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;

KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

KW stroke; tumour; cancer; herpesvirus infection; chromosome 3; asthma.

XX

OS Homo sapiens.

XX

PN WO200228902-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US031392.

XX

PR 05-OCT-2000; 2000US-0238557P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX

DR WPI; 2002-426103/45.

DR N-PSDB; AAD37440.

XX

PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,

PT useful for treating or preventing heart failure, malaria,

PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,

PT sepsis, stroke.

XX

PS Claim 1; Page 76-78; 141pp; English.

XX

CC The invention relates to a substantially purified nectin3alpha, beta,

CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.

CC Nectin DNA and protein are useful for treating a disease associated with

CC cell adhesion activity, adherens junction formation activity, epithelial

CC or endothelial barrier function activity, endothelial proliferation or

CC migration activity, viral polypeptide binding activity. The epithelial or

CC endothelial barrier function disorder which is treated by the above

CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

CC asthma, allergy, allograft rejection, metastasis of cancer cells,

CC paracellular transport disorders such as magnesium transport defects in

CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for

CC inhibiting angiogenesis in a mammal and treating endothelial migration,

CC proliferation or angiogenic condition of a tissue or a subject, such as

CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,

CC stroke, restenosis, tumour growth and treating herpesvirus infection.

CC Nectin is also useful for modulating proliferation or migration of an

CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular

CC smooth muscle cell). The present sequence is human nectin-3alpha protein

CC containing 7 amino acids deleted from the N-terminal end. Human nectin-

CC 3alpha gene is located on chromosome 3

XX

SQ Sequence 542 AA;

Query Match 93.3%; Score 1844; DB 5; Length 542;

Best Local Similarity 100.0%; Pred. No. 5.8e-143;

Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQVGFVQGEY 60

Db 51 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTAVVHHPQVGFVQGEY 110

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVLVEPTVSLIKG 120

Db 111 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVLVEPTVSLIKG 170

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSPNETATIIISQYKLFPTTR 180

Db 171 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSPNETATIIISQYKLFPTTR 230

QY 181 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLKCNADANP 240

Db 231 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLKCNADANP 290

QY 241 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300

Db 291 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 350

QY 301 PPTTTTQQTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 347

Db 351 PPTTTTQQTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 397

RESULT 4

AAE23283

ID AAE23283 standard; protein; 549 AA.

XX

AC AAE23283;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human nectin-3alpha protein.

XX

KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;

KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;

KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 73

FT /note= "N-glycosylated"

FT Domain 74. .152

FT /note= "Extracellular Ig domain"

FT Modified-site 83

FT /note= "N-glycosylated"

FT Modified-site 125

FT /note= "N-glycosylated"

FT Modified-site 186

FT /note= "N-glycosylated"

FT Domain 189. .250

FT /note= "Extracellular Ig domain"

FT Modified-site 222

FT /note= "N-glycosylated"

FT Domain 287. .342

FT /note= "Extracellular Ig domain"

FT Modified-site 331

FT /note= "N-glycosylated"

FT Domain 405. .424

FT /note= "Transmembrane domain"

FT Domain 425. .549

FT /note= "C-terminal domain"

XX

PN WO200228902-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US031392.

XX

PR 05-OCT-2000; 2000US-0238557P.

XX

PA (IMMV) IMMUNEX CORP.

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC FLAGpolyHis fusion protein
XX
SQ Sequence 426 AA;

Query Match 100.0%; Score 1976; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 5.8e-154;
Matches 369; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db |||||
QY 58 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
Db |||||
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
QY 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
Db |||||
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIISQYKLFPTTR 180
Db |||||
QY 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIISQYKLFPTTR 237
Db |||||
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANP 240
Db |||||
QY 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANP 297
Db |||||
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db |||||
QY 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357
Db |||||

RESULT 2
AAE23287
ID AAE23287 standard; protein; 634 AA.
XX
AC AAE23287;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-IgG1Fc region fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX

OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.

PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.

Claim 9; Page 100-102; 141pp; English.

CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 634 AA;

Query Match 93.8%; Score 1853; DB 5; Length 634;
Best Local Similarity 100.0%; Pred. No. 1.3e-143;
Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db |||||
QY 58 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
Db |||||
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
QY 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
Db |||||
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIISQYKLFPTTR 180
Db |||||
QY 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIISQYKLFPTTR 237
Db |||||
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANP 240
Db |||||
QY 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGNLKNADANP 297
Db |||||
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db |||||
QY 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357
Db |||||
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFLSTLTIKDDTIATRS 349
XX |||||

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 44.5662 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-15_COPY_58_426
Perfect score: 1976
Sequence: 1 GPIIIVEPHVTAVGKNVSLK.....GSSDYKDDDDKGSSHHHHH 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1976	100.0	426	5	AAE23289 Human nec
2	1853	93.8	634	5	AAE23287 Human nec
3	1844	93.3	542	5	AAE23281 Human del
4	1844	93.3	549	5	AAE23283 Human nec
5	1844	93.3	549	5	AAE23282 Mouse nec
6	1844	93.3	549	6	ABJ20222 Human IG
7	1844	93.3	555	4	AAM39143 Human pol
8	1767	89.4	549	4	AAG63982 Amino aci
9	1767	89.4	549	4	AAG63985 Amino aci
10	1767	89.4	549	5	AAE23291 Mouse nec
11	1706.5	86.4	387	5	AAE23290 Human nec
12	1615.5	81.8	559	4	AAM40929 Human pol
13	1604	81.2	504	5	AAE23284 Human del
14	1604	81.2	510	5	AAE23285 Mouse nec
15	1604	81.2	510	5	AAE23286 Human nec
16	1602	81.1	437	5	AAE23299 Human nec
17	1602	81.1	595	5	AAE23288 Human aci
18	1567	79.3	438	4	AAG63984 Amino aci
19	1567	79.3	438	5	AAE23293 Mouse nec
20	1567	79.3	510	4	AAG63983 Amino aci
21	1567	79.3	510	5	AAE23292 Mouse nec
22	1218	61.6	267	4	AAM93536 Human pol
23	594	30.1	258	5	ABB90250 Human pol
24	538.5	27.3	458	5	AAE23295 Human nec
25	538.5	27.3	514	6	ABJ20237 Human IG

26	538.5	27.3	517	3	AAAY32390	Aay32390 Herpesvir
27	538.5	27.3	517	5	AAE23294	Aae23294 Human nec
28	516	26.1	518	5	ABG77170	Abg77170 Prostate
29	492	24.9	497	5	AAE23303	Aae23303 Human nec
30	485.5	24.6	498	5	AAE23305	Aae23305 Human nec
31	480.5	24.3	510	4	AAB93365	Aab93365 Human pro
32	480.5	24.3	510	4	AAU00471	Aau00471 Human TAN
33	480.5	24.3	510	5	ABJ05562	Abj05562 Breast ca
34	480.5	24.3	510	6	ABJ20232	Abj20232 Human IG
35	480.5	24.3	510	6	ABR48229	Abra48229 Human bla
36	480.5	24.3	510	6	ABU56613	Abu56613 Lung canc
37	480.5	24.3	510	6	ABP97212	Abp97212 Tumour-as
38	480.5	24.3	510	7	ADB80512	Adb80512 Ovarian c
39	478.5	24.2	510	5	AAE23300	Aae23300 Human nec
40	478.5	24.2	510	6	ABJ20231	Abj20231 Human IG
41	474	24.0	511	5	AAE23301	Aae23301 Human nec
42	470	23.8	580	5	AAE23302	Aae23302 Human nec
43	401.5	20.3	538	5	AAE23297	Aae23297 Human nec
44	401.5	20.3	538	6	ABJ20238	Abj20238 Human IG
45	401.5	20.3	538	8	ADE86687	Ade86687 Human pol

ALIGNMENTS

RESULT 1
AAE23289
ID AAE23289 standard; protein; 426 AA.
XX

AC AAE23289;

DT 27-AUG-2002 (first entry)

XX Human nectin-3alpha-FLAGpolyHis fusion protein.

Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
paracellular transport disorder; kidney; diabetic retinopathy; allergy;
allograft rejection; metastasis; restenosis; inflammatory bowel disease;
oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.

OS Homo sapiens.

OS Unidentified.

OS Chimeric.

Key	Location/Qualifiers
Region	1..404
Region	/note= "Human nectin-3alpha protein"
Region	405..420
Region	/note= "FLAG peptide"
Region	421..426
Region	/note= "PolyHis tag"

WO200228902-A2.

11-APR-2002.

05-OCT-2001; 2001WO-US031392.

05-OCT-2000; 2000US-0238557P.

(IMMV) IMMUNEX CORP.

Baum FR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

WPI; 2002-426103/45.

Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
sepsis, stroke.

Claim 9; Page 104-105; 141pp; English.

Qy	235	NADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHP	LTFTNYSGVYICKVTNSLGORSQOK	294	
Db	270	LSEGQPPP-KYNWTRLDGPLPSGVRVKGDTLGF-PPLT	TEHSGVYVCHVSNELSSRDSQV	327	
Qy	295	VYISDP-----	-----P	302	
Db	328	TVEVLDPEDPGKQVDLVSASVIVGVIAALLFCLLVV	VVVLMSRYHRRKAQQMTQKYEEE	387	
Qy	303	TTTTLQPTI-----	-----QWHPST-----	ADIEDLATEPKLPPFLST	336
Db	388	LTLTRENSIRRLHSHSDPRSQPEBSVGLRAEGHPD	SLKDNSSCSVMSEEPGRSY--ST	445	
Qy	337	LATIKD-----	DTIATRS GSSDYKDDDDKGSSHHHH	368	
Db	446	LTTRVREIETQTELLSPGSGRTEEDDDQDEGIKQ	AMNH	482	

Search completed: April 12, 2004, 09:45:14
Job time : 30.9686 secs

DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP566B0846.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;

Query Match 70.4%; Score 1391; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 5.2e-110;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPPVA 145
Db 1 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPPVA 60

QY 146 HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKKHPALEKDIRYSFI 205
Db 61 HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKKHPALEKDIRYSFI 120

QY 206 LDIQYAPEVSVTGYDGNWFWGKGVNLCNADANPPPKSVWSRLDGQWPDGLLASDNTL 265
Db 121 LDIQYAPEVSVTGYDGNWFWGKGVNLCNADANPPPKSVWSRLDGQWPDGLLASDNTL 180

QY 266 HFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISDPPTTTTLQTIQWHPSTADIEDLAT 325
Db 181 HFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISDPPTTTTLQTIQWHPSTADIEDLAT 240

QY 326 EPKKLPPLSTLTIKDDTIAT 347
Db 241 EPKKLPPLSTLTIKDDTIAT 262

RESULT 7
Q8NC05 PRELIMINARY; PRT; 267 AA.
AC Q8NC05;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL "NEDO human cDNA sequencing project."
DT Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075105; BAC11404.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.

DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;

Query Match 61.6%; Score 1218; DB 4; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.6e-95;
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 35 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 94

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 95 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 154

QY 121 PDSLIDGGNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTR 180
Db 155 PDSLIDGGNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTR 214

QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLC 233
Db 215 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLC 267

RESULT 8
Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to nectin 3, DKFZP566B0846 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 43.6%; Score 862; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 4e-65;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 CVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPKSVWS 248
Db 1 CVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPKSVWS 60

QY 249 RLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISDPPTTTTLQ 308
Db 61 RLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISDPPTTTTLQ 120

QY 309 PTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIAT 347
Db 121 PTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIAT 159

RESULT 9
Q9ERF5 PRELIMINARY; PRT; 295 AA.
AC Q9ERF5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

Db 358 IPLTQT 363

RESULT 5

Q9JLJB8

ID	Q9JLJB8	PRELIMINARY;	PRT;	510 AA.
AC	Q9JLJB8;			
DT	01-OCT-2000	(TrEMBLrel. 15,	Created)	
DT	01-OCT-2000	(TrEMBLrel. 15,	Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25,	Last annotation update)	
DE	Cell adhesion molecule nectin-3 beta.			

OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=20209403; PubMed=10744716;
RA	Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA	Tachibana K., Mizoguchi A., Takai Y.;
RT	"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT	that shows homophilic and heterophilic cell-cell adhesion
RT	activities.";
RL	J. Biol. Chem. 275:10291-10299 (2000).
DR	EMBL; AF195834; AAF63686.1; --
DR	MGD; MGI:1930171; Pvrl3.
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR	GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR	GO; GO:0005515; F:protein binding; IPI.
DR	GO; GO:0007155; P:cell adhesion; IDA.
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	Pfam; PF00047; ig; 2.
DR	SMART; SM00409; Ig; 1.
DR	PROSITE; PS50835; IG LIKE; 3.
SQ	SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;

Db	118	QGRVLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESSTTSFPNETATIIISOYKLEPTR	180
Db	178	PDSLIDGGNETVAAVCVAAATGKPVAQIDWEGDLGEMESSTTSFPNETATIVSOYKLEPTR	237
QY	181	FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP	240
Db	238	FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP	297
QY	241	PPFKSVNSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	300
Db	298	PPFKSVNSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	357
QY	301	PPTTTT 306	
Db	358	IPLTQT 363	
RESULT 6			
Q9Y412			
ID	Q9Y412		
AC	Q9Y412;		
	PRELIMINARY;	PRT;	407 AA.

QY 121 PDSLIDGGNETVAAICIAATGKPVAAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 404
RESULT 2
Q9JLB9 PRELIMINARY; PRT; 549 AA.
ID Q9JLB9
AC Q9JLB9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoch-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;
Query Match 89.4%; Score 1767; DB 11; Length 549;
Best Local Similarity 94.2%; Pred. No. 7.3e-142;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
QY 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GSIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 404
RESULT 3
Q9D006 PRELIMINARY; PRT; 549 AA.
ID Q9D006
AC Q9D006;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2610301B19Rik protein.
GN PVRL3 OR 2610301B19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;
Query Match 87.2%; Score 1723; DB 11; Length 549;
Best Local Similarity 91.9%; Pred. No. 4.1e-138;
Matches 319; Conservative 16; Mismatches 12; Indels 0; Gaps 0;
QY 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GSIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 29.9686 Seconds
(without alignments)
3884.945.Million cell updates/sec

Title: US-09-972-268-15_COPY_58_426
Perfect score: 1976
Sequence: 1 GPIIVEPHVTAVGKNVSLK.....GSSDYKDDDDKGSHHHHH 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archheap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1844	93.3	549	4	Q9NQS3	Q9nqs3 homo sapien
2	1767	89.4	549	11	Q9JLB9	Q9jlb9 mus musculus
3	1723	87.2	549	11	Q9D006	Q9d006 mus musculus
4	1567	79.3	438	11	Q9JLB7	Q9jlb7 mus musculus
5	1567	79.3	510	11	Q9JLB8	Q9jlb8 mus musculus
6	1391	70.4	407	4	Q9Y412	Q9y412 homo sapien
7	1218	61.6	267	4	Q8NC05	Q8nc05 homo sapien
8	862	43.6	304	4	Q9BVA9	Q9bva9 homo sapien
9	534.5	27.0	295	11	Q9ERF5	Q9erf5 mesocricetu
10	528	26.7	298	6	Q9GL74	Q9gl74 cercopithec
11	526.5	26.6	295	6	Q9GL75	Q9gl75 bos taurus
12	480.5	24.3	510	4	Q96NY8	Q96ny8 homo sapien
13	480.5	24.3	510	4	Q96KL5	Q96kl5 homo sapien
14	476.5	24.1	483	11	Q9DBP8	Q9dbp8 mus musculus
15	464	23.5	508	11	Q8R007	Q8r007 mus musculus
16	464	23.5	508	11	Q8CED8	Q8ced8 mus musculus

17	420	21.3	530	11	Q80XJ5	Q80xj5 mus musculu
18	419	21.2	467	11	Q91VT9	Q91vt9 mus musculu
19	419	21.2	467	11	Q8C6F2	Q8c6f2 mus musculu
20	396.5	20.1	449	4	Q9UEI6	Q9uei6 homo sapien
21	394.5	20.0	412	11	Q9RIE1	Q9rie1 rattus norv
22	389.5	19.7	412	11	Q63611	Q63611 rattus norv
23	386.5	19.6	400	6	Q8HY16	Q8hy16 cebus apell
24	383.5	19.4	417	4	Q96BJ1	Q96bj1 homo sapien
25	381.5	19.3	403	6	Q8HY15	Q8hy15 lemur catta
26	378	19.1	408	11	Q91WP1	Q91wp1 mus musculu
27	376	19.0	408	11	Q8K094	Q8k094 mus musculu
28	375	19.0	408	11	Q8BVF6	Q8bvf6 mus musculu
29	371.5	18.8	401	6	Q08835	Q08835 cercopithec
30	337	17.1	412	6	Q8HY14	Q8hy14 oryctolagus
31	334	16.9	415	11	Q60977	Q60977 mus musculu
32	295	14.9	456	11	Q8R5M8	Q8r5m8 mus musculu
33	294	14.9	442	4	Q9BY67	Q9by67 homo sapien
34	289	14.6	445	11	Q8R4L1	Q8r4l1 mus musculu
35	285	14.4	445	11	Q8K3T6	Q8k3t6 mus musculu
36	281.5	14.2	443	4	Q8N2F4	Q8n2f4 homo sapien
37	264.5	13.4	394	13	Q7ZXX1	Q7zxx1 xenopus lae
38	263.5	13.3	801	5	Q86LF8	Q86lf8 drosophila
39	257.5	13.0	417	11	Q7TNL1	Q7tnl1 mus musculu
40	257.5	13.0	800	5	Q86LF9	Q86lf9 drosophila
41	256.5	13.0	333	4	Q86WB8	Q86wb8 homo sapien
42	253.5	12.8	336	11	Q9D6E7	Q9d6e7 mus musculu
43	253.5	12.8	336	11	Q80VG4	Q80vg4 mus musculu
44	236.5	12.0	435	4	Q8N3J6	Q8n3j6 homo sapien
45	236.5	12.0	437	4	Q8IZP8	Q8izp8 homo sapien

ALIGNMENTS

RESULT 1						
Q9NQS3	ID	Q9NQS3	PRELIMINARY;	PRT;	549	AA.
AC	Q9NQS3;					
DT	01-OCT-2000	(TremBLrel. 15, Created)				
DT	01-OCT-2000	(TremBLrel. 15, Last sequence update)				
DT	01-OCT-2003	(TremBLrel. 25, Last annotation update)				
DE	Nectin 3.					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RA	Reymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,					
RA	Dubreuil P., Lopez M.;					
RT	"Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that					
RT	interacts with afadin.";					
RL	Gene 0:0-0(2000).					
DR	EMBL; AF282874; AAF97597.1; -.					
DR	InterPro; IPR003599; Ig.					
DR	InterPro; IPR007110; Ig-like.					
DR	Pfam; PF00047; ig; 2.					
DR	SMART; SM00409; IG; 1.					
DR	PROSITE; PS50835; IG_LIKE; 3.					
SQ	SEQUENCE	549	AA;	61002	MW;	6D1104CCB4A9D731 CRC64;
Query Match						
Best Local Similarity 93.3%; Score 1844; DB 4; Length 549;						
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						

Qy	1	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKTHGKSSQTVAVHHPQYGFVSQGEY	60
Db	58	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKTHGKSSQTVAVHHPQYGFVSQGEY	117
Qy	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	177

RT "Structural and immunological characterization of the amino-terminal
RT domain of mammalian neural cell adhesion molecules.";
RL J. Biol. Chem. 261:3396-3401(1986).
RN [3]
RP IDENTIFICATION AS N-CAM.
RX MEDLINE=92111748; PubMed=1765159;
RA Premont R.T.;
RA "A bovine brain cDNA purported to encode calmodulin-insensitive
RT adenylyl cyclase has extensive identity with neural cell adhesion
RT molecules (N-CAMs).";
RT FEBS Lett. 295:230-231(1991).
RL -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC neurites, etc.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=P31836-1; Sequence=Displayed;
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- CAUTION: Was originally (Ref.1) thought to be a calmodulin-
CC independent adenylate cyclase.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X16451; CAA34470.1; -;
DR PIR; A32976; IJBONC.
DR HSSP; P40189; 1BQU.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 853 NEURAL CELL ADHESION MOLECULE 1, 140 kDa
FT ISOFORM.
FT DOMAIN 20 719 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 720 737 POTENTIAL.
FT DOMAIN 738 853 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 111 IG-LIKE C2-TYPE 1.
FT DOMAIN 116 205 IG-LIKE C2-TYPE 2.
FT DOMAIN 212 300 IG-LIKE C2-TYPE 3.
FT DOMAIN 307 412 IG-LIKE C2-TYPE 4.
FT DOMAIN 415 500 IG-LIKE C2-TYPE 5.
FT DOMAIN 527 604 FIBRONECTIN TYPE-III 1.
FT DOMAIN 633 700 FIBRONECTIN TYPE-III 2.
FT DOMAIN 152 156 HEPARIN-BINDING (POTENTIAL).
FT DOMAIN 161 165 HEPARIN-BINDING (POTENTIAL).
FT DISULFID 41 96 BY SIMILARITY.
FT DISULFID 139 189 BY SIMILARITY.
FT DISULFID 235 286 BY SIMILARITY.
FT DISULFID 328 394 BY SIMILARITY.
FT DISULFID 435 488 BY SIMILARITY.
FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 314 314 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 346 346 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 432 432 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 853 AA; 93893 MW; E12FD49231A7A368 CRC64;
Query Match 9.6%; Score 189; DB 1; Length 853;
Best Local Similarity 23.3%; Pred. No. 5.2e-07;
Matches 80; Conservative 63; Mismatches 133; Indels 68; Gaps 17;
QY 8 HVTAVWGKNVSLKCLIEVNETITQISWEKINGKSSQTVAVHHPQYGSVQGEYQGRVLFK 67
Db 222 NATANLGQSIVLVCNAEGFPEPT-VSWTK-----DGEQIENEDEKYLFS 265
QY 68 NYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG 127
Db 266 D---DSSELTIRKVDKNDEAEYVCIAEN-KAGEQDASIHLEKVFAPKITYVENQTAM--E 319
QY 128 GNETVAAICIAATGKPVAHIDWE---GDLGEMESTTTTFPNETATI-----ISQ 173
Db 320 LEEQVTLTC-EASGDPIPSITWRTSTRNISSEKASWTRPEKQETLDGHMVVRSHARVSS 378
QY 174 YKLFPTFPFARGRRITCVVKHPALEKDIRYSFILDIOYAPE---VSVTGYDGNWVGRKG 229
Db 379 LTLKSIQYTDAGEYVCTASN-TIGQDSQ-SMYLEVQYAPKLOGPVAVYTWEQN-----Q 430
QY 230 VNLKCNADANPPPFKSVWSRLDQWPDGGLASDNTLHF-----VHPLTFNYSQ 277
Db 431 VNITCEVFAYPSATIS-WFR-DGQ---LLPSSNYSNIKIYNTPSASYLEVTPDSENDFG 484
RESULT 12
OX2G HUMAN STANDARD; PRT; 278 AA.
AC P41217; Q8TB85; Q9H3J3;
DT 01-FEB-1995 (Rel. 31, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE OX-2 membrane glycoprotein precursor (CD200 antigen) (My033 protein).
GN MOX2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 5-278 FROM N.A. (ISOFORM 1).
RC TISSUE=Blood;
RX MEDLINE=87192943; PubMed=3032785;
RA McCaughan G.W., Clark M.J., Barclay A.N.;
RT "Characterization of the human homolog of the rat MRC OX-2 membrane
RT glycoprotein.";
RL Immunogenetics 25:329-335(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Fetal brain;
RA Mao Y.M., Xie Y., Zheng Z.H.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

Genew; HGNC:5273; HSPG2.
MIM; 142461; -.
MIM; 255800; -.
InterPro; IPR008985; ConA_like_lect_gl.
InterPro; IPR000742; EGF_2.
InterPro; IPR006209; EGF_like.
InterPro; IPR006210; IEGF.
InterPro; IPR007110; Ig-like.
InterPro; IPR003599; Ig.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003596; Ig_v.
InterPro; IPR000034; Laminin_B.
InterPro; IPR002049; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR002172; LDL_receptor_A.
InterPro; IPR000082; SEA_domain.
Pfam; PF00008; EGF; 4.
Pfam; PF00047; Ig; 22.
Pfam; PF00052; laminin_B; 3.
Pfam; PF00053; laminin_EGF; 7.
Pfam; PF00054; laminin_G; 3.
Pfam; PF00057; ldl_recept_a; 4.
Pfam; PF01390; SEA; 1.
PRINTS; PR00261; LDLRECEPTOR.
ProDom; PD003031; Laminin_B; 3.
SMART; SM00181; EGF; 15.
SMART; SM00180; EGF_Lam; 12.
SMART; SM00409; IG; 22.
SMART; SM00408; IGC2; 21.
SMART; SM00406; IGV; 7.
SMART; SM00281; LamB; 3.
SMART; SM00282; LamG; 3.
SMART; SM00192; LDLa; 4.
SMART; SM00200; SEA; 1.
PROSITE; PS00022; EGF_1; 9.
PROSITE; PS01186; EGF_2; 6.
PROSITE; PS50026; EGF_3; 4.
PROSITE; PS50835; IG_LIKE; 22.
PROSITE; PS50025; LAM_G_DOMAIN; 3.
PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
PROSITE; PS01209; LDLRA_1; 4.
PROSITE; PS50068; LDLRA_2; 4.
PROSITE; PS50024; SEA; 1.
KW Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; EGF-like domain; Disease mutation.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 4391 BASEMENT MEMBRANE-SPECIFIC HEPARAN
SULFATE PROTEOGLYCAN CORE PROTEIN.
FT DOMAIN 80 194 SEA.
FT DOMAIN 198 235 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 284 320 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 324 360 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 367 404 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 405 504 IG-LIKE C2-TYPE 1.
FT DOMAIN 521 530 LAMININ EGF-LIKE 1 (N-TERMINAL).
FT DOMAIN 531 730 LAMININ DOMAIN IV 1 (DOMAIN III A).
FT DOMAIN 731 763 LAMININ EGF-LIKE 1 (C-TERMINAL).
FT DOMAIN 764 813 LAMININ EGF-LIKE 2.
FT DOMAIN 814 871 LAMININ EGF-LIKE 3.
FT DOMAIN 879 923 LAMININ EGF-LIKE 4 (INCOMPLETE).
FT DOMAIN 924 933 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 934 1125 LAMININ DOMAIN IV 2 (DOMAIN III B).
FT DOMAIN 1126 1158 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 1159 1208 LAMININ EGF-LIKE 6.
FT DOMAIN 1209 1265 LAMININ EGF-LIKE 7.
FT DOMAIN 1275 1324 LAMININ EGF-LIKE 8.
FT DOMAIN 1325 1334 LAMININ EGF-LIKE 9 (N-TERMINAL).
FT DOMAIN 1335 1529 LAMININ DOMAIN IV 3 (DOMAIN III C).
FT DOMAIN 1530 1562 LAMININ EGF-LIKE 9 (C-TERMINAL).
FT DOMAIN 1563 1612 LAMININ EGF-LIKE 10.
FT DOMAIN 1613 1670 LAMININ EGF-LIKE 11.
FT DOMAIN 1677 1771 IG-LIKE C2-TYPE 2.

FT	DOMAIN	1772	1865	IG-LIKE C2-TYPE 3.
FT	DOMAIN	1866	1955	IG-LIKE C2-TYPE 4.
FT	DOMAIN	1956	2051	IG-LIKE C2-TYPE 5.
FT	DOMAIN	2052	2151	IG-LIKE C2-TYPE 6.
FT	DOMAIN	2152	2244	IG-LIKE C2-TYPE 7.
FT	DOMAIN	2245	2340	IG-LIKE C2-TYPE 8.
FT	DOMAIN	2341	2436	IG-LIKE C2-TYPE 9.
FT	DOMAIN	2437	2533	IG-LIKE C2-TYPE 10.
FT	DOMAIN	2534	2629	IG-LIKE C2-TYPE 11.
FT	DOMAIN	2630	2726	IG-LIKE C2-TYPE 12.

Query Match 10.0%; Score 198; DB 1; Length 4391;
Best Local Similarity 22.8%; Pred. No. 8.9e-07;
Matches 89; Conservative 55; Mismatches 147; Indels 100; Gaps 18;

Qy	2	PIIVE---PHVTAVWGKNVSLKCLIEVNETITQISWEKIHGSSQTVAVHPQYGFVSQG	58
Db	2926	PIYIEASSSHVTE--GQTLDLNCVVP-GQAHQVTVYKRGG----SLPARHQTHG	2973
Qy	59	EYQGRVLFKNYSLNDATITLHNIGFSDSKGYICKAVTFPLGNAQSSTTVTV-----	109
Db	2974	-----SQLRLHLVSPADSGEYVCRAASGPGPEQEAFTVTVPPEGSSYR	3018
Qy	110	LVEPTVSLIKGPDLSLIDGNETVAAICIAATGKPKVAHIDWEGDLGEMESTTTTFPNETAT	169
Db	3019	LRSPVIS-IDPPSSTVQQGD-ASFCKLIHDGAAPISLEWKTNRQNELEDNVHISP--GS	3074
Qy	170	IISQYKLFPTFRFARRITCVVVKHPALEKDIRYSFI-LDIQYAPEVSVTGYDGNWVFVGRK	228
Db	3075	IIT---IVGTRPSNHGTYRCVASN---AYGVAQSVVNLVSHGPPVTVSVLPEGPVVVKVGK	3128
Qy	229	GVNLKCNADANPPPFKSVWSRLDG-----QWPDGLLASDNTLHFVHPLTFNYSGVYICK	282
Db	3129	AVTLEC-VSAGEPRSSARWTRISSTPAKLEQRTYGLMDSHAVLQ-ISSAKPSDAGTYVCL	3186
Qy	283	VTNSLQSRSDQKVIYIS-----DPPTTTTLQ-----PTIQWH	314
Db	3187	AQNALGTAQKQVEVIVDTGAMAPGAPQVQAEAEELTVEAGHTATLRCSATGSPAPTIHW-	3245
Qy	315	PSTADIEDLATEPKLPPLSTLATIKDDTI	345
Db	3246	-----SKLRSPLPWQHRLEGDTL	3263

RESULT 11

NCAL_BOVIN

ID	NCAL_BOVIN	STANDARD;	PRT;	853 AA.
AC	P31836;			

DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)

DE (NCAM-140).

GN NCAM1 OR NCAM.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;

OC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Brain cortex;

RX MEDLINE=89378239; PubMed=2776887;

RA Lipkin V.M., Khrantsov N.V., Andreeva S.G., Moshnyakov M.V.,

RA Petukhova G.V., Rakitina T.V., Feshchenko E.A., Ishchenko K.A.,

RA Mirzoeva S.F., Chernova M.N., Dranytsyna S.M.;

RT "Calmodulin-independent bovine brain adenylyate cyclase. Amino acid

RL FEBS Lett. 254:69-73(1989).

RN [2]

RP SEQUENCE OF 20-36.

RX MEDLINE=86140120; PubMed=3512556;

RX Rougot G., Marshak D.R.;

Db 209 PAIMPMQKSFNATAERGEEMTLTCKASGSPDET-ISRFR----- 246

QY 58 GEYQGRVLFKN--YSL--NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP 113

Db 247 ---NGKLIENEEKYILKGSNTLTVRNIINKDGGSYVCKA-TNKAGEDQKQAFLOVFPVQ 302

QY 114 TVSLIKGPDSLIDGNET-----VAAICIAATGKPVAHIDWEGDL-GEMESTTTSPNE 166

Db 303 HILQLK-----NETTSENGHVTLVC-EAEGEPVPEITWKRAIDGVNMFSEGDKSPDG 352

QY 167 TATIISQYKLFPTFRAGRRITCVKHPALEKDIRY-----SFILDIQYAP- 212

Db 353 RIEVKQGH-----GRSSLHIRDVKLSDSGRYDCEAASRIGGHQSRMHLDIYAPK 402

QY 213 ----EVSVTGYDGNWFVGRKGVNLKCNADANPPPKSV-WSRLDGQWPDGLIASDNTLHF 267

Db 403 FVSNQTMYSWEGN-----PINISCDVTANPP--ASIHWR-----EXLLLPKANTTHL 449

QY 268 -----VHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTTTLQPTIQWHP 315

Db 450 KTHSVGRKMILEIAPTSDNDFGRYNCATNRIGTRFQEVILELADVPSPHGVKIELSQ 509

QY 316 STA-----DIEDLATEPEKKL 330

Db 510 TTAKISFNKPESHGGVPIHHYQVDVKEVASETWKI 544

RESULT 10

PGBM HUMAN

ID PCBM_HUMAN STANDARD; PRT; 4391 AA.

AC P98160; Q16287; Q9H3V5;

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Basement membrane-specific heparan sulfate proteoglycan core

DE protein precursor (HSPG) (perlecan) (PLC).

GN HSPG2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92112994; PubMed=1730768;

RA Kallunki P., Tryggvason K.;

RT "Human basement membrane heparan sulfate proteoglycan core protein: a

RT 467-kD protein containing multiple domains resembling elements of the

RT low density lipoprotein receptor, laminin, neural cell adhesion

RT molecules, and epidermal growth factor.";

RL J. Cell Biol. 116:559-571(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Colon, and Skin;

RX MEDLINE=92235084; PubMed=1569102;

RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;

RT "Primary structure of the human heparan sulfate proteoglycan from

RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple

RT domains homologous to the low density lipoprotein receptor, laminin,

RT neural cell adhesion molecules, and epidermal growth factor.";

RL J. Biol. Chem. 267:8544-8557(1992).

RN [3]

RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.

RX MEDLINE=20553141; PubMed=11101850;

RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,

RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,

RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,

RA Hentati F., Fontaine B.;

RT "Perlecan, the major proteoglycan of basement membranes, is altered in

RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";

RL Nat. Genet. 26:480-483(2000).

RN [4]

RP SEQUENCE OF 1016-1470 FROM N.A.

RC TISSUE=Colon;

RX MEDLINE=91365376; PubMed=1679749;

RA Dodge G.R., Kovalesky I., Chu M.L., Hassell J.R., McBride O.W.,

RA Yi H.F., Iozzo R.V.;

RT "Heparan sulfate proteoglycan of human colon: partial molecular

RT cloning, cellular expression, and mapping of the gene (HSPG2) to the

RT short arm of human chromosome 1.";

RL Genomics 10:673-680(1991).

RN [5]

RP SEQUENCE OF 890-1396 FROM N.A.

RC TISSUE=Fibrosarcoma;

RX MEDLINE=92120660; PubMed=1685141;

RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,

RA Tryggvason K.;

RT "Cloning of human heparan sulfate proteoglycan core protein,

RT assignment of the gene (HSPG2) to 1p36.1--p35 and identification of

RT a BamHI restriction fragment length polymorphism.";

RL Genomics 11:389-396(1991).

RN [6]

RP SEQUENCE OF 1-21 FROM N.A.

RX MEDLINE=94052171; PubMed=8234307;

RA Coher I.R., Graessel S., Murdoch A.D., Iozzo R.V.;

RT "Structural characterization of the complete human perlecan gene and

RT its promoter.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).

RN [7]

RP CARBOHYDRATE-LINKAGE SITE ASN-2121.

RX MEDLINE=22660472; PubMed=12754519;

RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;

RT "Identification and quantification of N-linked glycoproteins using

RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";

RL Nat. Biotechnol. 21:660-666(2003).

CC -!- FUNCTION: This protein is an integral component of basement

CC membranes. It is responsible for the fixed negative electrostatic

CC charge and is involved in the charge-selective ultrafiltration

CC properties. It serves as an attachment substrate for cells.

CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in

CC dimers or stellate structures. It interacts with other basement

CC membrane components such as laminin, prolargin and collagen type

CC IV.

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: Found in the basement membranes.

CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED

CC AND O-LINKED OLIGOSACCHARIDES.

CC -!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel

CC syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder

CC characterized by permanent myotonia (prolonged failure of muscle

CC relaxation) and skeletal dysplasia, resulting in reduced stature,

CC kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.

CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.

CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.

CC -!- SIMILARITY: Contains 3 laminin IV domains.

CC -!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 3 laminin G-like domains.

CC -!- SIMILARITY: Contains 4 EGF-like domains.

CC -!- SIMILARITY: Contains 1 SEA domain.

CC -----

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CC use by non-profit institutions as long as its content is in no way

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; X62515; CAA44373.1; -.

CC EMBL; M85289; AAA52700.1; -.

CC EMBL; AL445795; CAC18534.1; -.

CC EMBL; M64283; AAA52699.1; -.

CC EMBL; S76436; AAB21121.2; -.

CC EMBL; L22078; -; NOT_ANNOTATED_CDS.

CC PIR; A38096; A38096.

CC HSSP; P00740; 1EDM.

CC Siena-2DPAGE; P98160; -.

DR	Genew; HGNC:9705; PVR.	
DR	MIM; 173850; --	
DR	GO; GO:0005737; C:cytoplasm; TAS.	
DR	GO; GO:0005615; C:extracellular space; TAS.	
DR	GO; GO:0016021; C:integral to membrane; TAS.	
DR	GO; GO:0004872; F:receptor activity; TAS.	
DR	GO; GO:0007125; P:invasive growth; TAS.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; ig; 3.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS50835; IG LIKE; 3.	
KW	Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;	
KW	Repeat; Antigen; Alternative splicing; Polymorphism.	
FT	SIGNAL	1
FT	CHAIN	20
FT	DOMAIN	21
FT	DOMAIN	21
FT	TRANSMEM	344
FT	TRANSMEM	367
FT	DOMAIN	368
FT	DOMAIN	417
FT	DOMAIN	24
FT	DOMAIN	145
FT	DOMAIN	244
FT	DOMAIN	49
FT	DISULFID	166
FT	DISULFID	266
FT	DISULFID	266
FT	CARBOHYD	105
FT	CARBOHYD	120
FT	CARBOHYD	188
FT	CARBOHYD	218
FT	CARBOHYD	237
FT	CARBOHYD	278
FT	CARBOHYD	307
FT	CARBOHYD	313
FT	CARBOHYD	340
FT	VARSPLIC	331
FT	VARSPLIC	331
FT	VARSPLIC	332
FT	VARSPLIC	385
FT	VARSPLIC	392
FT	VARSPLIC	393
FT	VARIANT	67
FT	VARIANT	340
FT	SEQUENCE	417 AA; 45302 MW; D15C012CE853169B CRC64;
SQ	Query Match	19.4%; Score 383.5; DB 1; Length 417;
	Best Local Similarity	30.2%; Pred. No. 1.2e-22;
	Matches	95; Conservative 56; Mismatches 143; Indels 21; Gaps 9;
QY	1 GPIIVE--PHVTAVWGKNVSLKCLIEVNET----	ITQISWEKIHGKSSQTVAVH---PQ 51
Db	27 GDVVVQAPTQVPGFLGDSVTLPCYLQVPMNEVTHVSQLTWAR-HGESGSMVAFHQTCGPS	85
QY	52 YGFSVQGEYQGRVLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV	111
Db	86 YSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVA	143
QY	112 BP--TVSLIKGPDSLIDGNETVAACIAATGKPAHIDWEGDLGEMESTT--TSFPNET	167
Db	144 KPQNTAEVQKVQLT---GEPVPMARCVSTGGRPPAQITWHSDLGMPNTSQVPGFLSGT	199
QY	168 ATISQYKLPPTFRFARRRITCVVKHPALEKDIRYSFILDIQAPEVSVTGYDGNWFVGR	227
Db	200 VTVSLWILVPSSQVDGKNVTCVHEHSEFEKPOLLTVNLTVYYPPEVVISGYDNNWYLGQ	259
QY	228 KGVNLKCNADANPPPEKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL	287
Db	260 NEATLTCDARSNPEPTGYNWSTMGPLPPFAVAQGAQL-LIRPVDKPIINTLLICNTNAL	318

QY	288	QORSQKVIYISDPP	302
Db	319	GARQAELTVQVKEGP	333
RESULT 8			
ID	ICCR_DROME	STANDARD;	PRT; 764 AA.
AC	Q08180;		
DT	01-FEB-1995 (Rel. 31, Created)		
DT	01-FEB-1995 (Rel. 31, Last sequence update)		
DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DE	Irregular chiasm C-roughest protein precursor (IRREC protein).		
GN	RST.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorphia;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94102535; PubMed=7503814;		
RA	Ramos R.G., Igloi G.L., Lichte B., Baumann U., Maier D.,		
RA	Schneider T., Brandstaetter J.H., Froehlich A., Fischbach K.-F.;		
RT	"The irregular chiasm C-roughest locus of Drosophila, which affects		
RT	axonal projections and programmed cell death, encodes a novel		
RT	immunoglobulin-like protein.";		
RL	Genes Dev. 7:2533-2547 (1993).		
CC	-!- FUNCTION: REQUIRED FOR CORRECT AXONAL PATHWAY FORMATION IN		
CC	THE OPTIC LOBE AND FOR PROGRAMMED CELL DEATH IN THE DEVELOPING		
CC	RETINA.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- TISSUE SPECIFICITY: POSTEMBRYONIC EXPRESSION IS STRONG IN THE		
CC	DEVELOPING OPTIC LOBE AND IN THE EYE IMAGINAL DISC.		
CC	-!- DEVELOPMENTAL STAGE: STRONGLY EXPRESSED IN EMBRYOS. ALSO FOUND		
CC	IN LATE LARVAL AND PUPAL STAGES.		
CC	-!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.		
CC	-----		
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -		
CC	the European Bioinformatics Institute. There are no restrictions on its		
CC	use by non-profit institutions as long as its content is in no way		
CC	modified and this statement is not removed. Usage by and for commercial		
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/		
CC	or send an email to license@isb-sib.ch).		
CC	-----		
DR	EMBL; Z21641; CAA79756.1; --		
DR	EMBL; L11040; AAA16632.1; --		
DR	PIR; A49448; A49448.		
DR	FlyBase; FBgn003285; rst.		
DR	GO; GO:0016202; P:regulation of myogenesis; IMP.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	Pfam; PF00047; ig; 4.		
DR	SMART; SM00408; IGC2; 1.		
DR	PROSITE; PS50835; IG LIKE; 5.		
KW	Transmembrane; Immunoglobulin domain; Glycoprotein; Signal; Repeat;		
KW	Cell adhesion.		
FT	SIGNAL	1	POTENTIAL.
FT	CHAIN	20	IRREGULAR CHIASM C-ROUGHEST PROTEIN.
FT	DOMAIN	20	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	534	POTENTIAL.
FT	DOMAIN	557	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	21	IG-LIKE C2-TYPE 1.
FT	DOMAIN	117	IG-LIKE C2-TYPE 2.
FT	DOMAIN	245	GLY-RICH.
FT	DOMAIN	237	IG-LIKE C2-TYPE 3.
FT	DOMAIN	346	IG-LIKE C2-TYPE 4.
FT	DOMAIN	430	IG-LIKE C2-TYPE 5.
FT	DOMAIN	637	GLN-RICH (OPA-REPEAT).
FT	CARBOHYD	211	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	313	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	393	N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 313 313 N-LINKED (GLCNAC...) (POTENTIAL).
FT VARSPLIC 386 392 EHASASA -> HHQSCHN (in isoform Delta).
FT /FTid=VSP 002622.
FT VARSPLIC 393 417 Missing (in isoform Delta).
FT /FTid=VSP 002623.
SQ SEQUENCE 417 AA; 45464 MW; DA4AD0F64D2F6E1F CRC64;

Query Match 20.1%; Score 396.5; DB 1; Length 417;
Best Local Similarity 31.4%; Pred. No. 1.1e-23;
Matches 99; Conservative 55; Mismatches 140; Indels 21; Gaps 10;

QY 1 GPIIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51
Db 27 GDIIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGN 85
QY 52 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV 111
Db 86 YSEPKRLIEFVAARL--GTELRDASLRMFLGRVEDEGNYTCLFVFPQGSRSVDIWLRLVA 143
QY 112 EP--TVSLIKGPDSLIDGGNETVAICIAATGKPAHIDWEGDIGEMESTTTS--FPNET 167
Db 144 KPONTAEVQKVLQTLT---GKVPVAVRCVSTGGRPPAHITWHSGLGMPNTSQAPGFLSGT 199
QY 168 ATIIISOYKLFPTREARRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227
Db 200 VTITSLWILVPSQVDGKSVTKVEHSEFEXKPOLLTVNLTVYPPVEVISISGYDNNWYLSQ 259
QY 228 KGVNLKCNADANPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 260 NEATLTCDARSNPEPTGYNNWSTTMGPLPPFAVAQQAQL-LIRPVDKPINTTFCNVTNAL 318
QY 288 GQRSDQKVIYISDPP 302
Db 319 GARQAEITVQVKEGP 333

RESULT 7

PVR_HUMAN
ID PVR_HUMAN STANDARD; PRT; 417 AA.
AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168426; PubMed=2538245;
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and expression of a new member of the immunoglobulin superfamily.";
RL Cell 56:855-865(1989).
RN [2]
RP REVISIONS.
RA Racaniello V.R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91006015; PubMed=2170108;
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RA Takeuchi K., Takegami T., Nomoto A.;
RT "The poliovirus receptor protein is produced both as membrane-bound and secreted forms.";
RL EMBO J. 9:3217-3224(1990).
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyianni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
RA Shannon M., Brower A., Olsen A.S., Smith L.M.;

RT "Sequence analysis of a 1Mb region in 19q13.2 containing a zinc finger gene cluster.";
RT Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS.
RX MEDLINE=91239515; PubMed=1851992;
RA Koike S., Ise I., Nomoto A.;
RT "Functional domains of the poliovirus receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N glycosylation of the virus binding domain is not essential for function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P15151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P15151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
CC WWW= "http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC
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CC
CC EMBL; M24407; AAA36461.1; -.
DR EMBL; M24406; AAA36462.1; -.
DR EMBL; X64116; CAA45478.1; -.
DR EMBL; X64117; CAA45478.1; JOINED.
DR EMBL; X64118; CAA45478.1; JOINED.
DR EMBL; X64119; CAA45478.1; JOINED.
DR EMBL; X64120; CAA45478.1; JOINED.
DR EMBL; X64121; CAA45478.1; JOINED.
DR EMBL; X64122; CAA45478.1; JOINED.
DR EMBL; X64123; CAA45478.1; JOINED.
DR EMBL; X64116; CAA45479.1; -.
DR EMBL; X64117; CAA45479.1; JOINED.
DR EMBL; X64118; CAA45479.1; JOINED.
DR EMBL; X64119; CAA45479.1; JOINED.
DR EMBL; X64120; CAA45479.1; JOINED.
DR EMBL; X64121; CAA45479.1; JOINED.
DR EMBL; X64122; CAA45479.1; JOINED.
DR EMBL; X64123; CAA45479.1; JOINED.
DR EMBL; X64116; CAA45480.1; -.
DR EMBL; X64117; CAA45480.1; JOINED.
DR EMBL; X64118; CAA45480.1; JOINED.
DR EMBL; X64119; CAA45480.1; JOINED.
DR EMBL; X64120; CAA45480.1; JOINED.
DR EMBL; X64122; CAA45480.1; JOINED.
DR EMBL; X64123; CAA45480.1; JOINED.
DR EMBL; AC068948; AAF69803.1; -.
DR PIR; A43024; RWHUPD.
DR PIR; S12048; RWHUPA.

FT	DOMAIN	153	247	IG-LIKE C2-TYPE 1.
FT	DOMAIN	252	337	IG-LIKE C2-TYPE 2.
FT	DISULFID	54	131	BY SIMILARITY.
FT	DISULFID	174	229	BY SIMILARITY.
FT	DISULFID	274	320	BY SIMILARITY.
FT	CARBOHYD	128	128	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	315	315	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	339	467	ESPTAGAGATGGIIGGIIAIIATATAVAGTILICQORKE
FT				ORLOADEEELEGPSPYKPPPKAKLEPEMPSQLFTLGA
FT				SEHSPVKTPTFYFDAGVSCADQEMPRYHELPTLEERSGPLLG
FT				ATGLGP -> DTPQASRDVGLVWCAVGGTLLVLLLAGGFL
FT				ALILLRGRRRKSPGGGNDGRGSYDPKTVQVFGNGGPFVW
FT				RSASPEPMRPDGRDEDEEEEMKAEGLMLPPHESPCKDM
FT				ESHLDGSLISRAVYV (in isoform Alpha).
FT				/FTId=VSP 002630.
FT	VARSPLIC	468	530	Missing (in isoform Alpha).
FT				/FTId=VSP 002631.
FT	SEQUENCE	530 AA; 57317 MW; 0ED71BF2B231BBE CRC64;		
SQ				
Query Match 21.3%; Score 420; DB 1; Length 530;				
Best Local Similarity 31.8%; Pred. No. 2.2e-25;				
Matches 101; Conservative 50; Mismatches 137; Indels 30; Gaps 9;				
QY	5	VEPHVTAVGKNVSLKC--LIEVNEFITQISWEKIHGKSSQTVAVHHPOYGFVSVOGEY--	60	
Db	38	VLPEVRGLGTVLPCVLLPPTTTRVSVQVWQRLDG---TVVAAPHPSPFGVDFPNSQFS	94	
QY	61	QGRVLF-----KNYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVLEP-	113	
Db	95	KDRLSPVRRPETNADLRDATLAFRLGRVDEGNYTCEFATFPNGTRRGVTLRVIAQPE	154	
QY	114	-----TVSLIKGPDSLIDGNETVAICIAATGKPAHIDWEGDLGEMESTTTSFPN---E	166	
Db	155	NHAEAQEVITGPQSV-----AVARCVSTGGRPPARITWISSLGG-EAKDTQEPGIGAG	206	
QY	167	TATISQYKLFPTRFARGRRITCVVKKHFALEKDIRYSFILDIOYAPEVSVTGYDGNWFVG	226	
Db	207	TVTLISRYSLVPVGRADGVKVTCTVEHESFEEPIILLPVTLVRYPPPEVSISGYDDNWYLG	266	
QY	227	RKGVNLKCNADANPPPKSVWSRLDQWPDGLLASDNTLHFVHLELTNYSVGYICKVTNS	286	
Db	267	RSEAILTCDVRSNPEPTDYDWSVTSVGFPPASAVAQGSQQL-LVHSDVRMVNTTICTATNA	325	
QY	287	LQQRSDQKVIYISDPPTT 304		
Db	326	VGTGRAEQVILVRESPT 343		

RESULT 5
PVR2_HUMAN
ID PVR2_HUMAN STANDARD; PRT; 538 AA.
AC Q92692; O75455; Q96J29;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Herpes virus entry mediator B) (HvEB) (Nectin 2) (CD112 antigen).
GN PVRL2 OR PRR2 OR HVEB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95347610; PubMed=7622062;
RA Eberle F., Dubreuil P., Mattei M.-G., Devilard E., Lopez M.;
RT "The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the true homolog of the murine MPH gene.";
RL Gene 159:267-272(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98321161; PubMed=9657005;

RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
RT "A cell surface protein with herpesvirus entry activity (HvEB) confers
RT susceptibility to infection by mutants of herpes simplex virus type
RT 1, herpes simplex virus type 2, and pseudorabies virus.";
RL Virology 246:179-189(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 31-538 FROM N.A.
RA Yoshiura K., Murray J.C.;
RT "A transcriptional map in the region of 19ql3 derived using direct
RT sequencing and exon trapping.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 449-538 FROM N.A.
RX MEDLINE=99449047; PubMed=10520737;
RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
RA Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;
RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
RT PEREC1.";
RL DNA Seq. 9:89-101(1998).
CC -!- FUNCTION: RECEPTOR FOR ALPHAPERPEVIRUS (HSV-1, HSV-2 AND
CC PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Delta;
CC IsoId=Q92692-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;
CC TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:74-77(2000);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/204270028_g.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X80038; CAA56342.1; -.
DR EMBL; AF058448; AAC23797.1; -.
DR EMBL; BC003091; AAH03091.1; -.
DR EMBL; AF044968; AAC82348.1; -.
DR EMBL; AF044962; AAC82348.1; JOINED.
DR EMBL; AF044963; AAC82348.1; JOINED.

FT	DOMAIN	377	515	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	31	141	IG-LIKE V-TYPE.
FT	DOMAIN	145	243	IG-LIKE C2-TYPE 1.
FT	DOMAIN	247	334	IG-LIKE C2-TYPE 2.
FT	DOMAIN	437	443	POLY-GLU.
FT	DOMAIN	444	447	POLY-GLY.
FT	DISULFID	51	124	BY SIMILARITY.
FT	DISULFID	172	226	BY SIMILARITY.
FT	DISULFID	269	316	BY SIMILARITY.
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	72	72	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	286	286	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	307	307	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	515 AA; 57047 MW; BFAB00320DDE3785	CRC64;	

Query Match 27.0%; Score 534.5; DB 1; Length 515;
Best Local Similarity 37.8%; Pred. No. 2.3e-34;
Matches 113; Conservative 54; Mismatches 121; Indels 11; Gaps 5

QY

14

GKNVSLKCLIE--VN

ETITQISWEKIHGKSSQTVAVHHPQYGFVSQVQGRVLFKNYS

70

Db

44

GTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAINYPAMGVSVLAPYRVERVEFLRPS

103

QY

71

LNDAITLTHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDSDLIDG---

127

Db

104

FTDGTIRLSRLELEDEGVYICEFATFPAGNRESQNLNTVMAKPT-NWIEGTQAVLRAKKG

162

QY

128

-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQVKLPPTRFARGR

185

Db

163

KDDKVLVATCTGANGKPPSVSWETHLKGAEYQEIIRNPNGTIVISRYLVPSREDHRQ

222

QY

186

RITCVVKHPALEKDIRYSFILDIQYAPEVSVTCYDGNWFVGRKGVNLKCNADANPPPFKS

245

Db

223

SLACIVNYHM--DRFRESLTNLVQYEPEVTIEGFDGNWYLQMDVKLTCKADANPPATEY

280

QY

246

VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTT

304

Db

281

HWTTLNGSLPKGVEAQNRTLFFRGPINYSMAGTYICEATNPIGTRSGQVEVNITEFPYT

339

RESULT 4

PVR2

MOUSE

STANDARD;

PRT;

530 AA.

ID

PVR2

MOUSE

STANDARD;

PRT;

530 AA.

AC

P32507;

Q62096;

DT

01-OCT-1993

(Rel. 27, Created)

DT

16-OCT-2001

(Rel. 40, Last sequence update)

DT

15-MAR-2004

(Rel. 43, Last annotation update)

DE

Poliovirus receptor related protein 2 precursor

(Murine herpesvirus entry protein B) (mHvB) (Nectin 2) (Poliovirus receptor homolog).

GN

PVRL2

OR PVS

OR PVR

OR MPH.

OS

Mus musculus

(Mouse).

OC

Eukaryota;

Metazoa;

Chordata;

Craniata;

Vertebrata;

Euteleostomi;

OC

Mammalia;

Eutheria;

Rodentia;

Sciurognathi;

Muridae;

Murinae;

Mus.

OX

NCBI_TaxID=10090;

RN

[1]

RP

SEQUENCE FROM N.A. (ISOFORM ALPHA).

RX

MEDLINE=92219365;

PubMed=1560525;

RA

Morrison M.E.;

Racaniello V.R.;

RT

"Molecular cloning and expression of a murine homolog of the human poliovirus receptor gene."

RL

J. Virol. 66:2807-2813(1992).

RN

[2]

RP

SEQUENCE FROM N.A. (ISOFORM BETA).

RC

STRAIN=C57BL/6;

TISSUE=Brain;

RX

MEDLINE=94179228;

PubMed=8132569;

RA

Aoki J.;

Koike S.;

Ise I.;

Sato-Yoshida Y.;

Nomoto A.;

RT

"Amino acid residues on human poliovirus receptor involved in interaction with poliovirus."

RL

J. Biol. Chem. 269:8431-8438(1994).

RN	[3]	SEQUENCE FROM N.A. (ISOFORM BETA).
RP	STRAIN=FVB/N; TISSUE=Colon;	
RC	MEDLINE=22388257; PubMed=12477932;	
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,	
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,	
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,	
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,	
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,	
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,	
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,	
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,	
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,	
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,	
RA	Schmerch A., Schein J.E., Jones S.J.M., Marra M.A.;	
RT	"Generation and initial analysis of more than 15,000 full-length	
RT	human and mouse cDNA sequences."	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).	
RN	[4]	
RP	CHARACTERIZATION.	
RX	MEDLINE=99214397; PubMed=10196354;	
RA	Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;	
RT	"The murine homolog (Mph) of human herpesvirus entry protein B (HvEB)	
RT	mediates entry of pseudorabies virus but not herpes simplex virus	
RT	types 1 and 2."	
RL	J. Virol. 73:4493-4497(1999).	
CC	-I- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY	
CC	INTO CELLS.	
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein.	
CC	-I- ALTERNATIVE PRODUCTS:	
CC	Event=Alternative splicing; Named isoforms=2;	
CC	Name=Beta;	
CC	Isoid=P32507-1; Sequence=Displayed;	
CC	Name=Alpha;	
CC	Isoid=P32507-2; Sequence=VSP_002630, VSP_002631;	
CC	-I- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and	
CC	liver.	
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.	
CC	-I- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announ	
CC	or send an email to license@isb-sib.ch).	
DR	EMBL; M80206; AAA39734.1; -.	
DR	EMBL; D26107; BAA05103.1; -.	
DR	EMBL; BC059941; AAH59941.1; -.	
DR	PIR; A38211; HLMSP3.	
DR	PIR; A53437; A53437.	
DR	MGD; MGI:97822; Pvr12.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003596; Ig_v.	
DR	Pfam; PF00047; ig; 3.	
DR	SMART; SM00406; IGv; 1.	
DR	PROSITE; PS0835; IG LIKE; 3.	
KW	Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;	
KW	Repeat; Alternative splicing.	
FT	SIGNAL 1 31 POTENTIAL.	
FT	CHAIN 32 530 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.	
FT	DOMAIN 32 351 EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM 352 372 POTENTIAL.	
FT	DOMAIN 373 530 CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN 32 147 IG-LIKE V-TYPE.	

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EMBL; X76400; CAA53980.2; ALT_INIT.

EMBL; AF060231; AAC23798.1; -.

EMBL; AY029539; AAK33124.1; -.

EMBL; AF252867; AAG16648.1; -.

EMBL; AF196768; AAG16648.1; JOINED.

EMBL; AF196769; AAG16648.1; JOINED.

EMBL; AF196770; AAG16648.1; JOINED.

EMBL; AF196771; AAG16648.1; JOINED.

EMBL; AF196772; AAG16648.1; JOINED.

EMBL; AF196773; AAG16649.1; JOINED.

EMBL; AF196774; AAG16649.1; -.

EMBL; AF196768; AAG16649.1; JOINED.

EMBL; AF196769; AAG16649.1; JOINED.

EMBL; AF196770; AAG16649.1; JOINED.

EMBL; AF196771; AAG16649.1; JOINED.

EMBL; AF196772; AAG16649.1; JOINED.

EMBL; AF196773; AAG16649.1; JOINED.

Genew; HGNC:9706; PVRL1.

MIM; 600644; -.

MIM; 225000; -.

MIM; 225060; -.

GO; GO:0016021; C:integral to membrane; NAS.

GO; GO:0004895; F:cell adhesion receptor activity; NAS.

GO; GO:0015026; F:coreceptor activity; TAS.

GO; GO:0006955; P:immune response; NAS.

InterPro; IPR007110; Ig-like.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; ig; 2.

SMART; SM00406; IGV; 1.

PROSITE; PS50835; IG_LIKE; 2.

Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;

Repeat; Glycoprotein; Signal; Alternative splicing.

SIGNAL 1 30 POTENTIAL.

CHAIN 31 517 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.

DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).

TRANSMEM 356 376 POTENTIAL.

DOMAIN 377 517 CYTOPLASMIC (POTENTIAL).

DOMAIN 31 141 IG-LIKE V-TYPE.

DOMAIN 149 238 IG-LIKE C2-TYPE 1.

DOMAIN 247 334 IG-LIKE C2-TYPE 2.

DOMAIN 437 444 POLY-GLU.

DOMAIN 445 449 POLY-GLY.

DISULFID 51 124 BY SIMILARITY.

DISULFID 172 226 BY SIMILARITY.

DISULFID 269 316 BY SIMILARITY.

CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).

CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

EFYTPSPPEHGRAGPV -> AFCQLIYPGKGRTRARMF (in isoform Gamma).

/FTid=VSP 002624.

Missing (in isoform Gamma).

/FTid=VSP 002625.

FPYTPSPPEHGRAGPVPTAIGGVAGSILLVLIVVGIVV

ALRRRHTFKGDYSTKHHVYNGYSKAGIPQHPPMAQNLC

-> KRPQRGLGSAARLLAGTVAVFLILVAVLTVFFLYNRQ

QKSPPTDAGTDQPLSQKPEPSRQSSLVPEIDIQVHLD

PGRQQQEEEDLQKLSLQPPYVDLGVSFSPHSVTRTEPRG

ECP (in isoform Alpha).

/FTid=VSP 002626.

Missing (in isoform Alpha).

/FTid=VSP 002627.

SEQUENCE 517 AA; 57158 MW; DF34C8AEC893EE6D CRC64;

VARSPLIC 353 517

VARSPLIC 336 458

Query Match 27.3%; Score 538.5; DB 1; Length 517;

Best Local Similarity 37.8%; Pred. No. 1.1e-34;

Matches 113; Conservative 56; Mismatches 119; Indels 11; Gaps 5;

14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFKNYS 70

44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103

71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTVLVEPTVSLIKGPDSDLIDG--- 127

104 FTDGTIRLSRLEDEGVVCEPATFTPTGNRESQLNLTVMAKPT-NWIEGTQAVLRKKG 162

128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFNETATIIISQYKLFPTRFARGR 185

163 QDDKVLVATCTSANGKPPSVSWETRLKGEAEYQEIRNPNGTIVISRYRLVPSREAHQQ 222

186 RITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKS 245

223 SLACIVNYHM--DRFKESLTINVQYEPEVTIEGFDGNWYLRQMDVKLTCKADANPPATEY 280

246 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPTT 304

281 HWTTLNGSLPKGVEAQNRITLFEKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYT 339

RESULT 3

PVR1_PIG

ID_PVR1_PIG STANDARD; PRT; 515 AA.

AC Q9GL76;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).

GN PVRL1 OR PRR1 OR HVEC.

OS Sus scrofa (Pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

OX NCBI_TaxID=9823;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21176378; PubMed=11277703;

RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J., Cohen G.H.;

RA "Porcine HveC, a member of the highly conserved HveC/nectin 1 family, is a functional alphaherpesvirus receptor.";

RL Virology 281:315-328 (2001).

CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.

CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD) (By similarity).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

CC -----

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CC -----

DR EMBL; AF308632; AAG30281.1; -.

DR HSSP; P06907; LNEU.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;

KW Repeat; Glycoprotein; Signal.

FT SIGNAL 1 30 POTENTIAL.

FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.

FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 356 376 POTENTIAL.

DR EMBL; AF270977; AAF76195.1; -
DR EMBL; AF297665; AAG22808.1; -
DR MGD; MGI:1926483; Pvr1l.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0004872; F:receptor activity; IDA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30
FT CHAIN 31 515
FT DOMAIN 31 354
FT TRANSMEM 355 375
FT DOMAIN 376 515
FT DOMAIN 31 141
FT DOMAIN 145 243
FT DOMAIN 247 334
FT DOMAIN 436 442
FT DOMAIN 443 447
FT DISULFID 51 124
FT DISULFID 172 226
FT DISULFID 269 316
FT CARBOHYD 36 36
FT CARBOHYD 72 72
FT CARBOHYD 139 139
FT CARBOHYD 202 282
FT CARBOHYD 286 286
FT CARBOHYD 297 297
FT CARBOHYD 332 332
FT CONFLICT 138 138
FT CONFLICT 165 165
FT CONFLICT 342 342
FT CONFLICT 428 428
SQ SEQUENCE 515 AA; 57064 MW; FFF608EB5FFB7A0F CRC64;

Query Match 27.9%; Score 550.5; DB 1; Length 515;
Best Local Similarity 38.9%; Pred. No. 1.3e-35;
Matches 117; Conservative 57; Mismatches 116; Indels 11; Gaps 6;

QY 14 GKNVSLKCLIE--VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNVS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTWQKASNGSKQNMAIYNPTMGVSVLPPEYKRVFELRPS 103

QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG--- 127
Db 104 FIDGTIRLSGLELEDEGMVYICEFATPPTGNRESQLNLTVMAKPT-NWIEGTRAVLRARKG 162

QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTRFARGR 185
Db 163 QDNKVLVATCTSANGKPPPSAVSWETRLKGEAEYQEIIRNPNGTVTVISRYRLVPSREARHQ 222

QY 186 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLKCNADANPPPFKS 245
Db 223 SLACIVNY-HLDR-FRESLTINVOYEPVETVIEGFDGNWYLRQTDVKLTCKADANPPATEY 280

QY 246 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTT 305
Db 281 HWTTLNGLPKGVEAQNRTLFFRGPIYSLAGTYICEATNPIGTRSGQVEVNITEFPYTP 340

QY 306 T 306
Db 341 T 341

RESULT 2
PVR1 HUMAN
ID PVR1 HUMAN STANDARD; PRT; 517 AA.
AC Q15223; O75465; Q9HBE6; Q9HBW2;
DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR) (CD111 antigen).
DE (CD111 antigen).
GN PVRL1 OR PRR1 OR HVEC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95237621; PubMed=7721102;
RA Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C., Dubreuil P.;
RA "cDNA characterization and chromosomal localization of a gene related to the poliovirus receptor gene.";
RL Gene 155:261-265(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=98279152; PubMed=9616127;
RA Geraghty R.J., Krumenacher C., Cohen G.H., Eisenberg R.J., Spear P.G.;
RA "Entry of alphaherpesviruses mediated by poliovirus receptor-related protein 1 and poliovirus receptor.";
RL Science 280:1618-1620(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM GAMMA).
RX MEDLINE=21256041; PubMed=11356977;
RA Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J., Campadelli-Fiume G., Dubreuil P.;
RA "Novel, soluble isoform of the herpes simplex virus (HSV) receptor nectin1 (or prr1-HIGR-HVEC) modulates positively and negatively susceptibility to hsv infection.";
RL J. Virol. 75:5684-5691(2001).
RN [4]
RP SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE. MEDLINE=20392396; PubMed=10932188;
RX Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A., Helms J.A., Spritz R.A.;
RA "Mutations of PVRL1, encoding a cell-cell adhesion molecule/herpesvirus receptor, in cleft lip/palate-ectodermal dysplasia.";
RL Nat. Genet. 25:427-430(2000).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and delta). Secreted (isoform gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Name=Delta;
CC IsoId=Q15223-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q15223-2; Sequence=VSP_002626, VSP_002627;
CC Name=Gamma;
CC IsoId=Q15223-3; Sequence=VSP_002624, VSP_002625;
CC -!- DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is responsible for allelic forms known as Margarita island ectodermal dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001); WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
CC -----
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 5.89704 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-15_COPY_58_426

Perfect score: 1976

Sequence: 1 GPIIIEPHVTAVGKNVSLK.....GSSDYKDDDDKGSSHHHHH 369

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	550.5	27.9	515	1	PVR1_MOUSE Q9jkf6 mus musculus
2	538.5	27.3	517	1	PVR1_HUMAN Q15223 homo sapien
3	534.5	27.0	515	1	PVR1_PIG Q9gl76 sus scrofa
4	420	21.3	530	1	PVR2_MOUSE P32507 mus musculus
5	401.5	20.3	538	1	PVR2_HUMAN Q92692 homo sapien
6	396.5	20.1	417	1	PVR_CERAE P32506 cercopithec
7	383.5	19.4	417	1	PVR_HUMAN P15151 homo sapien
8	227.5	11.5	764	1	ICCR_DROME Q08180 drosophila
9	211.5	10.7	837	1	NCM2_MOUSE O35136 mus musculus
10	198	10.0	4391	1	PGBM_HUMAN P98160 homo sapien
11	189	9.6	853	1	NCAL_BOVIN P31836 bos taurus
12	187.5	9.5	278	1	OX2G_HUMAN P41217 homo sapien
13	181.5	9.2	2012	1	DSCA_HUMAN O60469 homo sapien
14	176	8.9	837	1	NCM2_HUMAN O15394 homo sapien
15	175	8.9	588	1	CL66_CHICK P42292 gallus gall
16	174	8.8	858	1	NCAL_RAT P13596 rattus norv
17	173.5	8.8	353	1	CEPU_CHICK Q90773 gallus gall
18	173.5	8.8	761	1	NCAL_HUMAN P13592 homo sapien
19	173.5	8.8	848	1	NCAL_HUMAN P13591 homo sapien
20	171.5	8.7	569	1	TACT_HUMAN P40200 homo sapien
21	171.5	8.7	3707	1	PGBM_MOUSE Q05793 mus musculus
22	170	8.6	847	1	CD22_HUMAN P20273 homo sapien
23	169.5	8.6	1091	1	NCAL_CHICK P13590 gallus gall
24	168.5	8.5	626	1	MAG_MOUSE P20917 mus musculus
25	166.5	8.4	626	1	MAG_HUMAN P20916 homo sapien
26	166.5	8.4	626	1	MAG_RAT P07722 rattus norv
27	165	8.4	725	1	NCAL_MOUSE P13594 mus musculus
28	165	8.4	1115	1	NCAL_MOUSE P13595 mus musculus
29	162.5	8.2	278	1	OX2G_MOUSE O54901 mus musculus
30	162.5	8.2	278	1	OX2G_RAT P04218 rattus norv
31	162	8.2	739	1	VCH1_MOUSE P29533 mus musculus
32	159.5	8.1	509	1	SHS1_RAT P97710 r protein-t
33	158	8.0	702	1	CEA5_HUMAN P06731 homo sapien

34	156	7.9	519	1	ECTO_RAT P16573 rattus norv
35	154.5	7.8	1018	1	CONT_HUMAN Q12860 homo sapien
36	152.5	7.7	1709	1	SN_HUMAN Q9bzz2 homo sapien
37	152	7.7	337	1	OPCM_CHICK Q98892 gallus gall
38	152	7.7	1088	1	NCAL_XENLA P16170 xenopus lae
39	152	7.7	1259	1	CAML_RAT Q05695 rattus norv
40	150.5	7.6	1694	1	SN_MOUSE Q62230 mus musculus
41	150	7.6	1092	1	NCAL_XENLA P36335 xenopus lae
42	148	7.5	344	1	NTRI_MOUSE Q99pj0 mus musculus
43	148	7.5	344	1	NTRI_RAT Q62718 rattus norv
44	147.5	7.5	1256	1	NRCA_MOUSE Q810u4 mus musculus
45	147	7.4	344	1	NTRI_HUMAN Q9p121 homo sapien

ALIGNMENTS

RESULT 1
PVR1_MOUSE ID PVR1_MOUSE STANDARD; PRT; 515 AA.
AC Q9JKF6; Q9ERL5; Q9J117;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).
GN PVRL1 OR PRR1 OR HVEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubreuil P., Campadelli-Fiume G.;
RT "The murine homolog of human nectin1 delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD."
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-lalpha to human nectin-lalpha (HvEC) in sequence and activity as a glycoprotein D receptor for alpha herpesvirus entry."
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF239762; AAF60333.1; -.

Db 194 TAKSVLRLTPKKEHNTNFSQQAQNTA-DRTYRSAKIRVEVKYAPKVKVNMGSLPGGAG 252

QY 221 GNWFEVGRKG-----VNLKCNADANPPPKSVWSRLDGGQWPDGLLASDN 263

Db 253 GS--VGGAGGGSVHMSTGRIVEHSQVRLECRADANPSDVRYRWFIND----EPIIGGQK 306

QY 264 TLHFVHPLTFNYSGVYI-CKVTNSLQORSQDKVIYISDPPT----- 303

Db 307 TEMVIRNVRKFDHAIKVEQVNSVGKSEDSSETLDISYAPSFRRPQSQMEADYGSVVSILT 366

QY 304 ---TTTLQPTIQW--HPS 316

Db 367 CEVDSNPQPEIVWQHPS 384

RESULT 13

T20992

hypothetical protein F15G9.4a - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T20992; T24733

R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20992

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5175 <WIL>

A;Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone F15G9

R;Kershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24733

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5175 <WI2>

A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: CESP:F15G9.4a

A;Map position: X

A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1

Query Match 10.1%; Score 200.5; DB 2; Length 5175;

Best Local Similarity 25.9%; Pred. No. 7.1e-06;

Matches 96; Conservative 48; Mismatches 153; Indels 73; Gaps 21;

QY 2 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGE 59

Db 793 PTIESPHTVRVNIERQVTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG- 847

QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSL 117

Db 848 -----NLLITDAQI-----EDQGQFTCIARN-TYQQSQSSTTLMVTGLVSPVLGH 891

QY 118 IKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLF 177

Db 892 VPPEEQLEIGQDLTLS--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSL 943

QY 178 PTRFARGR---RITCVVKHPALEKDIRYSFIL-----DIQYAPE-----VSVTGYDGNW- 223

Db 944 RLRCGNPKDEGKYTCIAVSPAGNSTLHINVQLIKKPEFVKPEGGIVFKPTISGMDEKHV 1003

QY 224 -----FVGRKGVNLKCNADANPPPKSVWSRLDGQWP-----DGLLASDNTLHFVH 269

Db 1004 AVVNSTHDVLDGEGFAIPCVCVSGTTPPI-ITW-YLDGR-PITPNRDFVTADNTL-IVR 1059

QY 270 PLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKK 329

Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTPMISPQSSSF-----NMVVDLFTIPCD 1114

QY 330 L---PFPLST 336

Db 1115 VYGDPKPVIT 1124

RESULT 14

T43290

hemicentin precursor - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000

C;Accession: T43290; T20993; T24734

R;Vogel, B.E.; Hedgecock, E.M.

submitted to the EMBL Data Library, June 1998

A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ

A;Reference number: Z22396

A;Accession: T43290

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-5198 <VOG>

A;Cross-references: EMBL:AF074901; PIDN:AAC26792.1

R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20993

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5198 <WIL>

A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

A;Experimental source: clone F15G9

R;Kershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24734

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5198 <WI2>

A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: him-4; F15G9.4b

A;Map position: X

A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100

Query Match 10.1%; Score 200.5; DB 2; Length 5198;

Best Local Similarity 25.9%; Pred. No. 7.1e-06;

Matches 96; Conservative 48; Mismatches 153; Indels 73; Gaps 21;

QY 2 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGE 59

Db 793 PTIESPHTVRVNIERQVTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG- 847

QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSL 117

Db 848 -----NLLITDAQI-----EDQGQFTCIARN-TYQQSQSSTTLMVTGLVSPVLGH 891

QY 118 IKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLF 177

Db 892 VPPEEQLEIGQDLTLS--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSL 943

QY 178 PTRFARGR---RITCVVKHPALEKDIRYSFIL-----DIQYAPE-----VSVTGYDGNW- 223

Db 944 RLRCGNPKDEGKYTCIAVSPAGNSTLHINVQLIKKPEFVKPEGGIVFKPTISGMDEKHV 1003

QY 224 -----FVGRKGVNLKCNADANPPPKSVWSRLDGQWP-----DGLLASDNTLHFVH 269

Db 1004 AVVNSTHDVLDGEGFAIPCVCVSGTTPPI-ITW-YLDGR-PITPNRDFVTADNTL-IVR 1059

QY 270 PLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKK 329

Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTPMISPQSSSF-----NMVVDLFTIPCD 1114

Db 326 VGTGRAEQVILVRDTPQASRDVGPLVW 352

RESULT 5

I68093

PRR2 delta - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000

C:Accession: I68093

R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.

Gene 159, 267-272, 1995

A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (pvr), is th

A:Reference number: I53950; MUID:95347610; PMID:7622062

A:Accession: I68093

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-538 <RES>

A:Cross-references: GB:S79172; NID:g1042204; PID:g1042205

C:Genetics:

A:Gene: PRR2delta

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 20.3%; Score 401.5; DB 2; Length 538;

Best Local Similarity 29.2%; Pred. No. 5e-22;

Matches 96; Conservative 57; Mismatches 133; Indels 43; Gaps 9;

QY 5 VEPHTAVWGKVNLSKCLII---EVNETITQISWEKIHGKSS-QTVAVHHPOYGFVSQGEY 60

Db 38 VLPEVRGQLGGTVLPCHELLPPVPGLYISLVTWQRPDAPANHQNVAAEFKMGPSFPSPK 97

QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108

Db 98 PGSERLSFVSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFFATPKGSRVGMTWLR 157

QY 109 VLVEP-----TVSLIKGPDSLIDGNETVAAICIAATGKPVAAHI-----DWEGLGE 155

Db 158 VIAKPKNAEAKQVTFSDP-----TTVALCISKEGRPPARISWLSLSDWEAKETQ 208

QY 156 MESTTTSFPNETATILSIQYKLFPTFRFARRITCVVKHPALEKDIRYSFILDIOYAPEVS 215

Db 209 VSGTLAG---TVVTSRFTLVPSGRADGVTVCKVEHSEFEPPALIPVTLVSRYPPEVS 264

QY 216 VTGYDGNWFVGRKGVNLKCNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNY 275

Db 265 ISGYDDNWYLGRDATALSCDVRNPEPTGYDWTSTSGTFPTSAVAQGSQ-L-VIHAVDSL 323

QY 276 SGVYICKVTNSLQGRSDQKVIYISDPPPT 304

Db 324 NTTFVCTVTNAVGMGRAEQVIFVRETPT 352

RESULT 6

B44194

poliovirus receptor (clone AGM-delta-1) - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: B44194

R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A:Title: A second gene for the African green monkey poliovirus receptor that has no puta

A:Reference number: A44194; MUID:93059651; PMID:1331508

A:Accession: B44194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <KOI>

A:Cross-references: GB:S48817

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 20.1%; Score 396.5; DB 2; Length 392;

Best Local Similarity 31.4%; Pred. No. 7.8e-22;

Matches 99; Conservative 55; Mismatches 140; Indels 21; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKVNLSKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51

Db 27 GDIIVQAPTQVPGFLGDSVTLPCLYQVPGMEETHVSQLTWSR-HGESGSMVAFHQTOGPN 85

QY 52 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 111

Db 86 YSEPKRLEFVAARL--GTELRDASLRMFLGRVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143

QY 112 EP--TVSLIKGPDSLIDGNETVAAICIAATGKPVAAHIDWEGDLGEMESTTTS--FPNET 167

Db 144 KPONTAEVQKVQLT---GKPVVPVAVRCVSTGGRPPAHITWHSIDLGMPTNSQAPGFLSGT 199

QY 168 ATIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227

Db 200 VTVTSLWILVPSSQVDGKSVTCKVEHSEFEKPOLLTVNLTVYVPPEVSISGYDNNWYLSQ 259

QY 228 KGVNLKCNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287

Db 260 NEATLTCDARSNPEPTGYNNWSTTMGPLPPFAVAQGAQL-LIRPVDKPINTTFCINVTNAL 318

QY 288 GQRSDQKVIYISDPP 302

Db 319 GARQAELTVQVKEGP 333

RESULT 7

A44194

poliovirus receptor (clone AGM-alpha-1) - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: A44194

R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A:Title: A second gene for the African green monkey poliovirus receptor that has no puta

A:Reference number: A44194; MUID:93059651; PMID:1331508

A:Accession: A44194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-417 <KOI>

A:Cross-references: GB:S48777

C:Superfamily: poliovirus receptor; immunoglobulin homology

C:Keywords: transmembrane protein

F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 20.1%; Score 396.5; DB 2; Length 417;

Best Local Similarity 31.4%; Pred. No. 8.5e-22;

Matches 99; Conservative 55; Mismatches 140; Indels 21; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKVNLSKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51

Db 27 GDIIVQAPTQVPGFLGDSVTLPCLYQVPGMEETHVSQLTWSR-HGESGSMVAFHQTOGPN 85

QY 52 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 111

Db 86 YSEPKRLEFVAARL--GTELRDASLRMFLGRVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143

QY 112 EP--TVSLIKGPDSLIDGNETVAAICIAATGKPVAAHIDWEGDLGEMESTTTS--FPNET 167

Db 144 KPONTAEVQKVQLT---GKPVVPVAVRCVSTGGRPPAHITWHSIDLGMPTNSQAPGFLSGT 199

QY 168 ATIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227

Db 200 VTVTSLWILVPSSQVDGKSVTCKVEHSEFEKPOLLTVNLTVYVPPEVSISGYDNNWYLSQ 259

QY 228 KGVNLKCNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287

Db 260 NEATLTCDARSNPEPTGYNNWSTTMGPLPPFAVAQGAQL-LIRPVDKPINTTFCINVTNAL 318

QY 288 GQRSDQKVIYISDPP 302

Db 319 GARQAELTVQVKEGP 333

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 9.76395 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-15_COPY_58_426
Perfect score: 1976
Sequence: 1 GPIIIBPHVTAVGKNVSLK.....GSSDYKDDDDKSSHHHHH 369

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1391	70.4	407	2 T08732	hypothetical prote
2	516	26.1	518	2 JC4024	poliovirus recepto
3	420	21.3	530	2 A53437	poliovirus recepto
4	419	21.2	467	1 HLMSP3	poliovirus recepto
5	401.5	20.3	538	2 I68093	PRR2 delta - human
6	396.5	20.1	392	2 B44194	poliovirus recepto
7	396.5	20.1	417	2 A44194	poliovirus recepto
8	396.5	20.1	478	2 I53960	PRR2 alpha - human
9	383.5	19.4	392	1 RWHUPD	poliovirus recepto
10	383.5	19.4	417	1 RWHUPA	poliovirus recepto
11	320	16.2	416	2 A54017	colon carcinoma-as
12	227.5	11.5	764	2 A49448	irregular chiasm C
13	200.5	10.1	5175	2 T20992	hypothetical prote
14	200.5	10.1	5198	2 T43290	hemacentin precurs
15	198	10.0	4391	2 A38096	perlecan precursor
16	189	9.6	853	1 IJBONC	neural cell adhesi
17	187.5	9.5	274	2 A47639	OX-2 membrane glyc
18	181.5	9.2	1896	2 T08851	Down syndrome cell
19	179	9.1	7962	2 I38346	elastic titin - hu
20	175	8.9	588	2 JH0506	adhesion molecule
21	175	8.9	588	2 A45254	surface glycoprote
22	174	8.8	858	1 IJRTNC	neural cell adhesi
23	173.5	8.8	761	1 IJHUNG	neural cell adhesi
24	171.5	8.7	569	2 A46462	T cell activation
25	171.5	8.7	765	2 C42632	cell adhesion mole
26	171.5	8.7	812	2 B42632	cell adhesion mole
27	171.5	8.7	932	2 A42632	cell adhesion mole
28	171.5	8.7	3707	2 S18252	heparan sulfate pr
29	170	8.6	847	2 JH0371	B-cell adhesion pr

30	169.5	8.6	1091	1 IJCHNL	neural cell adhesi
31	168.5	8.5	637	2 B33785	myelin-associated
32	166.5	8.4	582	1 BNRT3S	myelin-associated
33	166.5	8.4	626	1 A61084	myelin-associated
34	166.5	8.4	626	1 BNRT3	myelin-associated
35	165	8.4	725	1 IJMSNG	neural cell adhesi
36	165	8.4	1115	1 IJMSNL	neural cell adhesi
37	163	8.2	587	2 JH0464	DM-GRASP precursor
38	162.5	8.2	278	1 TDRTOX	OX-2 membrane glyc
39	162	8.2	739	2 JN0581	vascular cell adhe
40	158	8.0	702	2 A36319	carcinoembryonic a
41	156	7.9	458	2 S23969	cell-adhesion mole
42	154.5	7.8	1018	2 A54744	contactin 1 precur
43	153.5	7.8	1018	2 JC4211	neural adhesion pr
44	152	7.7	725	2 JE0099	neural cell adhesi
45	152	7.7	1088	1 IJXLNL	neural cell adhesi

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08732
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732
A;Molecule type: mRNA
A;Residues: 1-407 <OTT>
A;Cross-references: EMBL:AL050071
A;Experimental source: fetal kidney; clone DKFZp566B0846
C;Genetics:
A;Note: DKFZp566B0846.1

Query Match 70.4%; Score 1391; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 2.2e-95;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	86	SGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDLSLIDGGNETVAAICIAATGKPVA	145
Db	1	SGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDLSLIDGGNETVAAICIAATGKPVA	60
Qy	146	HIDWEGDLGEMESTTSPNETATIISQYKLFPTTFARRRITCVVKKHPALEKDIRYSFI	205
Db	61	HIDWEGDLGEMESTTSPNETATIISQYKLFPTTFARRRITCVVKKHPALEKDIRYSFI	120
Qy	206	LDIQAYEVSVTGYDGNWVFVGRKGNLKNADANPPFPKSVWSRLDGQWPDGLASDNTL	265
Db	121	LDIQAYEVSVTGYDGNWVFVGRKGNLKNADANPPFPKSVWSRLDGQWPDGLASDNTL	180
Qy	266	HFVHPLTFNYSGVYICKVTNSLQQRSDQKVIVISDPPTTTTLQPTIQWHPSTADIEDLAT	325
Db	181	HFVHPLTFNYSGVYICKVTNSLQQRSDQKVIVISDPPTTTTLQPTIQWHPSTADIEDLAT	240
Qy	326	EPKKLPFPLSTLATIKDDTIAT	347
Db	241	EPKKLPFPLSTLATIKDDTIAT	262

RESULT 2
JC4024
poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubi
Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene
A;Reference number: JC4024; MUID:95237621; PMID:7721102

; SEQ ID NO 8
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: humanized maell, version 1 heavy chain
US-08-466-163B-8

Query Match 43.9%; Score 1268; DB 4; Length 453;
Best Local Similarity 50.8%; Pred. No. 7.8e-105;
Matches 286; Conservative 38; Mismatches 91; Indels 148; Gaps 17;

QY	4	IVEPHVTAVWGKVN	SLKCLIEVNETITQISWEKIH	---	GKSSQT	VAV	----	HHPQYGF	SV	56
		:	:	:	:	:	:	:	:	
Db	11	LVQP	-----	GGSLRLSCAV	SGYSIT	SGYSWN	IRQAPG	KGLEW	VASITYD	GS
		:	:	:	:	:	:	:	:	
QY	57	QGEYQGRVLF	KNYSLNDA	TITLHNIG	FSDSG	KYTICK	AVTFPL	GN	NAQ	----
		:	:	:	:	:	:	:	:	
Db	65	KGRF	---	TISRDDS	KNTFY	LQMN	SLRAED	TAVY	CARGSH	YFGHWH
		:	:	:	:	:	:	:	:	
QY	112	EPTVSLIK	GPDSLID	GGNETV	AAICIA	ATGKPV	AHIDW	EGDL	GEMES	TTTSFP
		:	:	:	:	:	:	:	:	
Db	122	ASTKG	--	KGPSV	F	-----	PLA	-----	PSSK	STSGGTAA
		:	:	:	:	:	:	:	:	
QY	172	SQYKLF	PTRFAR	RRITCV	VVKHP	ALEK	DIRYS	FILDI	QYAP	E
		:	:	:	:	:	:	:	:	
Db	148	-----	LGCLVK	-----	-----	DYF	PEP	TVS	-----	163
		:	:	:	:	:	:	:	:	
QY	231	NLKC	NADAN	PPPKSV	WSRLD	GQWPD	GLLAS	DN	TLHF	VH
		:	:	:	:	:	:	:	:	
Db	164	-----	-----	WNSG	ALTSG	-----	VHTF	PAVL	QSSGL	YLS
		:	:	:	:	:	:	:	:	
QY	284	TNSL	QORS	DQKVI	YISDV	PFK	QTSS	-----	RS	CDK
		:	:	:	:	:	:	:	:	
Db	196	SSSL	GTQT	-----	YICNV	NH	KPSN	TKVD	KKVE	PKSCDK
		:	:	:	:	:	:	:	:	
QY	336	PKPK	DTL	MI	SRTPE	TCV	VVDV	SHED	PEV	KEN
		:	:	:	:	:	:	:	:	
Db	251	PKPK	DTL	MI	SRTPE	TCV	VVDV	SHED	PEV	KEN
		:	:	:	:	:	:	:	:	
QY	396	VL	TVL	HQD	WLNG	KEYK	CKVSN	KAL	PAP	IEKT
		:	:	:	:	:	:	:	:	
Db	311	VL	TVL	HQD	WLNG	KEYK	CKVSN	KAL	PAP	IEKT
		:	:	:	:	:	:	:	:	
QY	456	LT	CL	V	K	G	F	Y	P	S
		:	:	:	:	:	:	:	:	
Db	371	LT	CL	V	K	G	F	Y	P	S
		:	:	:	:	:	:	:	:	
QY	516	CSV	M	H	E	A	L	H	N	H
		:	:	:	:	:	:	:	:	
Db	431	CSV	M	H	E	A	L	H	N	H
		:	:	:	:	:	:	:	:	

Search completed: April 12, 2004, 09:49:26
Job time : 19.7595 secs

Db 130 PLAPSSKSTSGGTAALGCLVK-----DYPPEPVTVS----- 160
QY 231 NLKCNADANPPPFKSVWSRLDQWPDGLLASDNTLHFVH--PLTFNYSGVY-----ICKV 283
Db 161 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSVVTVP 192
QY 284 TNSLGQRSDQKVIYISDVPFKQTSS-----RSCDKTHTCPPCPAPEAEGAPSVFLFP 335
Db 193 SSSLGTQT-----YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFP 247
QY 336 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 395
Db 248 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 307
QY 396 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTTLPSSREEMTKNQVS 455
Db 308 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTTLPSSREEMTKNQVS 367
QY 456 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 515
Db 368 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 427
QY 516 CSVMHEALHNHYTQKSLSLSPG 537
Db 428 CSVMHEALHNHYTQKSLSLSPG 449

RESULT 14

US-08-466-151-8
; Sequence 8, Application US/08466151
; Patent No. 6037453
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,151
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466163
; FILING DATE: 06-Jun-1995
; APPLICATION NUMBER: 08/405617
; FILING DATE: 15-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/185899
; FILING DATE: 26-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/879495
; FILING DATE: 07-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/744768
; FILING DATE: 14-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Svoboda, Craig G.
; REGISTRATION NUMBER: 39,044
; REFERENCE/DOCKET NUMBER: P0718P2C1D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1489

; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 453 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-466-151-8

Query Match 43.9%; Score 1268; DB 3; Length 453;
Best Local Similarity 50.8%; Pred. No. 7.8e-105;
Matches 286; Conservative 38; Mismatches 91; Indels 148; Gaps 17;

QY 4 IVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIH---GKSSQTVAV---HHPPQYGFVS 56
Db 11 LVQP-----GGSRLSCAVSGYSITSGYSWNWIRQAPGKGLEWVASITYDGSTNYADSV 64
QY 57 QGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQ-----SSTTVTVLV 111
Db 65 KGRF---TISRDDSKNTFYQLMNSLRAEDTAVYYCARGSHYFGHWFAVWGQGTLVTVSS 121
QY 112 EPTVSLIKGPDLSLIDGGNETVAAICIAATCKPVAHIDWEGDLGEMESTTSPFNETATII 171
Db 122 ASTKG--KGFVSF-----PLA-----PSSKSTSGGTAA-- 147
QY 172 SQYKLFPTREARRRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFGVGRKGV 230
Db 148 -----LGCLVK-----DYFPEPVTVS----- 163
QY 231 NLKCNADANPPPFKSVWSRLDQWPDGLLASDNTLHFVH--PLTFNYSGVY-----ICKV 283
Db 164 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSVVTVP 195
QY 284 TNSLGQRSDQKVIYISDVPFKQTSS-----RSCDKTHTCPPCPAPEAEGAPSVFLFP 335
Db 196 SSSLGTQT-----YICNVNHKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGPSVFLFP 250
QY 336 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 395
Db 251 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 310
QY 396 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTTLPSSREEMTKNQVS 455
Db 311 VLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTTLPSSREEMTKNQVS 370
QY 456 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 515
Db 371 LTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 430
QY 516 CSVMHEALHNHYTQKSLSLSPG 538
Db 431 CSVMHEALHNHYTQKSLSLSPG 453

RESULT 15

US-08-466-163B-8
; Sequence 8, Application US/08466163B
; Patent No. 6329509
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Immunoglobulin Variants
; FILE REFERENCE: P0718P2C1D1
; CURRENT APPLICATION NUMBER: US/08/466,163B
; CURRENT FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: US 08/405,617
; PRIOR FILING DATE: 1995-03-15
; PRIOR APPLICATION NUMBER: US 08/185,899
; PRIOR FILING DATE: 1994-01-26
; PRIOR APPLICATION NUMBER: US 07/879,495
; PRIOR FILING DATE: 1992-05-07
; PRIOR APPLICATION NUMBER: US 07/744,768
; PRIOR FILING DATE: 1991-08-14
; NUMBER OF SEQ ID NOS: 64

Db 65 KGRF---TISADTSKNTAYLQMNSLRAEDTAVYYCSRW----- 99

QY 117 LIKGPDSLIDGGNETVAAICIAATGKPVAHIDW--EGDLGEMESTTTSPFNETATIIISQY 174

Db 100 -----GGDGFYA-----MDYWGQGTLLTVSSASTKGP-----SVF 129

QY 175 KLFPTRFARG---RRITCVVKHPALEKDIRYSFILDIQYAPE-VSVTGYDGNWFVGRKGV 230

Db 130 PLAPSSKSTSGGTAALGCLVK-----DYFPEPVTVS----- 160

QY 231 NLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH--PLTFNYSGVY-----ICKV 283

Db 161 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSVVTVP 192

QY 284 TNSLGQRSDQKVIYISDVPFKQTSS-----RSCDKTHTCPPCPAPEAEGAPSVFLFP 335

Db 193 SSSLGTQT-----YICNVNHNKPSNTKVDDKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP 247

QY 336 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 395

Db 248 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 307

QY 396 VLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS 455

Db 308 VLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS 367

QY 456 LTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPPVLDSGDSGFFLYSKLTVDKSRWQQGNVFS 515

Db 368 LTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPPVLDSGDSGFFLYSKLTVDKSRWQQGNVFS 427

QY 516 CSVMEALHNHYTQKSLSLSPG 537

Db 428 CSVMEALHNHYTQKSLSLSPG 449

RESULT 12

US-09-680-148-2

; Sequence 2, Application US/09680148

; Patent No. 6417335

; GENERAL INFORMATION:

; APPLICANT: BASEY, CAROL D.

; APPLICANT: BLANK, GREG S.

; TITLE OF INVENTION: PROTEIN PURIFICATION

; FILE REFERENCE: P1241RJD1

; CURRENT APPLICATION NUMBER: US/09/680,148

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: US 60/084,459

; PRIOR FILING DATE: 1998-05-06

; PRIOR APPLICATION NUMBER: US 09/304,465

; PRIOR FILING DATE: 1999-05-03

; NUMBER OF SEQ ID NOS: 2

; SEQ ID NO 2

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized.

; Patent No. 6417335

US-09-680-148-2

Query Match 44.0%; Score 1270.5; DB 4; Length 449;

Best Local Similarity 50.9%; Pred. No. 4.6e-105;

Matches 286; Conservative 42; Mismatches 83; Indels 151; Gaps 18;

QY 4 IVEPHVTAVWGKNVSLKCLIE-VNETITQISW-EKIHGKSSQTAVVHHPOYGF-----SV 56

Db 11 LVQP-----GSLRLSCAASGFNIKDTYIHWVRQAPGKLEWVARIYPTNGYTRYADSV 64

QY 57 QGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVS 116

Db 65 KGRF---TISADTSKNTAYLQMNSLRAEDTAVYYCSRW----- 99

QY 117 LIKGPDSLIDGGNETVAAICIAATGKPVAHIDW--EGDLGEMESTTTSPFNETATIIISQY 174

Db 100 -----GGDGFYA-----MDYWGQGTLLTVSSASTKGP-----SVF 129

QY 175 KLFPTRFARG---RRITCVVKHPALEKDIRYSFILDIQYAPE-VSVTGYDGNWFVGRKGV 230

Db 130 PLAPSSKSTSGGTAALGCLVK-----DYFPEPVTVS----- 160

QY 231 NLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVH--PLTFNYSGVY-----ICKV 283

Db 161 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSVVTVP 192

QY 284 TNSLGQRSDQKVIYISDVPFKQTSS-----RSCDKTHTCPPCPAPEAEGAPSVFLFP 335

Db 193 SSSLGTQT-----YICNVNHNKPSNTKVDDKVEPKSCDKTHTCPPCPAPELLGGPSVFLFP 247

QY 336 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 395

Db 248 PKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVS 307

QY 396 VLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS 455

Db 308 VLTVLHQDLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVS 367

QY 456 LTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPPVLDSGDSGFFLYSKLTVDKSRWQQGNVFS 515

Db 368 LTCLVKGFPYPSDIAVEWESNGQPENNYKTTPPPVLDSGDSGFFLYSKLTVDKSRWQQGNVFS 427

QY 516 CSVMEALHNHYTQKSLSLSPG 537

Db 428 CSVMEALHNHYTQKSLSLSPG 449

RESULT 13

US-09-304-465A-2

; Sequence 2, Application US/09304465A

; Patent No. 6489447

; GENERAL INFORMATION:

; APPLICANT: BASEY, CAROL D.

; APPLICANT: BLANK, GREG S.

; TITLE OF INVENTION: PROTEIN PURIFICATION

; FILE REFERENCE: P1241R1

; CURRENT APPLICATION NUMBER: US/09/304,465A

; PRIOR FILING DATE: 1999-05-03

; PRIOR APPLICATION NUMBER: US 60/084,459

; PRIOR FILING DATE: 1998-05-06

; NUMBER OF SEQ ID NOS: 2

; SEQ ID NO 2

; LENGTH: 449

; TYPE: PRT

; ORGANISM: Artificial sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized.

; Patent No. 6489447

US-09-304-465A-2

Query Match 44.0%; Score 1270.5; DB 4; Length 449;

Best Local Similarity 50.9%; Pred. No. 4.6e-105;

Matches 286; Conservative 42; Mismatches 83; Indels 151; Gaps 18;

QY 4 IVEPHVTAVWGKNVSLKCLIE-VNETITQISW-EKIHGKSSQTAVVHHPOYGF-----SV 56

Db 11 LVQP-----GSLRLSCAASGFNIKDTYIHWVRQAPGKLEWVARIYPTNGYTRYADSV 64

QY 57 QGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVS 116

Db 65 KGRF---TISADTSKNTAYLQMNSLRAEDTAVYYCSRW----- 99

QY 117 LIKGPDSLIDGGNETVAAICIAATGKPVAHIDW--EGDLGEMESTTTSPFNETATIIISQY 174

Db 100 -----GGDGFYA-----MDYWGQGTLLTVSSASTKGP-----SVF 129

QY 175 KLFPTRFARG---RRITCVVKHPALEKDIRYSFILDIQYAPE-VSVTGYDGNWFVGRKGV 230

CLASSIFICATION: 44.6%; Score 1287.5; DB 5; Length 454;
Best Local Similarity 51.7%; Pred. No. 1.4e-106;
Matches 294; Conservative 35; Mismatches 87; Indels 153; Gaps 19;
PCT-US93-07832-22
1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQ--ISWEK-IHGKSSQTAVVHHPOYGFVSQ 57
8 GPFLVKP-----GASVKISCKTS-GYTFTEYTHMMKQSHGKSLIEWIGFNPKNKGSSH 60
58 GE--YQGRVLFKNYSLNDATITLHNIGFSDSGKYIC-----KAVTFPLGNAQSST 105
61 NQRFMDKATLAVDKSTSTAYMELRSLTSEDSDGIYYCARWGLNYGDFVRYDFVWGA--GT 118
106 TVTVLVEPTVSLIKGPDSLIDGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPFN 165
119 TVTVSSAST---KGPSVF-----PLA-----PSSKSTSG 144
166 ETATILSQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWF 224
145 GTAA-----LGCLVK-----DYFPEPVTVS-----164
225 VGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGGLASDNTLHFVH--PLTFNYSGVY--- 279
165 -----WNSGALTSG-----VHTFPAVLQSSGLYSL 190
280 --ICKVTNSLQGRSDQKVIYISDVPFKQTSS-----RSCDKTHTCPPCPAPEAEGAP 329
191 SVTVPSSSLGTQT-----YICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPPELLGGP 245
330 SVFLFPPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNS 389
246 SVFLFPPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNS 305
390 TYRVSVLTVLHODWLNKGKVKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRHEM 449
306 TYRVSVLTVLHODWLNKGKVKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRHEM 365
450 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQ 509
366 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQ 425
510 QGNVFSCSVMEALHNHYTQKSLSLSPGK 538
426 QGNVFSCSVMEALHNHYTQKSLSLSPGK 454

Query Match 44.6%; Score 1287.5; DB 5; Length 454;
Best Local Similarity 51.7%; Pred. No. 1.4e-106;
Matches 294; Conservative 35; Mismatches 87; Indels 153; Gaps 19;
PCT-US93-07832-22
1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQ--ISWEK-IHGKSSQTAVVHHPOYGFVSQ 57
8 GPFLVKP-----GASVKISCKTS-GYTFTEYTHMMKQSHGKSLIEWIGFNPKNKGSSH 60
58 GE--YQGRVLFKNYSLNDATITLHNIGFSDSGKYIC-----KAVTFPLGNAQSST 105
61 NQRFMDKATLAVDKSTSTAYMELRSLTSEDSDGIYYCARWGLNYGDFVRYDFVWGA--GT 118
106 TVTVLVEPTVSLIKGPDSLIDGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPFN 165
119 TVTVSSAST---KGPSVF-----PLA-----PSSKSTSG 144
166 ETATILSQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWF 224
145 GTAA-----LGCLVK-----DYFPEPVTVS-----164
225 VGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGGLASDNTLHFVH--PLTFNYSGVY--- 279
165 -----WNSGALTSG-----VHTFPAVLQSSGLYSL 190
280 --ICKVTNSLQGRSDQKVIYISDVPFKQTSS-----RSCDKTHTCPPCPAPEAEGAP 329
191 SVTVPSSSLGTQT-----YICNVNHKPSNTKVDKKEPKSCDKTHTCPPCPAPPELLGGP 245
330 SVFLFPPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNS 389
246 SVFLFPPKPKDMLISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQVNS 305
390 TYRVSVLTVLHODWLNKGKVKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRHEM 449
306 TYRVSVLTVLHODWLNKGKVKCVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRHEM 365
450 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQ 509
366 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDSDGSGFFLYSKLTVDKSRWQ 425
510 QGNVFSCSVMEALHNHYTQKSLSLSPGK 538
426 QGNVFSCSVMEALHNHYTQKSLSLSPGK 454

RESULT 9
US-09-049-672A-8
; Sequence 8, Application US/09049672A

Patent No. 6135941
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Lal, Preeti
APPLICANT: Tang, Y. Tom
APPLICANT: Yue, Henry
APPLICANT: Au-Young, Janice
APPLICANT: Corley, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah R.
TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/049,672A
FILING DATE: HEREWITH
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Cerrone, Michael C
REGISTRATION NUMBER: 39,132
REFERENCE/DOCKET NUMBER: PF-0497 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGTUT11
CLONE: 2747531
US-09-049-672A-8

Query Match 44.2%; Score 1275.5; DB 3; Length 467;
Best Local Similarity 51.7%; Pred. No. 1.7e-105;
Matches 283; Conservative 44; Mismatches 85; Indels 135; Gaps 17;
Qy 14 GKNVSLKCLIEVNETITQIS--W-EKIHGKSSQTAVVHHPOYGFVSQGE-YQGRV-LFKN 68
Db 34 GASVQVSVTS-GFTLSDLSVHVVRQAPGQGLEWMGGLAPENGEAVYAQKFLGRLTSED 92
Qy 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLID-G 127
Db 93 TSADTAYMFLNLSGSDSAIYYCARQHY-----DFFDFW 127
Qy 128 GNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTRFARGRI 187
Db 128 GQGTMTVTVSSASTKGP-----SVFPLAPSSKSTSGTAA-----L 162
Qy 188 TCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFVGRKGVNLKCNADANPPPFKSV 246
Db 163 GCLVK-----DYFPEPVTVS-----177
Qy 247 WSRLDGQWPDGGLASDNTLHFVH--PLTFNYSGVY-----ICKVTNSLQGRSDQKVIYIS 299
Db 178 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSVTVVPSSSLGTQT-----YIC 220

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QY 106 TVTVLVEPTVSLIKGPDSDLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFN 165
Db 119 TVTVSSAST-----KGPSVF-----PLA-----PSSKSTSG 144
QY 166 ETATIISQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWF 224
Db 145 GTAA-----LGCLVK-----DYFPEPTVS----- 164
QY 225 VGRKGVNLKCNADANPPFKSVWSRLDGQWPDGLLASDNTLHFVH--PLTFNYSGVY--- 279
Db 165 -----WNSGALTSG-----VHTFPAVLQSSGLYSLS 190
QY 280 --ICKVTNSLQQRSDQKVIYISDVPPFKQTSS-----RSCDKTHTCPPCPAPEAEGAP 329
Db 191 SVTVPSSSLGTQT-----YICNVNHNKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGP 245
QY 330 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 389
Db 246 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 305
QY 390 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEM 449
Db 306 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEM 365
QY 450 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 509
Db 366 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 425
QY 510 QGNVFSCVMHEALHNHYTQKSLSLSPGK 538
Db 426 QGNVFSCVMHEALHNHYTQKSLSLSPGK 454
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RESULT 7

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US-09-705-686-22
; Sequence 22, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; City: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,686
; FILING DATE: 02-No. 6639055-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709PID3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-705-686-22
Query Match 44.6%; Score 1287.5; DB 4; Length 454;
Best Local Similarity 51.7%; Pred. No. 1.4e-106;
Matches 294; Conservative 35; Mismatches 87; Indels 153; Gaps 19;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQ--ISWEK-IHGKSSQTAVVHHPQYGFVSQ 57
Db 8 GPFLVKP-----GASVKISCKTS-GYTFTEYTMHWMKQSHGKSLEWIGFNPKNKGSSH 60
QY 58 GE--YQGRVLFKNYSLNDATITLHNIGFSDSGKYIC-----KAVTFPLGNAQSST 105
Db 61 NQREMDKATLAVDKSTSTAYMBELSLTSEDSGIYYCARWGLNYGFDVRYFDVWGA--GT 118
QY 106 TVTVLVEPTVSLIKGPDSDLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFN 165
Db 119 TVTVSSAST-----KGPSVF-----PLA-----PSSKSTSG 144
QY 166 ETATIISQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWF 224
Db 145 GTAA-----LGCLVK-----DYFPEPTVS----- 164
QY 225 VGRKGVNLKCNADANPPFKSVWSRLDGQWPDGLLASDNTLHFVH--PLTFNYSGVY--- 279
Db 165 -----WNSGALTSG-----VHTFPAVLQSSGLYSLS 190
QY 280 --ICKVTNSLQQRSDQKVIYISDVPPFKQTSS-----RSCDKTHTCPPCPAPEAEGAP 329
Db 191 SVTVPSSSLGTQT-----YICNVNHNKPSNTKVDKKEPKSCDKTHTCPPCPAPELLGGP 245
QY 330 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 389
Db 246 SVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 305
QY 390 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEM 449
Db 306 TYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEM 365
QY 450 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 509
Db 366 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQ 425
QY 510 QGNVFSCVMHEALHNHYTQKSLSLSPGK 538
Db 426 QGNVFSCVMHEALHNHYTQKSLSLSPGK 454
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RESULT 8

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PCT-US93-07832-22
; Sequence 22, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; City: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
```


Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-22

Query Match 44.6%; Score 1287.5; DB 3; Length 454;
Best Local Similarity 51.7%; Pred. No. 1.4e-106;
Matches 294; Conservative 35; Mismatches 87; Indels 153; Gaps 19;
QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQ--ISWEK-IHGKSSQTVAVHHPQYGFVSQ 57
Db 8 GPELVKP-----GASVKISCKTS-GYTFEYTMHMKQSHGKSLEWIGFNPKNKGSSH 60
QY 58 GE--YQGRVLFKKNYSLNDATITLHNIGFSDSGKYIC-----KAVTFPLGNAQSST 105
Db 61 NQRFMDKATLAVDKSTSTAYMELRSLTSEDSGIYYCARWRGLNYGFDVYFDVWGA--GT 118
QY 106 TVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPN 165
Db 119 TVTVSSAST-----KGPSVF-----PLA-----PSSKSTSG 144
QY 166 ETATIISQYKLPPTFRFARGRRITCVVKBPALEKDIRYSFILDIQYAPE-VSVTGYDGNWF 224
Db 145 GTAA-----LGCLVK-----DYFEPVTVS----- 164
QY 225 VGRKGVLKCNADANPPPFKSVWSRLDQGWPDGLLASDNTLHFVH--PLTFNYSGVY--- 279
Db 165 -----WNSGALTSG-----VHTFPAVLQSSGLYSLS 190
QY 280 --ICKVTNSLQGRSDQKVIYISDVFPKQTSS-----RSCDKTHTCPPCPAPEAGAP 329

Db 191 SVVTVPSSSLGTQ-----YICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPPELLGGP 245
QY 330 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 389
Db 246 SVFLFPPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNS 305
QY 390 TYRVVSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM 449
Db 306 TYRVVSVLTIVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEM 365
QY 450 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQ 509
Db 366 TKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRWQ 425
QY 510 QGNVFSCSVMEHALHNHYTQKSLSLSPGK 538
Db 426 QGNVFSCSVMEHALHNHYTQKSLSLSPGK 454
RESULT 6
US-08-146-206C-22
; Sequence 22, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 454 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-22

Query Match 44.6%; Score 1287.5; DB 4; Length 454;
Best Local Similarity 51.7%; Pred. No. 1.4e-106;
Matches 294; Conservative 35; Mismatches 87; Indels 153; Gaps 19;
QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQ--ISWEK-IHGKSSQTVAVHHPQYGFVSQ 57
Db 8 GPELVKP-----GASVKISCKTS-GYTFEYTMHMKQSHGKSLEWIGFNPKNKGSSH 60
QY 58 GE--YQGRVLFKKNYSLNDATITLHNIGFSDSGKYIC-----KAVTFPLGNAQSST 105
Db 61 NQRFMDKATLAVDKSTSTAYMELRSLTSEDSGIYYCARWRGLNYGFDVYFDVWGA--GT 118


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; NAME/KEY: tICAM(185)/IgG fusion protein
; OTHER INFORMATION: amino acid residues 1-453 =
; OTHER INFORMATION: tICAM(453); amino acid residues 454-680 = amino
; OTHER INFORMATION: acid residues 216-442 of human IGG1 heavy chain
US-08-227-496C-15

Query Match      45.1%; Score 1300.5; DB 3; Length 680;
Best Local Similarity 48.6%; Pred. No. 1.8e-107;
Matches 302; Conservative 48; Mismatches 133; Indels 139; Gaps 21;

QY 14 GKNVSLKCLIE-----VNETITQISWEK-----IHGKSSQ---TVAVHHPOYG--FSVQ 57
Db 101 GKNLTLCQVEGGAPRANLTVVLLRGEKELKREPAVGEPAEVTITVLVRRDHGANFSCR 160
QY 58 GEY----QGRVLFKN-----YSLN-----
Db 161 TELDLRPQGLELFENTSAPIQLQTFVLPAFPPLQVSPRVLEVDQTGTVVCSLDGLFPVSE 220
QY 73 -----DATITLHNIGFS-----DSG--KYICKAVTFPLGNAQSST--T 106
Db 221 AQVHLALGDQRLNPTVIYGNDSFSAKASVSVTAEDEGTQRLTCAVI---LGNQSQETLQT 277
QY 107 VTVLVEPTVSLIKGPDLSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNE 166
Db 278 VTIYSFPAPNVILTKPEVSEGTETV-----KCEAH-----PRAKVTLNGVPAQ 321
QY 167 TATIISQYKLFPTFRFARGRRITCVVK-----HPALEKDIRYSFILDIOYAPEVSVTG 218
Db 322 PLGPRAQLLLKATPEDNGRFSFCSATLEVAGQLIHKNQTRCLR-----VLYGPRLDERD 375
QY 219 YDGNW-FVGRKGVNLKCNADANP-PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYS 276
Db 376 CPGNWTWPENSQQTPMCQAWGNPLPELKCL---KDGTFP--LPIGESV-----TVTRDLE 425
QY 277 GVIYICKVTNSLQORSQDKVIYISDVPPFKQTSSRSCDKTHTCPPCPAPEAEGAPSVFLPPP 336
Db 426 GTYLCRARSTQGEVTRKVTNV-----LSPRYEDKTHTCPPCPAPELLGGPSVFLPPP 478
QY 337 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV 396
Db 479 KPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSV 538
QY 397 LTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEMTKNQVSL 456
Db 539 LTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREELTKNQVSL 598
QY 457 TCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 516
Db 599 TCLVKGFPYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 658
QY 517 SVMHEALHNHYTQKSLSLSPGK 538
Db 659 SVMHEALHNHYTQKSLSLSPGK 680
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RESULT 2
US-09-301-593-18
; Sequence 18, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
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; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 453
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-18

Query Match      44.8%; Score 1292.5; DB 4; Length 453;
Best Local Similarity 51.9%; Pred. No. 5e-107;
Matches 294; Conservative 38; Mismatches 86; Indels 149; Gaps 20;

QY 1 GPIIVEPHVTAVMGKNVSLKCLIEVNETITQ--ISW-EKIHGKSSQTVAVHHPOYGF-SV 56
Db 7 GPELVKP-----GASVKMSCKTS-RYTFEYTIHWVRQSHGKSLEWIGGINPNNGIPNY 59
QY 57 QGEYQGR-VLFKNYSLNDATITLHNIGFSDSGKYICK---AVTFPLGNAQ-----SSTTV 107
Db 60 NQKFKGRAATLVGKSSSTAYMELRSLTSEDSAVVFCARRRIAYGYDEGHAMDYWGQTSV 119
QY 108 TVLVEPTVSLIKGPDLSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNET 167
Db 120 TVSSAST---KGPSVF-----PLA-----PSSKSTSGGT 145
QY 168 ATIISQYKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFG 226
Db 146 AA-----LGCLVK-----DYFPEPTVS----- 163
QY 227 RKGVNLCNADANPPFPKSVWSRLDQWPDGLLASDNTLHFVH--PLTFNYSGVY----- 279
Db 164 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSV 191
QY 280 ICKVTNSLQORSQDKVIYISDVPPFKQTSS-----RSCDKTHTCPPCPAPEAEGAPSV 331
Db 192 VTPSSSLGTQT-----YICNVNHPKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSV 246
QY 332 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 391
Db 247 FLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY 306
QY 392 RVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEMTK 451
Db 307 RVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPSREEMTK 366
QY 452 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 511
Db 367 NOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQG 426
QY 512 NVFSCSVMEALHNHYTQKSLSLSPGK 538
Db 427 NVFSCSVMEALHNHYTQKSLSLSPGK 453
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RESULT 3
US-09-301-593-30
; Sequence 30, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 17.7595 Seconds
(without alignments)
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Title: US-09-972-268-14_COPY_58_595
Perfect score: 2886
Sequence: 1 GPIIIVPHVTAVGKNVSLK.....MHEALHNHYTKLSLSPGK 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1300.5	45.1	680	3	US-08-227-496C-15
2	1292.5	44.8	453	4	US-09-301-593-18
3	1292	44.8	472	4	US-09-301-593-30
4	1287.5	44.6	454	2	US-07-934-373C-22
5	1287.5	44.6	454	3	US-08-437-642B-22
6	1287.5	44.6	454	4	US-08-146-206C-22
7	1287.5	44.6	454	4	US-09-705-686-22
8	1287.5	44.6	454	5	PCT-US93-07832-22
9	1275.5	44.2	467	3	US-09-049-672A-8
10	1274.5	44.2	459	1	US-08-157-101A-7
11	1270.5	44.0	449	4	US-09-679-397-2
12	1270.5	44.0	449	4	US-09-680-148-2
13	1270.5	44.0	449	4	US-09-304-465A-2
14	1268	43.9	453	3	US-08-466-151-8
15	1268	43.9	453	4	US-08-466-163B-8
16	1268	43.9	453	4	US-08-802-096-8
17	1267.5	43.9	476	3	US-08-487-550-4
18	1267.5	43.9	476	4	US-09-526-098-4
19	1266.5	43.9	473	3	US-09-049-672A-4
20	1266	43.9	451	2	US-08-887-352B-18
21	1266	43.9	451	3	US-09-109-207C-18
22	1266	43.9	451	3	US-09-282-505-2
23	1266	43.9	451	3	US-09-054-255-2
24	1266	43.9	451	3	US-09-296-005-18
25	1266	43.9	451	4	US-09-282-846-2
26	1266	43.9	451	4	US-09-680-145-2
27	1266	43.9	451	4	US-09-920-171-18

28	1265.5	43.8	452	3	US-09-027-449-71	Sequence 71, Appl
29	1265.5	43.8	452	3	US-09-026-985-71	Sequence 71, Appl
30	1265.5	43.8	452	4	US-09-121-952A-71	Sequence 71, Appl
31	1265.5	43.8	452	4	US-09-234-340A-71	Sequence 71, Appl
32	1264	43.8	451	2	US-08-887-352B-14	Sequence 14, Appl
33	1264	43.8	451	2	US-08-887-352B-16	Sequence 16, Appl
34	1264	43.8	451	3	US-08-466-151-65	Sequence 65, Appl
35	1264	43.8	451	3	US-09-109-207C-14	Sequence 14, Appl
36	1264	43.8	451	3	US-09-109-207C-16	Sequence 16, Appl
37	1264	43.8	451	3	US-09-296-005-14	Sequence 14, Appl
38	1264	43.8	451	3	US-09-296-005-16	Sequence 16, Appl
39	1264	43.8	451	4	US-09-920-171-14	Sequence 14, Appl
40	1264	43.8	451	4	US-09-920-171-16	Sequence 16, Appl
41	1263	43.8	488	4	US-09-499-846-12	Sequence 12, Appl
42	1262.5	43.7	704	4	US-09-590-656-2	Sequence 2, Appli
43	1262.5	43.7	704	4	US-09-733-764-2	Sequence 2, Appli
44	1260.5	43.7	446	3	US-08-397-411-7	Sequence 7, Appli
45	1259	43.6	476	2	US-08-378-939-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-08-227-496C-15
; Sequence 15, Application US/08227496C
; Patent No. 6130202
; GENERAL INFORMATION:
; APPLICANT: Greve, Jeffrey M.
; APPLICANT: McClelland, Alan
; TITLE OF INVENTION: Multimeric Forms of Human
; TITLE OF INVENTION: Rhinovirus Receptor Protein
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 400 Morgan Lane
; CITY: West Haven
; STATE: Connecticut
; COUNTRY: USA
; ZIP: 06516
; COMPUTER READABLE FORM:
; MEDIUM TYPE: diskette, 1.44 Mb storage
; COMPUTER: Dell OptiPlex GX1
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect 8.0 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/227,496C
; FILING DATE: 04/14/94
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/903,069
; FILING DATE: 06/22/92
; APPLICATION NUMBER: 07/704,984
; FILING DATE: 05/24/91
; APPLICATION NUMBER: 07/556,238
; FILING DATE: 07/20/90
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara A. Shimei
; REGISTRATION NUMBER: 29,862
; REFERENCE/DOCKET NUMBER: MTI 214.2C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (203) 812-2786
; TELEFAX: (203) 812-5492
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 680 amino acid residues
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: protein
; HYPOTHETICAL: no
; FRAGMENT TYPE: complete sequence
; FEATURE:

Query Match	55.5%;	Score 1602;	DB 10;	Length 426;
Best Local Similarity	98.7%;	Pred. No. 2.6e-115;		
Matches 302;	Conservative	0;	Mismatches 4;	Indels 0;
Gaps	0			
QY	1	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEY	60	
Db	58	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEY	117	
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG	120	
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG	177	
QY	121	PDSLIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR	180	
Db	178	PDSLIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR	237	
QY	181	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP	240	
Db	238	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP	297	
QY	241	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD	300	
Db	298	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD	357	
QY	301	VPEKQT	306	
Db	358	PPTTTT	363	

RESULT 14
 US-09-959-845-6
 ; Sequence 6, Application US/09959845
 ; Publication No. US20030008334A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Yoshimi TAKAI
 ; APPLICANT: Hiroyuki NAKANISHI
 ; APPLICANT: Keiko SATO
 ; APPLICANT: Kenichi TAKAHASHI
 ; TITLE OF INVENTION: Protein Nectin-3
 ; FILE REFERENCE: 2001-1678A/LC/00653
 ; CURRENT APPLICATION NUMBER: US/09/959,845
 ; CURRENT FILING DATE: 2001-12-31
 ; PRIOR APPLICATION NUMBER: PCT/JP01/01871
 ; PRIOR FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: JP 2000-065595
 ; PRIOR FILING DATE: 2000-03-09
 ; NUMBER OF SEQ ID NOS: 14
 ; SOFTWARE: PatentIn ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 438
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-959-845-6

Query Match	54.8%;	Score 1582;	DB 10;	Length 438;
Best Local Similarity	95.5%;	Pred. No. 9.5e-114;		
Matches 294;	Conservative 9;	Mismatches 5;	Indels 0;	Gaps 0;

Qy	1	GPII	VPHVTA	VGKNVSLKCLIEVN	ETITQISWEIKHGKSSQTVA	VHHPQYGF	SVOGEY	60
Dd	58	GSII	VPHVTA	VGKNVSLKCLIEVN	ETITQISWEIKHGKSTQ	TVAVHHPQYGF	SVOGDY	117
Qy	61	QRVL	FKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT	VTVLVEPTVS	LKG	120		
Dd	118	QRVL	FKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT	VTVLVEPTVS	LKG	177		
Qy	121	PD	SLIDGGNETVA	AICIAATGKPVAHIDWEGDLGEMES	TTSFPNETATIISQYKL	FPTR	180	
Dd	178	PD	SLIDGGNETVA	AVCVAAATGKPVAQIDWEGDLGEMES	TTSFPNETATIVSQYL	FPTR	237	
Qy	181	FARGRRITCVVKHPALEKD	IRYSFILDIQYAPEVSV	TYDGNWFVGRKGVNLKC	NADANP	240		
Dd	238	FARGRRITCVVKHPALEKD	IRYSFILDIQYAPEVSV	TYDGNWFVGRKGVNLKC	NADANP	297		

Qy	241	PPFKSVWSRLDQGWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVYIYISD	300
Db	298	PPFKSVWSRLDQGWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVYIYISD	357
Qy	301	VPFKQTSS	308
Db	358	IPLTQTSS	365

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RESULT 15
US-09-972-268-19
; Sequence 19, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES,
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 438
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-19

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Query Match 54.8%; Score 1582; DB 10; Length 438;
Best Local Similarity 95.5%; Pred. No. 9.5e-114;
Matches 294; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY	241	PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	300
Dd	298	PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYCKVSNSLGQRSDQKVIYISD	357
QY	301	VPFKQTSS	308
Dd	358	IPLTQTSS	365

Search completed: April 12, 2004, 10:25:28
Job time : 45.9625 sec

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; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-6

Query Match      55.9%; Score 1613; DB 10; Length 549;
Best Local Similarity 73.4%; Pred. No. 5.2e-116;
Matches 326; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

QY      1 GPIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db      58 GPIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117

QY      61 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKG 120
Db      118 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKG 177

QY      121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 180
Db      178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 237

QY      181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db      238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297

QY      241 PPKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 300
Db      298 PPKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 357

QY      301 VPFKQTSSRSCDKTHTCPPCPAPEAGAPSV-----FLFPK-----PKDTLMISRTPEVT 351
Db      358 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIA 403

QY      352 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNSTY-----RVVSVTLVHQQDWL 405
Db      404 TIIASVVGALFIVLVSVLAGIFCYRRRRTRFRGDYFAKNYIPPSDMQKESQIDVLQQDEL 463

QY      406 NGKEYCKVSNKALPAPIEKTISK 429
Db      464 DSYDPDSVKKENK---NPVNNLIRK 484

RESULT 12
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
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; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match      55.9%; Score 1613; DB 14; Length 549;
Best Local Similarity 73.4%; Pred. No. 5.2e-116;
Matches 326; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

QY      1 GPIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db      58 GPIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117

QY      61 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKG 120
Db      118 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKG 177

QY      121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 180
Db      178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 237

QY      181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db      238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297

QY      241 PPKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 300
Db      298 PPKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 357

QY      301 VPFKQTSSRSCDKTHTCPPCPAPEAGAPSV-----FLFPK-----PKDTLMISRTPEVT 351
Db      358 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIA 403

QY      352 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNSTY-----RVVSVTLVHQQDWL 405
Db      404 TIIASVVGALFIVLVSVLAGIFCYRRRRTRFRGDYFAKNYIPPSDMQKESQIDVLQQDEL 463

QY      406 NGKEYCKVSNKALPAPIEKTISK 429
Db      464 DSYDPDSVKKENK---NPVNNLIRK 484

RESULT 13
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15
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Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSFPNETATIIISQYKLFPTTR 237

QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357

QY 301 VPFKQTSS 308

Db 358 VPFKQTSS 365

RESULT 9

US-09-972-268-2

; Sequence 2, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2

; LENGTH: 542

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-972-268-2

Query Match 55.9%; Score 1613; DB 10; Length 542;

Best Local Similarity 73.4%; Pred. No. 5.1e-116;

Matches 326; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

QY 1 GPIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 51 GPIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 110

QY 61 QGRVLPKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 111 QGRVLPKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 170

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSFPNETATIIISQYKLFPTTR 180

Db 171 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSFPNETATIIISQYKLFPTTR 230

QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANP 240

Db 231 FARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANP 290

QY 241 PPFKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300

Db 291 PPFKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 350

QY 301 VPFKQTSSRSCDKTHTCPPCPAPEAGAPSV-----FLFPPK----PKDTLMISRTPEVT 351

Db 351 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTTIA 396

QY 352 CVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYNSTY-----RVVSVLTVLHQDWL 405

Db 397 TTIASVVGALFIVLVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODEL 456

QY 406 NGKEYKCKVSNKALPAPIEKTISK 429

Db 457 DSYDPSVKKENK---NPVNNLIRK 477

RESULT 10

US-09-972-268-4

; Sequence 4, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 549

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are fr

; OTHER INFORMATION: m human Nectin-3 alpha

US-09-972-268-4

Query Match 55.9%; Score 1613; DB 10; Length 549;

Best Local Similarity 73.4%; Pred. No. 5.2e-116;

Matches 326; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

QY 1 GPIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GPIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY 61 QGRVLPKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLPKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSFPNETATIIISQYKLFPTTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSFPNETATIIISQYKLFPTTR 237

QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357

QY 301 VPFKQTSSRSCDKTHTCPPCPAPEAGAPSV-----FLFPPK----PKDTLMISRTPEVT 351

Db 358 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTTIA 403

QY 352 CVVVDVSHEDPEVKFNWYVDGVEVHNNAKTKPREEQYNSTY-----RVVSVLTVLHQDWL 405

Db 404 TTIASVVGALFIVLVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODEL 463

QY 406 NGKEYKCKVSNKALPAPIEKTISK 429

Db 464 DSYDPSVKKENK---NPVNNLIRK 484

RESULT 11

US-09-972-268-6

; Sequence 6, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

```
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10
```

```
Query Match 56.8%; Score 1638; DB 10; Length 510;
Best Local Similarity 84.8%; Pred. No. 5.5e-118;
Matches 318; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSRS-----CDK-----THTCPPCA 322
Db 358 VPFKQTSSIAVAGAVIGAVLALFIATVTLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 323 PEAGAPSVFLFPPK 337
Db 418 ERSPLPQKDLFQPE 432
```

```
RESULT 7
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; ORGANISM: homo sapiens
```

```
US-09-972-268-12
Query Match 56.8%; Score 1638; DB 10; Length 510;
Best Local Similarity 84.8%; Pred. No. 5.5e-118;
Matches 318; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSRS-----CDK-----THTCPPCA 322
Db 358 VPFKQTSSIAVAGAVIGAVLALFIATVTLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 323 PEAGAPSVFLFPPK 337
Db 418 ERSPLPQKDLFQPE 432

RESULT 8
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31
```

```
Query Match 56.7%; Score 1636; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 6.4e-118;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
```

QY	242	PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDQKVIYISDV	301
Db	278	PSYN-WTRLDGPLSGVRVDGDTLGF-PPLTTEHSGIYVCHVSNEFSSRDSQVTVVDVLAD	335
QY	302	PFKQ-----TSSRSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMISRTPEVTCV	353
Db	336	PQEDSGKQVDLVSASRSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMISRTPEVTCV	395
QY	354	VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK	413
Db	396	VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK	455
QY	414	VSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE	473
Db	456	VSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE	515
QY	474	SNQOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS	533
Db	516	SNQOPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS	575
QY	534	LSPGK	538
Db	576	LSPGK	580

RESULT 4

```

US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE THEREOF
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

```

Query Match	57.0%;	Score 1645;	DB 10;	Length 387;
Best Local Similarity	100.0%;	Pred. No. 1.1e-118;		
Matches 310;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY	60	
Db	58	GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY	117	
Qy	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120	
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	177	
Qy	121	PDSLIDGGNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR	180	
Db	178	PDSLIDGGNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR	237	
Qy	181	FARGRRITCVVXHPALEKDIRYSPILDIQYAPEVSVTGYDGNWFVGRKGNLKCNDANP	240	
Db	238	FARGRRITCVVXHPALEKDIRYSPILDIQYAPEVSVTGYDGNWFVGRKGNLKCNDANP	297	
Qy	241	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRDQKVIYISD	300	

Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357

Qy 301 VPFKQTSSRS 310
|||||

Db 358 VPFKQTSSRS 367

RESULT 5

```

US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

```

Query Match 56.8%; Score 1638; DB 10; Length 504;
Best Local Similarity 84.8%; Pred. NO. 5.4e-118;
Matches 318; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

QY	1	GPIIVEPHVTA	VWGKNVSLKCLIEVNETITQISWEKIHGKSSQT	VAVHHPQYGF	SVQGEY	60
Db	52	GPIIVEPHVTA	VWGKNVSLKCLIEVNETITQISWEKIHGKSSQT	VAVHHPQYGF	SVQGEY	111
QY	61	QGRVLFKNYS	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQS	STTVTLVEPTV	SLIKG	120
Db	112	QGRVLFKNYS	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQS	STTVTLVEPTV	SLIKG	171
QY	121	PDSLIDGGNET	VAAICIAATGKPVAHIDWEGDLGEMESTTISFPNETATII	ISQYKLF	FPTR	180
Db	172	PDSLIDGGNET	VAAICIAATGKPVAHIDWEGDLGEMESTTISFPNETATII	ISQYKLF	FPTR	231
QY	181	FARGRRITCV	VVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP			240
Db	232	FARGRRITCV	VVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANP			291
QY	241	PPFKSVWSRLD	GQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORS	DQKVIYISD		300
Db	292	PPFKSVWSRLD	GQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORS	DQKVIYISD		351
QY	301	VPEKQOTSSR	-----CDK-----	-----THTCPC	CPA	322
Db	352	VPEKQOTSS	IAVAGAVIGAVLALFIIAIFVTVLTPRKKRPSYLDKVIDLP	PTHKPP	PLYE	411
QY	323	PEAEGAPS	VFLEPPK			337
Db	412	ERSPPL	POKDLFQPE			426

RESULT 6

US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VPFKQTSSRSCDKTHTCPPCPAPEAGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHE 360
Db 358 VPFKQTSSRSCDKTHTCPPCPAPEAGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHE 417
QY 361 DPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 420
Db 418 DPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 477
QY 421 APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPEN 480
Db 478 APIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPEN 537
QY 481 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 538
Db 538 NYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 595

RESULT 2
US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match 97.9%; Score 2824.5; DB 10; Length 634;
Best Local Similarity 92.2%; Pred. No. 1.7e-209;
Matches 532; Conservative 2; Mismatches 4; Indels 39; Gaps 1;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VPFKQT-----SSRSCDKTHTCPPCP 321
Db 358 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKODTTIATRSCDKTHTCPPCP 417
QY 322 APEAGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 381
Db 418 APEAGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNATK 477
QY 382 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 441
Db 478 PREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVY 537
QY 442 LPPSREEMTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 501
Db 538 LPPSREEMTKNQVSLTCLVKGYFSPYSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKL 597
QY 502 TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 538
Db 598 TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 634

RESULT 3
US-09-972-268-36
; Sequence 36, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion Construct
US-09-972-268-36

Query Match 59.1%; Score 1705.5; DB 10; Length 580;
Best Local Similarity 61.7%; Pred. No. 4e-123;
Matches 336; Conservative 61; Mismatches 129; Indels 19; Gaps 9;
QY 9 VTAVWGKNVSLKCLII-EVNETITQISWEKIH-GKSSQTVAVHHPQYGFVSQGEYQGRVL 65
Db 40 VTVVLGQDAKLPQYRGDSGEQGVQVAVARVDAGEGAQELALLHSKYGLHVS PAYEGRVE 99
QY 66 FKNYSLN-DATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 123
Db 100 QPPPPRNPDLGSLVLRNAVQADEGEYECRVSTFFPAGSFQARLRLRVLPPLPSLNPGP-A 158
QY 124 LIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 183
Db 159 LEEGQGLTLAASC-TAEGSPAPSVTWDTEVKGTTSSRSFKHSRAAVTSEFHLVPSRSMN 217
QY 184 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGN--WFGVGRKGVNLKCNADANP 241
Db 218 GQPLTCVSHPGLLQDQRITHILVSLFABASVRGLEDQNLWLHIGREGAMLKCLSEGQPP 277

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 44.9625 Seconds
(without alignments)
3146.189 Million cell updates/sec

Title: US-09-972-268-14_COPY_58_595
Perfect score: 2886
Sequence: 1 GPIIVEPHVTAVWGKNVSLK.....MHEALHNHYTQKLSLSPGK 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1:	/cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17:	/cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18:	/cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2886	100.0	595	10	US-09-972-268-14	Sequence 14, Appl
2	2824.5	97.9	634	10	US-09-972-268-13	Sequence 13, Appl
3	1705.5	59.1	580	10	US-09-972-268-36	Sequence 36, Appl
4	1645	57.0	387	10	US-09-972-268-16	Sequence 16, Appl
5	1638	56.8	504	10	US-09-972-268-8	Sequence 8, Appl
6	1638	56.8	510	10	US-09-972-268-10	Sequence 10, Appl
7	1638	56.8	510	10	US-09-972-268-12	Sequence 12, Appl
8	1636	56.7	437	10	US-09-972-268-31	Sequence 31, Appl
9	1613	55.9	542	10	US-09-972-268-2	Sequence 2, Appl
10	1613	55.9	549	10	US-09-972-268-4	Sequence 4, Appl
11	1613	55.9	549	10	US-09-972-268-6	Sequence 6, Appl
12	1613	55.9	549	14	US-10-161-572-45	Sequence 45, Appl
13	1602	55.5	426	10	US-09-972-268-15	Sequence 15, Appl
14	1582	54.8	438	10	US-09-959-845-6	Sequence 6, Appl
15	1582	54.8	438	10	US-09-972-268-19	Sequence 19, Appl

16	1582	54.8	510	10	US-09-959-845-4	Sequence 4, Appl
17	1582	54.8	510	10	US-09-972-268-18	Sequence 18, Appl
18	1581	54.8	549	10	US-09-959-845-2	Sequence 2, Appl
19	1581	54.8	549	10	US-09-972-268-17	Sequence 17, Appl
20	1415	49.0	555	12	US-10-463-260-6	Sequence 6, Appl
21	1332	46.2	779	10	US-09-910-600-16	Sequence 16, Appl
22	1332	46.2	779	10	US-09-910-600-30	Sequence 30, Appl
23	1314.5	45.5	698	9	US-09-875-338-9	Sequence 9, Appl
24	1314.5	45.5	698	14	US-10-077-023-9	Sequence 9, Appl
25	1300.5	45.1	680	8	US-08-469-583A-15	Sequence 15, Appl
26	1297	44.9	594	9	US-09-815-108-22	Sequence 22, Appl
27	1297	44.9	594	14	US-10-229-584-22	Sequence 22, Appl
28	1295.5	44.9	480	14	US-10-077-023-135	Sequence 135, Appl
29	1292.5	44.8	453	14	US-10-159-006-18	Sequence 18, Appl
30	1292	44.8	472	14	US-10-159-006-30	Sequence 30, Appl
31	1290.5	44.7	480	14	US-10-077-023-133	Sequence 133, Appl
32	1281	44.4	489	15	US-10-104-047-3329	Sequence 3329, Ap
33	1279.5	44.3	471	15	US-10-108-260A-4285	Sequence 4285, Ap
34	1278	44.3	478	15	US-10-104-047-3812	Sequence 3812, Ap
35	1275.5	44.2	979	15	US-10-418-836-10	Sequence 10, Appl
36	1275	44.2	481	12	US-10-463-260-5	Sequence 5, Appl
37	1272.5	44.1	480	9	US-09-875-338-5	Sequence 5, Appl
38	1272.5	44.1	480	14	US-10-077-023-5	Sequence 5, Appl
39	1271	44.0	1194	14	US-10-191-029-10	Sequence 10, Appl
40	1270.5	44.0	448	14	US-10-171-452A-42	Sequence 42, Appl
41	1270.5	44.0	448	14	US-10-171-452A-54	Sequence 54, Appl
42	1270.5	44.0	448	15	US-10-353-708-42	Sequence 42, Appl
43	1270.5	44.0	448	15	US-10-353-708-54	Sequence 54, Appl
44	1270.5	44.0	449	14	US-10-253-366-2	Sequence 2, Appl
45	1270.5	44.0	449	14	US-10-316-694-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match 100.0%; Score 2886; DB 10; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.8e-214;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTVTVLVEPTVSLIKG 177

Qy 301 VPFKQTSRSCDKTHTCPAPABGAPSV-----FLFPPK-----PKDTLMISRTPEVT 351
Db 364 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPPFLSTLATIKDDTIA 409
Qy 352 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTY-----RVSVLTVLHQDWL 405
Db 410 TIIASVVGALFIVLSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDEL 469
Qy 406 NG-----KEYKCKVSN 416
Db 470 DSYPDVSVKKEKKNPVNN 486

RESULT 14
AAE23289
ID AAE23289 standard; protein; 426 AA.

AC AAE23289;

DT 27-AUG-2002 (first entry)

DE Human nectin-3alpha-FLAGpolyHis fusion protein.

XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.

XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.

XX
FH Key Location/Qualifiers
FT Region 1..404
FT /note= "Human nectin-3alpha protein"
FT Region 405..420
FT /note= "FLAG peptide"
FT Region 421..426
FT /note= "polyHis tag"

XX WO200228902-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMV) IMMUNEX CORP.

XX PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.

XX Claim 9; Page 104-105; 141pp; English.

XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in

CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha-
CC FLAGpolyHis fusion protein

XX
SQ Sequence 426 AA;

Query Match 55.5%; Score 1602; DB 5; Length 426;
Best Local Similarity 98.7%; Pred. No. 3.4e-101;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GPIIVPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIVPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTP 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTP 237
Qy 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGDGNWFVGRKGVNLKCNADANP 297
Qy 241 PPFKSVWSRLDGQWPDGILLASDNTLHFVHPLTFNYSGVYICKVQTSNLSGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGILLASDNTLHFVHPLTFNYSGVYICKVQTSNLSGQSDQKVIYISD 357
Qy 301 VPFKQT 306
Db 358 PPTTTT 363

RESULT 15

AAG63984

ID AAG63984 standard; protein; 438 AA.

XX
AC AAG63984;

XX 26-NOV-2001 (first entry)

XX Amino acid sequence of murine nectin-3.

XX Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.

XX Mus sp.

XX WO200166736-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP001871.

XX 09-MAR-2000; 2000JP-00065595.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX (TAKA/) TAKAHASHI K.

XX Takahashi K, Takai Y, Nakanishi H, Sato K;

XX WPI; 2001-570771/64.

XX N-PSDB; AAH78181.

XX New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and

AAE23282;
29-AUG-2003 (revised)
27-AUG-2002 (first entry)
Mouse nectin-3-human nectin 3alpha fusion protein.
Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
paracellular transport disorder; kidney; diabetic retinopathy; allergy;
allograft rejection; metastasis; restenosis; inflammatory bowel disease;
oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
chromosome 3.
Homo sapiens.
Mus musculus.
Chimeric.
Key Location/Qualifiers
Region 1..7 /note= "Mouse nectin-3 protein"
Region 8..549 /note= "Human nectin-3alpha protein"
WO200228902-A2.
11-APR-2002.
05-OCT-2001; 2001WO-US031392.
05-OCT-2000; 2000US-0238557P.
(IMMV) IMMUNEX CORP.
Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
WPI; 2002-426103/45.
N-PSDB; AAD37441.
Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
sepsis, stroke.
Claim 1; Page 80-82; 141pp; English.
The invention relates to a substantially purified nectin3alpha, beta,
gamma and nectin-4 polypeptides and their corresponding polynucleotides.
Nectin DNA and protein are useful for treating a disease associated with
cell adhesion activity, adherens junction formation activity, epithelial
or endothelial barrier function activity, endothelial proliferation or
migration activity, viral polypeptide binding activity. The epithelial or
endothelial barrier function disorder which is treated by the above
mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
asthma, allergy, allograft rejection, metastasis of cancer cells,
paracellular transport disorders such as magnesium transport defects in
the kidney or inflammatory bowel disease. Nectin DNA is also useful for
inhibiting angiogenesis in a mammal and treating endothelial migration,
proliferation or angiogenic condition of a tissue or a subject, such as
ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
stroke, restenosis, tumour growth and treating herpesvirus infection.
Nectin is also useful for modulating proliferation or migration of an
endothelial cell, an epithelial cell or a smooth muscle cell (vascular
smooth muscle cell). The present sequence is a fusion protein containing
mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
standardise OS field)
Sequence 549 AA;
Query Match 55.9%; Score 1613; DB 5; Length 549;
Best Local Similarity 73.4%; Pred. No. 8.1e-102;
Matches 326; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

QY 1 GPIIPEPHVTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWVGRKGNLKNADANP 240
Db 238 FARGRRITCVVKKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWVGRKGNLKNADANP 297
QY 241 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 VPFKQTSSRSCDKTHTCPPCPAPEGAPSV-----FLFPPK-----PKDTLMISRTPEVT 351
Db 358 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKLFFPLSTLATIKDDTTIA 403
QY 352 CVVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY-----RVVSVLTVHLQDWL 405
Db 404 TIIASVVGAGLFIIVLSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDEL 463
QY 406 NGKEYKCKVSNKALPAPIEKTISK 429
Db 464 DSYPSVKKENK--NPVNNLRK 484
RESULT 12
ABJ20222
ID ABJ20222 standard; protein; 549 AA.
XX
AC ABJ20222;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human IG gene related protein SEQ ID No 45.
XX
KW Breast cancer; p53 pathway modulating agent; IG; colon cancer;
KW kidney cancer; lung cancer; ovary cancer; human.
XX
OS Homo sapiens.
XX
PN WO200299040-A2.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017313.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 22-OCT-2001; 2001US-0338733P.
PR 15-FEB-2002; 2002US-0357253P.
PR 15-FEB-2002; 2002US-0357600P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Lioubin MN;
XX
DR WPI; 2003-148660/14.
XX
PT Identifying a candidate p53 pathway modulators that are useful as targets
PT for therapeutics or for diagnosing cancers associated with defective p53
PT function, by providing an assay system having a purified IG polypeptide
PT or nucleic acid.
XX

Db 231 FARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 290
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 291 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 350
QY 301 VPFKQTSSRSCDKTHTCPPCPAPEAEGAPSV-----FLFPPK-----PKDTLMISRTPEVT 351
Db 351 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIA 396
QY 352 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY-----RVVSVLTVLHQDWL 405
Db 397 TIIASVVGALFIVLVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDEL 456
QY 406 NGKEYKCKVSNKALPAPIEKTISK 429
Db 457 DSYPDVSKENK---NPVNNLIRK 477

RESULT 10
AAE23283
ID AAE23283 standard; protein; 549 AA.
XX
AC AAE23283;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha protein.

XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.

XX
FH Key Location/Qualifiers
FT Modified-site 73 /note= "N-glycosylated"
FT Domain 74. .152 /note= "Extracellular Ig domain"
FT Modified-site 83 /note= "N-glycosylated"
FT Modified-site 125 /note= "N-glycosylated"
FT Modified-site 186 /note= "N-glycosylated"
FT Domain 189. .250 /note= "Extracellular Ig domain"
FT Modified-site 222 /note= "N-glycosylated"
FT Domain 287. .342 /note= "Extracellular Ig domain"
FT Modified-site 331 /note= "N-glycosylated"
FT Domain 405. .424 /note= "Transmembrane domain"
FT Domain 425. .549 /note= "C-terminal domain"

XX WO200228902-A2.
XX 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX

DR WPI; 2002-426103/45.
DR N-PSDB; AAD37442.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 89-91; 141pp; English.
XX

CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha DNA.
CC Human nectin-3alpha gene is located on chromosome 3
XX
SQ Sequence 549 AA;

Query Match 55.9%; Score 1613; DB 5; Length 549;
Best Local Similarity 73.4%; Pred. No. 8.1e-102;
Matches 326; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIIISQYKLPTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIIISQYKLPTR 237
QY 181 FARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSRSCDKTHTCPPCPAPEAEGAPSV-----FLFPPK-----PKDTLMISRTPEVT 351
Db 358 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIA 403
QY 352 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY-----RVVSVLTVLHQDWL 405
Db 404 TIIASVVGALFIVLVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDEL 463
QY 406 NGKEYKCKVSNKALPAPIEKTISK 429
Db 464 DSYPDVSKENK---NPVNNLIRK 484

RESULT 11
AAE23282
ID AAE23282 standard; protein; 549 AA.
XX

Db 418 ERSPLPQKDLFQPE 432

RESULT 7

AAE23286

ID AAE23286 standard; protein; 510 AA.

XX

AC AAE23286;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human nectin-3beta protein.

XX

KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;

KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;

KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

XX stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Modified-site 73

FT /note= "N-glycosylated"

FT 74..152

FT /note= "Extracellular Ig domain"

FT 83

FT Modified-site /note= "N-glycosylated"

FT 125

FT Modified-site /note= "N-glycosylated"

FT 186

FT Modified-site /note= "N-glycosylated"

FT 189..250

FT Domain /note= "Extracellular Ig domain"

FT 222

FT Modified-site /note= "N-glycosylated"

FT 287..342

FT Domain /note= "Extracellular Ig domain"

FT 331

FT Modified-site /note= "N-glycosylated"

FT 386..510

FT Domain /note= "Intracellular C-terminal domain"

XX

WO200228902-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US031392.

XX

PR 05-OCT-2000; 2000US-0238557P.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX

DR WPI; 2002-426103/45.

DR N-PSDB; AAD37445.

XX

PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,

PT useful for treating or preventing heart failure, malaria,

PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,

PT sepsis, stroke.

XX

PS Claim 1; Page 98-99; 141pp; English.

XX

CC The invention relates to a substantially purified nectin3alpha, beta,

CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.

CC Nectin DNA and protein are useful for treating a disease associated with

CC cell adhesion activity, adherens junction formation activity, epithelial

CC or endothelial barrier function activity, endothelial proliferation or

CC migration activity, viral polypeptide binding activity. The epithelial or

CC endothelial barrier function disorder which is treated by the above

CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

CC asthma, allergy, allograft rejection, metastasis of cancer cells,

CC paracellular transport disorders such as magnesium transport defects in

CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for

CC inhibiting angiogenesis in a mammal and treating endothelial migration,

CC proliferation or angiogenic condition of a tissue or a subject, such as

CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,

CC stroke, restenosis, tumour growth and treating herpesvirus infection.

CC Nectin is also useful for modulating proliferation or migration of an

CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular

CC smooth muscle cell). The present sequence is human nectin-3beta protein.

CC Human nectin-3beta gene is located on chromosome 3

XX

SQ Sequence 510 AA;

Query Match 56.8%; Score 1638; DB 5; Length 510;

Best Local Similarity 84.8%; Pred. No. 1.5e-103;

Matches 318; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

QY 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGNETVAAICIAATGKVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180

Db 178 PDSLIDGNETVAAICIAATGKVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

QY 181 FARGRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 240

Db 238 FARGRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 297

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD 357

QY 301 VPFKQTSSRS-----CDK-----THTCPPCPA 322

Db 358 VPFKQTSSIAVAGAVIGALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPLYE 417

QY 323 PEAEGAPSVFLFPPK 337

Db 418 ERSPLPQKDLFQPE 432

RESULT 8

AAE23299

ID AAE23299 standard; protein; 437 AA.

XX

AC AAE23299;

XX

DT 27-AUG-2002 (first entry)

XX

DE Human nectin-3gamma protein.

XX

KW Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;

KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;

KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

XX stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX

OS Homo sapiens.

XX

PN WO200228902-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US031392.

XX

PR 05-OCT-2000; 2000US-0238557P.

XX

CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX
SQ Sequence 504 AA;

Query Match 56.8%; Score 1638; DB 5; Length 504;
Best Local Similarity 84.8%; Pred. No. 1.4e-103;
Matches 318; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

Qy 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEY 60
Db |||||
52 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEY 111

Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171

Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db |||||
172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 231

Qy 181 FARGRRITCVVKGHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANP 240
Db |||||
232 FARGRRITCVVKGHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANP 291

Qy 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db |||||
292 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 351

Qy 301 VPFKQTSSRS-----CDK-----THTCPPCPA 322
Db ||||| : ||| :
352 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTLLTPRKRPYSYLDKVIDLPPTHKPPPLYE 411

Qy 323 PEAGAPSVFLFPPK 337
Db : ||| :
412 ERSPLPQKDLFQPE 426

RESULT 6
AAE23285
ID AAE23285 standard; protein; 510 AA.
XX
AC AAE23285;
XX
DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin-3beta fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..6
FT /note= "Mouse nectin-3 pprotein"
FT Region 7..510
FT /note= "Human nectin-3beta protein"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.

XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37444.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 94-95; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 510 AA;

Query Match 56.8%; Score 1638; DB 5; Length 510;
Best Local Similarity 84.8%; Pred. No. 1.5e-103;
Matches 318; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

Qy 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEY 60
Db |||||
58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEY 117

Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db |||||
178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

Qy 181 FARGRRITCVVKGHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANP 240
Db |||||
238 FARGRRITCVVKGHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANP 297

Qy 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db |||||
298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

Qy 301 VPFKQTSSRS-----CDK-----THTCPPCPA 322
Db ||||| : ||| :
358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTLLTPRKRPYSYLDKVIDLPPTHKPPPLYE 417

Qy 323 PEAGAPSVFLFPPK 337
Db : ||| :
323 PEAGAPSVFLFPPK 337

XX DE Human nectin-3beta-FLAGpolyHis fusion protein.

XX KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;

KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;

KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.

XX OS Homo sapiens.

OS Unidentified.

OS Chimeric.

XX FH Key Location/Qualifiers

FT Region 1. .365

FT /note= "Human nectin-3alpha protein"

FT Region 366. .381

FT /note= "FLAG peptide"

FT Region 382. .387

FT /note= "PolyHis tag"

XX WO200228902-A2.

PN 11-APR-2002.

PD 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

PR (IMMV) IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

PI WPI; 2002-426103/45.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,

PT useful for treating or preventing heart failure, malaria,

PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,

PT sepsis, stroke.

XX Claim 9; Page 105-107; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,

CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.

CC Nectin DNA and protein are useful for treating a disease associated with

CC cell adhesion activity, adherens junction formation activity, epithelial

CC or endothelial barrier function activity, endothelial proliferation or

CC migration activity, viral polypeptide binding activity. The epithelial or

CC endothelial barrier function disorder which is treated by the above

CC asthma, allergy, allograft rejection, metastasis of cancer cells,

CC paracellular transport disorders such as magnesium transport defects in

CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for

CC inhibiting angiogenesis in a mammal and treating endothelial migration,

CC proliferation or angiogenic condition of a tissue or a subject, such as

CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,

CC stroke, restenosis, tumour growth and treating herpesvirus infection.

CC Nectin is also useful for modulating proliferation or migration of an

CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular

CC smooth muscle cell). The present sequence is human nectin-3beta-

CC FLAGpolyHis fusion protein

XX SQ Sequence 387 AA;

Query Match 57.0%; Score 1645; DB 5; Length 387;

Best Local Similarity 100.0%; Pred. No. 3.4e-104;

Matches 310; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLPFTR 180

Db 178 PDSLIDGGNETVAACIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLPFTR 237

QY 181 FARRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240

Db 238 FARRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297

QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLGQRSDQKVIYISD 300

Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVIKVTNSLGQRSDQKVIYISD 357

QY 301 VPFKQTSSRS 310

Db 358 VPFKQTSSRS 367

RESULT 5

AAE23284

ID AAE23284 standard; protein; 504 AA.

XX

AC AAE23284;

XX 27-AUG-2002 (first entry)

XX Human deleted nectin-3beta protein.

DE

XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;

KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;

KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;

KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX Homo sapiens.

OS WO200228902-A2.

XX 11-APR-2002.

PF 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMV) IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

XX N-PSDB; AAD37443.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,

PT useful for treating or preventing heart failure, malaria,

PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,

PT sepsis, stroke.

XX Claim 1; Page 89-91; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,

CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.

CC Nectin DNA and protein are useful for treating a disease associated with

CC cell adhesion activity, adherens junction formation activity, epithelial

CC or endothelial barrier function activity, endothelial proliferation or

CC migration activity, viral polypeptide binding activity. The epithelial or

CC endothelial barrier function disorder which is treated by the above

CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

CC asthma, allergy, allograft rejection, metastasis of cancer cells,

CC paracellular transport disorders such as magnesium transport defects in

CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for

CC inhibiting angiogenesis in a mammal and treating endothelial migration,

CC proliferation or angiogenic condition of a tissue or a subject, such as

CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,

CC stroke, restenosis, tumour growth and treating herpesvirus infection.

CC Nectin is also useful for modulating proliferation or migration of an

CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular

CC smooth muscle cell). The present sequence is human nectin-3beta-

CC FLAGpolyHis fusion protein

Db 358 PPTTTTLQTIQWHPSTADIEDLATEPKKLPFPFLSTLTIATIKDDTIATRSCDKTHTCPPCP 417
QY 322 APEAEGAPSVLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNVYVDGVEVHNAKTK 381
Db 418 APEAEGAPSVLFPKPKDMLMISRTPEVTCVVVDVSHEDPEVKFNVYVDGVEVHNAKTK 477
QY 382 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVY 441
Db 478 PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQV 537
QY 442 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 501
Db 538 LPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSF 597
QY 502 TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 538
Db 598 TVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 634

RESULT 3
AAE23302
ID AAE23302 standard; protein; 580 AA.
XX
AC AAE23302;
XX 27-AUG-2002 (first entry)
XX Human nectin-4-IgG1 Fc region fusion protein.
XX Human; nectin-4; therapy; cell adhesion; cell proliferation; tumour;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; sepsis; herpesvirus infection; asthma; chromosome 1; cancer;
KW immunoglobulin G1.
XX
OS Homo sapiens.
XX
Key Location/Qualifiers
FT Peptide 1..26
FT Protein /label= Signal_peptide 27..580
FT /note= "Mature nectin-4-IgG1 Fc region fusion protein" 27..580
FT Domain /note= "Soluble/extracellular domain" 350..580
FT Region /note= "Human IgG1 Fc region" 350..580
XX
WO200228902-A2.
XX
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
(IMMV) IMMUNEX CORP.
XX
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37453.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
XX Claim 6; Page 134-136; 141pp; English.
PS
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC

CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-4 protein fused to human immunoglobulin G1 (IgG1) Fc region.
CC Human nectin-4 gene is located on chromosome 1
XX
SQ Sequence 580 AA;

Query Match 59.1%; Score 1705.5; DB 5; Length 580;
Best Local Similarity 61.7%; Pred. No. 4.2e-108;
Matches 336; Conservative 61; Mismatches 129; Indels 19; Gaps 9;
QY 9 VTAVWGNVSLKCLI--EVNETITQISWEKIH-GKSSQTVAVHHPOYGFVSQGEYQGRVL 65
Db 40 VTVLGQDAKLPCFYRGDSGEQGVQVAVARVDAGEGAQELALHLSKYGLHVSAPYGRVE 99
QY 66 FKNYSLN--DATITLHNIGFSGKIYICKAVTFPLGNAQSTTVTLVEPTVSLIKGPD 123
Db 100 QPPPPNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQARLRLRVLPPLSLNPGP-A 158
QY 124 LIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIIISQYKLFPTRFAR 183
Db 159 LEEGQGLTLAASC-TAEGSPAPSVTWDTEVKTSSRSFKHSRAAVTSEFHLVPSRSMN 217
QY 184 GRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTVGYDGN--WFGVGRKGNLKNADANPP 241
Db 218 GQPLTCVVSHPGLLQDQRIITHLVSVFLAASVVRGLEQDNLWHIGREGAMLKCLSEGQPP 277
QY 242 PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDV 301
Db 278 PSYN-WTRLDGPLPSGVRVDGDTLGF-PPLTTEHSGIYVCHVSNEFSSRDSQVTVDLAD 335
QY 302 PFKQ-----TSSRSCDKTHTCPPCPAPEAGAPSVLFPPKPKDTLMISRTPEVTCV 353
Db 336 PQEDSGKQVDLVASASRSCDKTHTCPPCPAPEAGAPSVLFPPKPKDTLMISRTPEVTCV 395
QY 354 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 413
Db 396 VVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCK 455
QY 414 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE 473
Db 456 VSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWE 515
QY 474 SNGQPNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS 533
Db 516 SNGQPNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLS 575
QY 534 LSPGK 538
Db 576 LSPGK 580

RESULT 4
AAE23290
ID AAE23290 standard; protein; 387 AA.
XX
AC AAE23290;
XX
DT 27-AUG-2002 (first entry)

CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 595 AA;

Query Match 100.0%; Score 2886; DB 5; Length 595;
Best Local Similarity 100.0%; Pred. No. 9.3e-189;
Matches 538; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVEY 60
Db |||||
58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVEY 117
||
Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
||
Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 180
Db |||||
178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 237
||
Qy 181 FARGRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 240
Db |||||
238 FARGRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 297
||
Qy 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 300
Db |||||
298 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 357
||
Qy 301 VPFKQTSRSSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE 360
Db |||||
358 VPFKQTSRSSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE 417
||
Qy 361 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 420
Db |||||
418 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 477
||
Qy 421 APIEKTISKAKGPPEQVYTLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNGQPEN 480
Db |||||
478 APIEKTISKAKGPPEQVYTLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNGQPEN 537
||
Qy 481 NYKTPPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 538
Db |||||
538 NYKTPPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 595
||

RESULT 2
AAE23287
ID AAE23287 standard; protein; 634 AA.
XX
AC AAE23287;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-IgG1Fc region fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.

XX Homo sapiens.
OS Unidentified.
OS Chimeric.
XX WO200228902-A2.
XX 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 100-102; 14lpp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 634 AA;

Query Match 97.9%; Score 2824.5; DB 5; Length 634;
Best Local Similarity 92.2%; Pred. No. 1.6e-184;
Matches 532; Conservative 2; Mismatches 4; Indels 39; Gaps 1;

Qy 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVEY 60
Db |||||
58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVEY 117
||
Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
||
Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 180
Db |||||
178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 237
||
Qy 181 FARGRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 240
Db |||||
238 FARGRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 297
||
Qy 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 300
Db |||||
298 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 357
||
Qy 301 VPFKQTSRSSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE 360
Db |||||
358 VPFKQTSRSSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHE 417
||
Qy 361 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 420
Db |||||
418 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALP 477
||
Qy 421 APIEKTISKAKGPPEQVYTLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNGQPEN 480
Db |||||
478 APIEKTISKAKGPPEQVYTLPPSREEMTKNQVSLTCLVKGPYPSDIAVEWESNGQPEN 537
||
Qy 481 NYKTPPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 538
Db |||||
538 NYKTPPVLDSGSEFFLYSKLTVDKSRWQQGNVFSCSVMEALHNHYTQKSLSLSPGK 595
||

RESULT 2
AAE23287
ID AAE23287 standard; protein; 634 AA.
XX
AC AAE23287;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-IgG1Fc region fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 64.9772 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-14_COPY_58_595
Perfect score: 2886
Sequence: 1 GPIIIVEPHVTAVWGNVSLK.....MHEALHNHYTQKSLSLSPGK 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	2886	100.0	595	5 AAE23288	Aae23288 Human nec
2	2824.5	97.9	634	5 AAE23287	Aae23287 Human nec
3	1705.5	59.1	580	5 AAE23302	Aae23302 Human nec
4	1645	57.0	387	5 AAE23290	Aae23290 Human nec
5	1638	56.8	504	5 AAE23284	Aae23284 Human del
6	1638	56.8	510	5 AAE23285	Aae23285 Mouse nec
7	1638	56.8	510	5 AAE23286	Aae23286 Human nec
8	1636	56.7	437	5 AAE23299	Aae23299 Human nec
9	1613	55.9	542	5 AAE23281	Aae23281 Human del
10	1613	55.9	549	5 AAE23283	Aae23283 Human nec
11	1613	55.9	549	5 AAE23282	Aae23282 Mouse nec
12	1613	55.9	549	6 ABJ20222	Abj20222 Human IG
13	1609.5	55.8	555	4 AAM39143	Aam39143 Human pol
14	1602	55.5	426	5 AAE23289	Aae23289 Human nec
15	1582	54.8	438	4 AAG63984	Aag63984 Amino aci
16	1582	54.8	438	5 AAE23293	Aae23293 Mouse nec
17	1582	54.8	510	4 AAG63983	Aag63983 Amino aci
18	1582	54.8	510	5 AAE23292	Aae23292 Mouse nec
19	1581	54.8	549	4 AAG63982	Aag63982 Amino aci
20	1581	54.8	549	4 AAG63985	Aag63985 Amino aci
21	1581	54.8	549	5 AAE23291	Aae23291 Mouse nec
22	1545.5	53.6	559	4 AAM40929	Aam40929 Human pol
23	1332	46.2	779	5 AAU87088	Aau87088 Siglec-BM
24	1332	46.2	779	5 AAU87081	Aau87081 Sialic ac
25	1326.5	46.0	564	3 AAY94406	Aay94406 Human ACA

26	1326.5	46.0	598	3 AAY94404	Aay94404 Human ACA
27	1320.5	45.8	744	3 AAY94408	Aay94408 Human VCA
28	1315	45.6	717	6 ABP72600	Abp72600 Human LP2
29	1314.5	45.5	698	5 AAU81012	Aau81012 B7-relate
30	1314.5	45.5	698	6 AAO16237	Aao16237 B7-relate
31	1300.5	45.1	680	2 AAR48037	Aar48037 tICAM(453
32	1300.5	45.1	680	6 ABU07273	Abu07273 Human exp
33	1297	44.9	594	4 AAU09817	Aau09817 Murine FG
34	1295.5	44.9	480	6 AAO16239	Aao16239 B7-relate
35	1295	44.9	592	4 AAB83838	Aab83838 Amino aci
36	1294.5	44.9	557	4 AAY97590	Aay97590 Flt1 rece
37	1294.5	44.9	557	5 ABP52443	Abp52443 Mutation
38	1292.5	44.8	453	2 AAY50151	Aay50151 Antibody
39	1292	44.8	472	2 AAY50157	Aay50157 Chimeric
40	1292	44.8	595	2 AAW86003	Aaw86003 Anti-5T4
41	1291	44.7	503	6 ABP72602	Abp72602 Human LP2
42	1290.5	44.7	480	6 AAO16238	Aao16238 B7-relate
43	1284.5	44.5	448	5 ABB99224	Abb99224 Chimeric
44	1282.5	44.4	567	4 AAY97593	Aay97593 Flt1 rece
45	1282.5	44.4	567	5 ABP52446	Abp52446 Mutation

ALIGNMENTS

RESULT 1
AAE23288
ID AAE23288 standard; protein; 595 AA.
XX
AC AAE23288;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta-IgG1Fc region fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 102-104; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or

Db 245 KTKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPM 304

QY 489 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 538

Db 305 LDSGGSFFLYSKLTVDKSRWQQGNIFSCVMHEALHNRYFTQKSLSLSPGK 354

RESULT 14

Q8N4Y9 PRELIMINARY; PRT; 521 AA.

AC Q8N4Y9; 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;

RA Strausberg R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC033178; A45874.1; -.

DR PIR; A60764; A60764.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 4.

DR SMART; SM00407; IGcl; 3.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; 2.

KW Hypothetical protein.

SQ SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;

Query Match 39.8%; Score 1149; DB 4; Length 521;

Best Local Similarity 91.3%; Pred. No. 4.2e-88;

Matches 210; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 309 RSCDKTHTCPPCPAPEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 368

Db 292 KSCDTPPPCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKW 351

QY 369 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 428

Db 352 YVDGVEVHNAKTKPREEQNFSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 411

QY 429 KAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPV 488

Db 412 KTKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPM 471

QY 489 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 538

Db 472 LDSGGSFFLYSKLTVDKSRWQQGNIFSCVMHEALHNRYFTQKSLSLSPGK 521

RESULT 15

Q8NF17 PRELIMINARY; PRT; 509 AA.

AC Q8NF17; 22, Created)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE FLJ00385 protein (Fragment).

GN FLJ00385.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;

RT "The nucleotide sequence of a long cDNA clone isolated from human spleen.";

RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AK090464; BAC03445.1; -.

DR PIR; A45874; A45874.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00407; IGcl; 3.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 2.

FT NON_TER 1

SQ SEQUENCE 509 AA; 56111 MW; 089498D8076E863C CRC64;

Query Match 39.3%; Score 1134; DB 4; Length 509;

Best Local Similarity 91.2%; Pred. No. 7.4e-87;

Matches 208; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 309 RSCDKTHTCPPCPAPEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 368

Db 211 KSCDTPPPCPCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKW 270

QY 369 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 428

Db 271 YVDGVEVHNAKTKPREEQNFSTFRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 330

QY 429 KAKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYKTTPPV 488

Db 331 KTKGQPREPQVYTLPPSRREMTKNQVSLTCLVKGFYPSDIAVEWESSGQPENNYNTTPPM 390

QY 489 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 536

Db 391 LDSGGSFFLYSKLTVDKSRWQQGNIFSCVMHEALHNRYFTQKSLSLSP 438

Search completed: April 12, 2004, 09:45:13

Job time : 45.694 secs

QY 206 LDIQYABEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTL 265
Db 121 LDIQYABEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTL 180
QY 266 HFVHPLTENYSGVYICKVTNSLQSRSDOKVIYISDVPFKQTSRSSCDKTHTCPPCPAPEA 325
Db 181 HFVHPLTENYSGVYICKVTNSLQSRSDOKVIYISDPPTTTLQ-----PTI 226
QY 326 EGAPSV-----FLFPPK----PKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVH 376
Db 227 QWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGGLFIVLVSVLGIFCY 286
QY 377 NAKTKPREEQNSTY-----RVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK 429
Db 287 RRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDPYPDSVKKENK---NPVNNLIRK 342
RESULT 12
Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025985; AAH25985.1; -.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000923; BlueCu 1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER BLUE; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
Query Match 40.1%; Score 1157; DB 4; Length 473;
Best Local Similarity 47.8%; Pred. No. 7.6e-89;
Matches 267; Conservative 46; Mismatches 107; Indels 138; Gaps 18;
QY 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQIS--WEKIH---GKSSQTVAVHHPOYGFS 55
Db 34 GPGLLKPSVT-----LSLTCTVS-GDSVASSSYWGVRQPPGKGLEWIGTINFSGNMY 86
QY 56 VQGEYQGRV-LFKNYSLNDATITLHNI GFS DSGKYICKAVTFPLG-NAQSSTVTVLVLEP 113
Db 87 YSPSLRSRVMTSADMSNSFYLKLDVSVAADTAVYCAAGHLVMGFAGHWGQGLVSVSP 146
QY 114 TVSLIKGPDLSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESITTSFPNETATIISQ 173
Db 147 AST--KGPSVF-----PLAPCSRSTS-----ESTAA----- 170
QY 174 YKLFPTRFARRRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFVGRKGVNL 232
Db 171 -----LGCLVK-----DYFPEPVTVS----- 186
QY 233 KCNADANPPFKSVWSRLDGQWPDGLLASDNTLHFVH--PLTFNYSGVY-----ICKVTN 285
Db 187 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSVTVTPSS 220

QY 286 SLGQRSDQKVIYISDVPFKQTSRSSCDKTHT-----CPPCPAPEAEGAPSVFLFPPKPKXD 340
Db 221 SLGKTKT-----YTCNVVDHKPSNTKVDKRVESKYGPSPCSPAPEFLGPGSVFLFPPKPKXD 275
QY 341 TLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVL 400
Db 276 TLMISRTPEVTCVVDVSEQDEPEQFNWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVL 335
QY 401 HQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLV 460
Db 336 HQDWLNGKEYKCKVSNKGLPSSIEKTIISKAKGQPREPQVYTLPPSQEEMTKNQVSLTCLV 395
QY 461 KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSKLTVDKSRWQQGNVFSQSVMH 520
Db 396 KGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFELYSRLLTVDKSRWQEGNVFSQSVMH 455
QY 521 EALHNHYTQKSLSLSPGK 538
Db 456 EALHNHYTQKSLSLSPGK 473
RESULT 13
Q86TT2 PRELIMINARY; PRT; 354 AA.
AC Q86TT2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Human full-length cDNA clone CS0DI019YF20 of placenta of Homo sapiens (Human) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Genoscope;
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Li W.B., Gruber C., Jessee J., Polayes D.;
RT "Full-length cDNA libraries and normalization."
RL Submitted (FEB-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX248278; CAD62606.1; -.
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Plasmid.
FT NON TER 1 1
SQ SEQUENCE 354 AA; 39125 MW; 23B80BF4D2B87A92 CRC64;
Query Match 39.8%; Score 1149; DB 4; Length 354;
Best Local Similarity 91.7%; Pred. No. 2.4e-88;
Matches 211; Conservative 7; Mismatches 12; Indels 0; Gaps 0;
QY 309 RSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNW 368
Db 125 KSCDTFPPCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQFKW 184
QY 369 YVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 428
Db 185 YVDGVEVHNAKTKPREEQNSTFRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 244
QY 429 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 488

DR	InterPro; IPR001254; Peptidase S1.	RA	Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
DR	InterPro; IPR001314; Peptidase S1A.	RA	Masuko Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
DR	InterPro; IPR000294; VitK_dep_GLA.	RA	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
DR	Pfam; PF00008; EGF; 2.	RT	"NEDO human cDNA sequencing project.";
DR	Pfam; PF00594; gla; 1.	RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR	Pfam; PF00047; ig; 2.	DR	EMBL; AK075105; BAC11404.1; -.
DR	Pfam; PF00089; trypsin; 1.	DR	InterPro; IPR003599; Ig.
DR	PRINTS; PR00722; CHYMOTRYPSIN.	DR	InterPro; IPR007110; Ig-like.
DR	PRINTS; PR00010; EGFLOOD.	DR	Pfam; PF00047; ig; 1.
DR	PRINTS; PR00001; GLABLOOD.	DR	SMART; SM00409; IG; 1.
DR	SMART; SM00181; EGF; 2.	DR	PROSITE; PS50835; IG_LIKE; 2.
DR	SMART; SM00179; EGF_CA; 1.	KW	Hypothetical protein.
DR	SMART; SM00069; GLA; 1.	SQ	SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;
DR	SMART; SM00407; IGC1; 2.		
DR	SMART; SM00020; Tryp_SPC; 1.		
DR	PROSITE; PS00010; ASX_HYDROXYL; 1.	Query Match	42.2%; Score 1218; DB 4; Length 267;
DR	PROSITE; PS00022; EGF_1; 1.	Best Local Similarity	99.6%; Pred. No. 2.4e-94;
DR	PROSITE; PS01186; EGF_2; 1.	Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
DR	PROSITE; PS01187; EGF_CA; 1.		
DR	PROSITE; PS00011; GLU CARBOXYLATION; 1.	QY	1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
DR	PROSITE; PS50835; IG_LIKE; 2.	Db	35 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 94
DR	PROSITE; PS00290; IG_MHC; 1.		
DR	PROSITE; PS00240; TRYPSIN_DOM; 1.	QY	61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
DR	PROSITE; PS00134; TRYPSIN_HIS; 1.	Db	95 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 154
DR	PROSITE; PS00135; TRYPSIN_SER; 1.		
SQ	SEQUENCE 679 AA; 75552 MW; 0B0023AE70A067A1 CRC64;	QY	121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFPT 180
		Db	155 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFPT 214
		QY	181 FARGRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLK 233
		Db	215 FARGRRITCVVKHHPALEKDIRYSFILDIOYAPEVSVTYDGNWFWGKGVNLK 267
		RESULT 11	
		Q9Y412	
		ID Q9Y412	PRELIMINARY; PRT; 407 AA.
		AC Q9Y412;	
		DT 01-NOV-1999 (TrEMBLrel. 12, Created)	
		DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)	
		DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
		DE Hypothetical protein (Fragment).	
		GN DKFZP566B0846.	
		OS Homo sapiens (Human).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
		OX NCBI_TaxID=9606;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RC TISSUE=Kidney;	
		RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;	
		RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.	
		DR EMBL; AL050071; CAB43256.1; -.	
		DR PIR; T08732; T08732.	
		DR InterPro; IPR007110; Ig-like.	
		DR PROSITE; PS50835; IG_LIKE; 2.	
		KW Hypothetical protein.	
		FT NON TER 1	
		SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;	
		Query Match	40.1%; Score 1158; DB 4; Length 407;
		Best Local Similarity	67.1%; Pred. No. 5e-89;
		Matches 241; Conservative 16; Mismatches 70; Indels 32; Gaps 5;	
		QY	86 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLDGGNETVAAICIAATGKPV 145
		Db	1 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLDGGNETVAAICIAATGKPV 60
		QY	146 HIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRRITCVVKHHPALEKDIRYSFI 205
		Db	61 HIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRRITCVVKHHPALEKDIRYSFI 120
		RESULT 10	
		Q8NC05	
		ID Q8NC05	PRELIMINARY; PRT; 267 AA.
		AC Q8NC05;	
		DT 01-OCT-2002 (TrEMBLrel. 22, Created)	
		DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)	
		DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)	
		DE Hypothetical protein FLJ90624.	
		OS Homo sapiens (Human).	
		OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
		OX NCBI_TaxID=9606;	
		RN [1]	
		RP SEQUENCE FROM N.A.	
		RC TISSUE=Placenta;	
		RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,	
		RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,	

Db 180 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQT----- 219

QY 296 IYISDVPFKQTSS-----RSCDKTHTCPPCPAPEAAGAPSVFLFPPKPKDITLMISRT 347

Db 220 -YICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDITLMISRT 278

QY 348 PEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 407

Db 279 PEVTCVAVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNG 338

QY 408 KEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSRDEMTKNQVSLTCLVKGYFSPSD 467

Db 339 KEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPSRDELTKNQVSLTCLVKGYFSPSD 398

QY 468 IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNY 527

Db 399 IAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNY 458

QY 528 TQKSLSLSPGK 538

Db 459 TQKSLSLSPGK 469

RESULT 8

Q7Z5W1

ID Q7Z5W1 PRELIMINARY; PRT; 470 AA.

AC Q7Z5W1;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

RA Strausberg R.;

RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC053984; AAK53984.1; -.

KW Hypothetical protein.

SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 43.4%; Score 1251.5; DB 4; Length 470;

Best Local Similarity 58.9%; Pred. No. 8.2e-97;

Matches 267; Conservative 28; Mismatches 61; Indels 97; Gaps 14;

QY 114 TVSLIKGPDSLIDGN-----ETVAAICIAATGK--PVAHID-W-EGDLGEMESTTSTFP 164

Db 87 TISRENAKDSLVLQWNSLRVGDAAVYYCARGAGRWAPLGAFDIWGQGTMTVTVSSASTKGP 146

QY 165 NETATIISQYKLFPTREFARG--RRITCVVVKHPALEKDIRYSFILDIQAPE-VSVTGYD 220

Db 147 -----SVFPLAPSSKSTSGTAAALGCLVK-----DYFPEPVTVS--- 180

QY 221 GNWVVGKGVNLKCNADANPPPKSVMSRLDQWPDGLLASDNTLHFVH--PLTFNYSGV 278

Db 181 -----WNSGALTSG-----VHTFPAVLQSSGL 202

QY 279 Y-----ICKVTNSLQQRSDQKVIYISDVPFKQTSS-----RSCDKTHTCPPCPAPEA 325

Db 203 YSLSSVTVTPSSSLGTQT-----YICNVNHNKPSNTKVDKKVEPKSCDKTHTCPPCPAPEL 257

QY 326 EGAPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 385

Db 258 LGGPSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREE 317

QY 386 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 445

Db 318 QYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPOVYITLPPS 377

QY 446 REEMTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 505

Db 378 RDELTKNQVSLTCLVKGYFSPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDK 437

QY 506 SRWQQGNVFCSCVMHEALHNYTKQSLSLSPGK 538

Db 438 SRWQQGNVFCSCVMHEALHNYTKQSLSLSPGK 470

RESULT 9

Q96PQ8

ID Q96PQ8 PRELIMINARY; PRT; 679 AA.

AC Q96PQ8;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Factor VII active site mutant immunoconjugate.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21477448; PubMed=11593034;

RA Hu Z., Garen A.;

RT "Targeting tissue factor on tumor vascular endothelial cells and tumor cells for immunotherapy in mouse models of prostatic cancer.";

RL Proc. Natl. Acad. Sci. U.S.A. 98:12180-12185 (2001).

RN [2]

RP SEQUENCE FROM N.A.

RA Hu Z., Garen A.;

RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF272774; AAK58686.2; -.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0005509; F:calcium ion binding; IEA.

DR GO; GO:0004263; F:chymotrypsin activity; IEA.

DR GO; GO:0004295; F:trypsin activity; IEA.

DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.

DR InterPro; IPR000152; Asx_hydroxyl_S.

DR InterPro; IPR009003; Cys_Ser_trypsin.

DR InterPro; IPR00742; EGF_2.

DR InterPro; IPR001881; EGF_Ca.

DR InterPro; IPR001438; EGF_II.

DR InterPro; IPR006209; EGF_like.

DR InterPro; IPR002383; GLA_blood.

DR InterPro; IPR006210; IEGF.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_cl.

DR InterPro; IPR003006; Ig_MHC.

Db 238 FARRRITCVVKKHFALEKDIRYSFILDQYAPESVTDYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGGLASDNTLHFVHPLTFNYSVGVYCKVNSNSLGORSQDKVIYISD 357
QY 301 VPFKQTSRSSCDKTHCTPPCPAPEAEGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHE 360
Db 358 PP-TTTTLOPTQVWHSSP----ADVQDIATEHKKLPPLSTLATLKDGTIGTIIASVVG 412
QY 361 DPEVKFNWYVDGVEVHNAKTKPREEQYNSTY-----RVSVLTVLHQDWLNGKEYKCKV 414
Db 413 ALFLVLVSILAGVFCYRRRTFRGDYFAKNYTPPSDMQKESQIDVLHQDELDSYPDSVK 472
QY 415 SNKALPAPIEKTISK 429
Db 473 ENK---NPVNNLIRK 484

RESULT 6
Q7Z351 ID Q7Z351 PRELIMINARY; PRT; 482 AA.
AC Q7Z351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686N02209.
GN DKFZp686N02209.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; EDA75F1901D1A034 CRC64;

Query Match 44.0%; Score 1269; DB 4; Length 482;
Best Local Similarity 50.4%; Pred. No. 2.8e-98;
Matches 283; Conservative 52; Mismatches 98; Indels 128; Gaps 17;

QY 1 GPIIVEPHVTAVGKNVSLKCLIE-VNETITQISW-EKIHGSSQTAV-----HHPQYG 53
Db 27 GGSVVQP-----GRSLRLSCIASGFSFGSAMHWRQIPGKLEWAVAVISYDGNHKLYS 80
QY 54 FSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP 113
Db 81 DSVKGRF---TISRDNKSKLLFLHVNLSLTSADTAIYYCAR-----DFHSKTTTSIFGLIP 131
QY 114 TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQ 173
Db 132 LYFYYSAMDY---WGRGTTTVIVSSASTKGP-----SVFPLAPSSKSTSGGTAA---- 176
QY 174 YKLPFTRFARRRITCVVKKHFALEKDIRYSFILDQYAPE-VSVTGYDGNWFVGRKGVNL 232
Db 177 -----LGCLVK-----DYFPEPVTVS----- 192
QY 233 KCNADANPPPFKSVWSRLDQWPDGGLASDNTLHFVH--PLTFNYSGVY-----ICKVTN 285
Db 193 -----WNSGALTSG-----VHTFPAVLQSSGLYSLSSVVTVPSS 226
QY 286 SLGQRSQDKVIYISDVPFKQTS-----RSCDKTHTCPCPAPEAEGAPSVFLFPPK 337
Db 227 SLGTQT-----YICNVNHKPSNTKVDKKVEPKSCDKTHTCPCPAPELLGGPSVFLFPPK 281
QY 338 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 397

Db 282 PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVL 341
QY 398 TVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSREEMTKNQVSLT 457
Db 342 TVLHQDWLNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYVTLPPSRDELTKNQVSLT 401
QY 458 CLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 517
Db 402 CLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFS 461
QY 518 VMHEALHNHYTQKSLSLSPGK 538
Db 462 VMHEGLHNHYTQKSLSLSPGK 482

RESULT 7
Q7Z7P5 ID Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheraia; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
KW Hypothetical protein.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 43.4%; Score 1253.5; DB 4; Length 469;
Best Local Similarity 60.8%; Pred. No. 5.5e-97;
Matches 262; Conservative 26; Mismatches 53; Indels 90; Gaps 12;

QY 129 NETVAAICIAATGKPVAHID-W-EGDLGEMESTTSPNETATISQYKLFTRFARG-- 184
Db 108 DDTALFYCATKSRGQVGDFDSWGQGTTLTVSSASTKGP-----SVFPLAPSSKSTSGG 160
QY 185 -RRITCVWKHPALEKDIRYSFILDQYAPE-VSVTGYDGNWFVGRKGVNLKCNADANPPP 242
Db 161 TAALGCLVK-----DYFPEPVTVS----- 179
QY 243 FKSWSRLDQWPDGGLASDNTLHFVH--PLTFNYSGVY-----ICKVTNSLGORSQDKV 295

Db 298 PPFKSVMSRLDGMPPDGLLASDNTLHFVHPLTVNYSGVYVCKVSNLSLQORSQDKVIYISD 357

QY 301 VPFXQTSS 308

Db 358 IPLTQTSS 365

RESULT 4

Q9JLB9 PRELIMINARY; PRT; 549 AA.

AC Q9JLB9; 17, Created)

DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)

DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Cell adhesion molecule nectin-3 alpha.

GN PVRL3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=20209403; PubMed=10744716;

RX Sato-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,

RA Tachibana K., Mizoguchi A., Takai Y.;

RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules

RT that shows homophilic and heterophilic cell-cell adhesion

RT activities.";

RL J. Biol. Chem. 275:10291-10299(2000).

DR EMBL; AF195833; AAF63685.1; -.

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005913; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;

Query Match 54.8%; Score 1581; DB 11; Length 549;

Best Local Similarity 72.4%; Pred. No. 1.7e-124;

Matches 315; Conservative 29; Mismatches 77; Indels 14; Gaps 4;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60

Db 58 GSIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGDY 117

QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDCGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180

Db 178 PDSLIDCGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237

QY 181 FARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297

QY 241 PPFKSVMSRLDGMPPDGLLASDNTLHFVHPLTVNYSGVYICKVTNSLQORSQDKVIYISD 300

Db 298 PPFKSVMSRLDGMPPDGLLASDNTLHFVHPLTVNYSGVYICKVTNSLQORSQDKVIYISD 357

QY 301 VPFXQTSSRSCDKTHTCPPCPAPEGAPSVLFPFKPKDTLMISRTPEVTCVVDVSHS 360

Db 358 PP-TTTTLOPTVQWSSP-ADVQDIATEHKKLPFPLSTLATLKDDTIGTIIASVWGG 412

QY 361 DPEVKFNWYVDGVEVHNAKTPREEQYNSTY-----RVVSVLTVLHQDLNKGKEYCKV 414

Db 413 ALFLVLVSLAGVFCYRRRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSYPDSVKK 472

QY 415 SNKALPAPIEKTISK 429

Db 473 ENK---NPVNNLIRK 484

RESULT 5

Q9D006 PRELIMINARY; PRT; 549 AA.

AC Q9D006; 17, Created)

DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)

DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE 2610301B19Rik protein.

GN PVRL3 OR 2610301B19RIK.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momabaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

DR EMBL; AK011949; BAB27933.1; -.

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005913; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

SQ SEQUENCE 549 AA; 60703 MW; 32775CBE7319B32 CRC64;

Query Match 53.3%; Score 1537; DB 11; Length 549;

Best Local Similarity 70.6%; Pred. No. 8.7e-121;

Matches 307; Conservative 32; Mismatches 82; Indels 14; Gaps 4;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60

Db 58 GSIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGDY 117

QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDCGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180

Db 178 PDSLIDCGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237

QY 181 FARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPT 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPT 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VPFKQTSSRCDKTHTCPPEAPAEAGPSV-----FLFPPK-----PKDTLMISRTPEVT 351
Db 358 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFPLSTLTIKODTIA 403
QY 352 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNSTY-----RVVSVLTVLHQDWL 405
Db 404 TTIASVVGALFIVLVSVLGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDEL 463
QY 406 NGKEYKCKVSNKALPAPIEKTISK 429
Db 464 DSYDPSVKKENK---NPVNNLIRK 484

RESULT 2

Q9JLB7
ID Q9JLB7 PRELIMINARY; PRT; 438 AA.
AC Q9JLB7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 gamma.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195835; AAF63687.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;

Query Match 54.8%; Score 1582; DB 11; Length 438;
Best Local Similarity 95.5%; Pred. No. 1e-124;
Matches 294; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPT 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPT 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VPFKQTSS 308
Db 358 IPLTQTSS 365

RESULT 3

Q9JLB8
ID Q9JLB8 PRELIMINARY; PRT; 510 AA.
AC Q9JLB8;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 beta.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195834; AAF63686.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;

Query Match 54.8%; Score 1582; DB 11; Length 510;
Best Local Similarity 95.5%; Pred. No. 1.3e-124;
Matches 294; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPT 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPT 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 43.694 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-14_COPY_58_595
Perfect score: 2886
Sequence: 1 GPIIVEPHVTAVWGKNVSLK.....MHEALHNHYTQKSLSLSPGK 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1613	55.9	549	4 Q9NQS3	Q9nqe3 homo sapien
2	1582	54.8	438	11 Q9JLB7	Q9jlb7 mus musculu
3	1582	54.8	510	11 Q9JLB8	Q9jlb8 mus musculu
4	1581	54.8	549	11 Q9JLB9	Q9jlb9 mus musculu
5	1537	53.3	549	11 Q9D006	Q9d006 mus musculu
6	1269	44.0	482	4 Q7Z351	Q7z351 homo sapien
7	1253.5	43.4	469	4 Q7Z7P5	Q7z7p5 homo sapien
8	1251.5	43.4	470	4 Q7Z5W1	Q7z5w1 homo sapien
9	1234.5	42.8	679	4 Q96PQ8	Q96pq8 homo sapien
10	1218	42.2	267	4 Q8NC05	Q8nc05 homo sapien
11	1158	40.1	407	4 Q9Y412	Q9y412 homo sapien
12	1157	40.1	473	4 Q8TC63	Q8tc63 homo sapien
13	1149	39.8	354	4 Q86TT2	Q86tt2 homo sapien
14	1149	39.8	521	4 Q8N4Y9	Q8n4y9 homo sapien
15	1134	39.3	509	4 Q8NF17	Q8nf17 homo sapien
16	910.5	31.5	337	6 Q95M34	Q95m34 equus cabal

17	876	30.4	470	11 Q7TMK1	Q7tmk1 mus musculu
18	864.5	30.0	463	11 Q99LC4	Q99lc4 mus musculu
19	855.5	29.6	437	11 Q9R1A4	Q9r1a4 mus musculu
20	853.5	29.6	469	11 Q8R3V9	Q8r3v9 mus musculu
21	835.5	29.0	473	11 Q9D8L4	Q9d8l4 mus musculu
22	805.5	27.9	473	11 Q99L25	Q99l25 mus musculu
23	800	27.7	468	11 Q99L31	Q99l31 mus musculu
24	799	27.7	474	11 Q8R3H6	Q8r3h6 mus musculu
25	784.5	27.2	473	11 Q91Z05	Q91z05 mus musculu
26	631	21.9	304	4 Q9BVA9	Q9bva9 homo sapien
27	534.5	18.5	295	11 Q9ERF5	Q9erf5 mesocricetu
28	528	18.3	298	6 Q9GL74	Q9gl74 cercopithec
29	526.5	18.2	295	6 Q9GL75	Q9gl75 bos taurus
30	469.5	16.3	510	4 Q96NY8	Q96ny8 homo sapien
31	469.5	16.3	510	4 Q96K15	Q96k15 homo sapien
32	455	15.8	613	4 Q96EY0	Q96ey0 homo sapien
33	451.5	15.6	483	11 Q9DBP8	Q9dbp8 mus musculu
34	451.5	15.6	508	11 Q8R007	Q8r007 mus musculu
35	451.5	15.6	508	11 Q8CED8	Q8ced8 mus musculu
36	451	15.6	613	4 Q8WUK1	Q8wuk1 homo sapien
37	449.5	15.6	597	4 Q9BQB8	Q9bqb8 homo sapien
38	447.5	15.5	597	4 Q9BU10	Q9bul0 homo sapien
39	446	15.5	614	4 Q96GA6	Q96ga6 homo sapien
40	445.5	15.4	597	4 Q96BB9	Q96bb9 homo sapien
41	437.5	15.2	588	4 Q8WUX4	Q8wux4 homo sapien
42	437.5	15.2	618	4 Q96AA6	Q96aa6 homo sapien
43	427	14.8	530	11 Q80XJ5	Q80xj5 mus musculu
44	420.5	14.6	614	11 Q7TMT6	Q7tmt6 mus musculu
45	419	14.5	467	11 Q91VT9	Q91vt9 mus musculu

ALIGNMENTS

RESULT 1
Q9NQS3
ID Q9NQS3 PRELIMINARY; PRT; 549 AA.
AC Q9NQS3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;

Query Match 55.9%; Score 1613; DB 4; Length 549;
Best Local Similarity 73.4%; Pred. No. 3.4e-127;
Matches 326; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

Qy	1	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 60
Db	58	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 117
Qy	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

Db 139 VDISQNDPEVRFSWFIDDDVEVHTAQTHAPEKQSNSTLRSVSELPVHRDWLNGKTFCKV 198

QY 415 SNKALPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWES 474

Db 199 NSGAFFAPAPIEKISLKPEGTPRGPQVYTMAPPKEEMTSQVSIITCMVKGFYPPDIYTEWK 258

QY 475 NGOPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKQSLSL 534

Db 259 NGQPQENYKNTPTMTDGTGSYFLYSKLVNKKETWQQGNTFTCSVLHEGLHNHHTKSLSH 318

QY 535 SPGK 538

Db 319 SPGK 322

RESULT 15

GCAA MOUSE STANDARD; PRT; 330 AA.

AC P01863;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig gamma-2A chain C region, A allele.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=81076554; PubMed=6777755;

RA Sikorav J.-L., Auffray C., Rougeon F.;

RT "Structure of the constant and 3' untranslated regions of the murine

RT Balb/c gamma 2a heavy chain messenger RNA.";

RL Nucleic Acids Res. 8:3143-3155(1980).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=81198976; PubMed=6262729;

RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;

RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene

RT and evolution of heavy chain genes: further evidence for intervening

RT sequence-mediated domain transfer.";

RL Nucleic Acids Res. 9:1365-1381(1981).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=81223894; PubMed=6787604;

RA Ollo R., Auffray C., Mochamps C., Rougeon F.;

RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes

RT suggests that exons can be exchanged between genes in a multigenic

RT family.";

RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).

RN [4]

RP MYELOMA PROTEIN MOPC 173.

RX MEDLINE=74175517; PubMed=4831970;

RA Bourgois A., Fougereau M., Rocca-Serra J.;

RT "Determination of the primary structure of a mouse IgG2a

RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications

RT for the evolution of immunoglobulin structure and function.";

RL Eur. J. Biochem. 43:423-435(1974).

RN [5]

RP DISULFIDE BONDS.

RX MEDLINE=73056887; PubMed=4565406;

RA de Preval C., Fougereau M.;

RT "Determination of the primary structure of a mouse gamma G2a

RT immunoglobulin. Identification of the disulfide bridges.";

RL Eur. J. Biochem. 30:452-462(1972).

CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.

CC -----

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CC -----

DR EMBL; V00798; CAA24178.1; -. 1

DR PIR; A02152; G2MSA. 2

DR PDB; 1E4W; 12-JUL-01. 3

DR PDB; 1E4X; 12-JUL-01. 4

DR PDB; 1MNU; 06-MAY-99. 5

DR InterPro; IPR007110; Ig-like. 6

DR InterPro; IPR003597; Ig_c1. 7

DR InterPro; IPR003006; Ig_MHC. 8

DR Pfam; PF00047; ig; 2. 9

DR SMART; SM00407; IGc1; 2. 10

DR PROSITE; PS50835; IG_LIKE; 3. 11

DR PROSITE; PS00290; IG_MHC; 1. 12

KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.

FT NON TER 1 98

FT DOMAIN 6 98

FT DOMAIN 121 220

FT DOMAIN 229 325

FT DISULFID 15 15

FT DISULFID 27 82

FT DISULFID 107 107

FT DISULFID 110 110

FT DISULFID 112 112

FT DISULFID 144 204

FT DISULFID 250 308

FT MOD RES 330 330

SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 27.8%; Score 801; DB 1; Length 330;

Best Local Similarity 52.3%; Pred. No. 2.4e-49;

Matches 158; Conservative 38; Mismatches 74; Indels 32; Gaps 5;

QY 266 HFVHPLTFNY-----SGVYI--CKVTNSLQGRSDQKVIYISDVPEFKQTSSRSCDKTH-- 315

Db 32 YFPEPVTLTNWNSGSLSSGVHTFPFPAVLQSDLYTLSSSVTVTSSTWP---SQSITCNVAHPA 88

QY 316 -----TCPP--CPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVD 356

Db 89 SSTKVKKIEPRGPTIKPCPPCKCPAPNLLGGPSVFIFPPKIKDVLMISSLSPITCVVVD 148

QY 357 VSHEDPEVKFNWYVDGVEVHNATKPREEQYNSTYRVVSVLTVHLQDNLNGKEYCKKVS 416

Db 149 VSEDDPDVQISWFWNNVEVHTAQCTHREDYNSLTIRVVSALPIQHDWMSGKEFKCKVNN 208

QY 417 KALPAPIEKTISKAKGQPREPQVYTLPPSRREEMTKNQVSLTCLVKGFYPSDIAVEWESNG 476

Db 209 KDLPAPIERTISKPKGVRAPQVYVLPPEEEMTKKQVTLTCWVTDMPEDIIYVEWTNNG 268

QY 477 OPENNYKTTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTKQSLSLSP 536

Db 269 KTELNYKNTEPVLDSDGSYFMYSKLRVEKKNWVERNSYSCSVVHEGLHNHHTTKSFSRTP 328

QY 537 GK 538

Db 329 GK 330

Search completed: April 12, 2004, 09:39:50

Job time : 9.59785 secs

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Db      211 PSPIKTIKPRGKARTPQVYTIIPPREQMSKNKVSILTCMVTFSYPASISVEWERNGELE 270
      Qy      480 NNYKTTTPVLDSGFFLYSKLTVDKSRWQGNVFCVMHEALHNHYTKSLSLSPGK 538
      Db      271 QDYKNTLPVLDSDSYFLYKLSVDITDWMRGDIYTCVVHEALHNHYTKSLSRSPGK 329

RESULT 14
GCA_RAT
ID_GCA_RAT STANDARD; PRT; 322 AA.
AC P20760;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2A chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M13804; AAA41376.1; ALT_INIT.
DR PIR; PS0019; PS0019.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON_TER 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 115 212 IG-LIKE 2.
FT DOMAIN 221 317 IG-LIKE 3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 136 196
FT DISULFID 242 300
FT CARBOHYD 172 172
SQ SEQUENCE 322 AA; 35186 MW; E8EA136A9DE01EDB CRC64;

Query Match 28.1%; Score 811.5; DB 1; Length 322;
Best Local Similarity 53.0%; Pred. No. 4.2e-50;
Matches 161; Conservative 42; Mismatches 60; Indels 41; Gaps 8;

QY 254 WPDGLLASDNTLHFVHPLTFN---YSGVYICKVTNSLQGRSDQKVIYISDVPEKQTSR- 309
Db 41 WNSGALSSG-----VH--TFPAVLQSGLY--TLTSSV-----TVPSSTWSSQA 79

QY 310 -SCDKTH-----TCPPCPAPEAGAPSVFLPPPKDITLMISRTPEVTCVV 354
Db 80 VTCNVAHPASSTKVDKIVPRECNPCGCTGSE-VSSVFIFPPKTKDVLITLTPKVTGV 138

QY 355 VDVSHEDPEVKFNWYVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKV 414

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[illegible]

Db 34 PEPVTVTN--SGSLSSGVHTFPAVLQSDLYTLSSSVTV-----PSSPRPSETVTCNVAHP 87

Qy 286 SLGQRSDQKVIYISDVFPFKQTSSRSCDKTHTCPP--CPAPEAEGAPSVFLFPKPKDTLM 343

Db 88 ASSTKVDDKKIV-----PRDCG-----CKPCICTVPEVS---SVFIFFPKPKDVL 129

Qy 344 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVQLHOD 403

Db 130 ITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQD 189

Qy 404 WLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGF 463

Db 190 WLNKKEFKCRVNSAAPPAPIEKTISKTKGPKAPQVYTIPPPKEQMAKDKVSLTCTMITDF 249

Qy 464 YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVSCSVMHEAL 523

Db 250 FPEDITVEWQWNGQPAENYKNTQPIMTNGSYFVYSKLVNQQKSWEAGNTFTCSVLHEGL 309

Qy 524 HNHYTQKSLSLSPGK 538

Db 310 HNHHTKSLSHSPGK 324

RESULT 12

GC1M_MOUSE STANDARD; PRT; 393 AA.

AC P01869;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Ig gamma-1 chain C region, membrane-bound form.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=80045036; PubMed=115593;

RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Mano Y.;

RT "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene.";

RL Cell 18:559-568(1979).

RN [2]

RP SEQUENCE OF 323-393 FROM N.A.

RX MEDLINE=82197626; PubMed=6804950;

RA Tyler B.M., Cowman A.F., Gerondakis S.D., Adams J.M., Bernard O.;

RT "mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmembrane sequence and a 28-residue intracellular domain.";

RT Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).

RN [3]

RP SEQUENCE OF 323-366 FROM N.A.

RX MEDLINE=82115295; PubMed=6799207;

RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M., Eisenberg D., Wall R.;

RT "Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma chains.";

RL Cell 26:19-27(1981).

RN [4]

RP SEQUENCE OF 1-44 FROM N.A.

RX MEDLINE=82222190; PubMed=6283537;

RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;

RT "Nucleotide sequences of gene segments encoding membrane domains of immunoglobulin gamma chains.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=Membrane-bound;

CC Isoid=P01869-1; Sequence=Displayed;

CC Name=Secreted;

CC Isoid=P01868-1; Sequence=External;

CC Note=May be the major isoform;

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CC -----

DR EMBL; V00793; CAA24172.1; -

DR EMBL; V00793; CAA24173.1; -

DR EMBL; V00793; CAA24174.1; -

DR PIR; B02159; G1MSM.

DR PDB; 15C8; 23-MAR-99.

DR PDB; 1AE6; 18-MAR-98.

DR PDB; 1CL7; 12-JAN-00.

DR PDB; 1F11; 06-FEB-01.

DR PDB; 1F58; 29-DEC-99.

DR PDB; 1KC5; 24-JUL-02.

DR PDB; 1KCR; 11-MAY-02.

DR PDB; 25C8; 09-JUL-99.

DR MGD; MGI:96446; Igh-4.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00407; Igc1; 2.

DR PROSITE; PS50835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 1.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW Alternative splicing; Transmembrane; 3D-structure.

FT NON_TER 1 1

FT DOMAIN 1 97 CH1.

FT DOMAIN 98 110 HINGE.

FT DOMAIN 111 217 CH2.

FT DOMAIN 218 324 CH3.

FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 138 198 N-LINKED (GLCNAC. .).

FT CARBOHYD 174 174 POTENTIAL.

FT DISULFID 244 302 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 340 357

FT DOMAIN 358 393

SQ SEQUENCE 393 AA; 43386 MW; 4CC88343B7A1CE27 CRC64;

Query Match 28.6%; Score 825.5; DB 1; Length 393;

Best Local Similarity 50.0%; Pred. No. 5.7e-51;

Matches 157; Conservative 52; Mismatches 65; Indels 40; Gaps 8;

Qy 240 PPPFKSVWSRLDQWPDGL-----LASDNTLHFVHPLTFNYSGVYICKVTN- 285

Db 34 PEPVTVTN--SGSLSSGVHTFPAVLQSDLYTLSSSVTV---PSSPRPSETVTCNVAHP 87

Qy 286 SLGQRSDQKVIYISDVFPFKQTSSRSCDKTHTCPP--CPAPEAEGAPSVFLFPKPKDTLM 343

Db 88 ASSTKVDDKKIV-----PRDCG-----CKPCICTVPEVS---SVFIFFPKPKDVL 129

Qy 344 ISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVQLHOD 403

Db 130 ITLTPKVTCTVVVDISKDDPEVQFSWFVDDVEVHTAQTQPREEQFNSTFRSVSELPIMHQD 189

Qy 404 WLNKKEYCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSREEMTKNQVSLTCLVKGF 463

Db 190 WLNKKEFKCRVNSAAPPAPIEKTISKTKGPKAPQVYTIPPPKEQMAKDKVSLTCTMITDF 249

Qy 464 YPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSLKLTVDKSRWQQGNVSCSVMHEAL 523

Db 250 FPEDITVEWQWNGQPAENYKNTQPIMTNGSYFVYSKLVNQQKSWEAGNTFTCSVLHEGL 309

Qy 524 HNHYTQKSLSLSPG 537

Matches 161; Conservative 48; Mismatches 55; Indels 43; Gaps 8;	
QY	254 WPDGLLASDNTLHFVHPLTFN---YSGVY-----ICKVTN-SLGQRS 291
Db	41 WNSGALSSG-----VH--TFPAVLQSGLYTLTSSVTPSSWPSQVTCNVAHPASSTKV 93
QY	292 DQKVIYISDVFFKQTSRSCDKTHTCPPCPAPEAEGAPSVLFPKPKDTLMISRTPEVT 351
Db	94 DKKIV-----PRNCG--GDCXPCICTGSE--VSSVFIFPPKPKDVLITILTPKVT 139
QY	352 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYK 411
Db	140 CVVVDISQDDPEVHFSWFVDVVEVHTAQTRPPEEQFNSTERSVSELPILHQDWLNGRTER 199
QY	412 CKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVE 471
Db	200 CKVTSAAFPSPIEKTIKPEGRITQVPHVYTMSPTEKEMTQNEVSIITCMVKGFYPPIYVE 259
QY	472 WESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKS 531
Db	260 WQWNGQPQENYKNTPTMTDTSYFLYSLNKKVKEKQQGNFTFCSVLHEGLHNHHTKS 319
QY	532 LSLSPGK 538
Db	320 LSHSPGK 326

RESULT 9	
GC3M_MOUSE	STANDARD; PRT; 333 AA.
AC	P03987;
DT	01-FEB-1991 (Rel. 17, Created)
DT	01-FEB-1991 (Rel. 17, Last sequence update)
DT	10-OCT-2003 (Rel. 42, Last annotation update)
DE	Ig gamma-2B chain C region.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCBI_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=89232738; PubMed=3149946;
RA	Brueggemann M.;
RT	"Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL	Gene 74:473-482(1988).
CC	-!- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR	PIR; PS0018; PS0018.
DR	HSSP; P01842; 7FAB.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PF00047; Ig; 3.
DR	SMART; SM00407; IGcl; 2.
DR	PROSITE; PS50835; IG LIKE; 3.
DR	PROSITE; PS00290; IG_MHC; 1.
KW	Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT	NON_TER 1 1
FT	DOMAIN 6 96 IG-LIKE 1.
FT	DOMAIN 124 223 IG-LIKE 2.
FT	DOMAIN 232 328 IG-LIKE 3.
FT	DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT	DISULFID 27 80
FT	DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT	DISULFID 147 207
FT	DISULFID 253 311
SQ	SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 29.0%; Score 836; DB 1; Length 333;
Best Local Similarity 53.6%; Pred. No. 8.2e-52;
Matches 162; Conservative 43; Mismatches 71; Indels 26; Gaps 5;

QY	254 WPDGLLASDNTLHFVHPLTFN---YSGVYICKVTNSILGQRSQDKVIYISDVFPKQTSR- 309
Db	41 WNSGALSSD-----VH--TFPAVLQSGLY--TLTSSVTSSWPSQVTCNVAHPASSTKV 91
QY	310 -----SCDKTHTCPPCPAPEAEGAPSVLFPKPKDTLMISRTPEVTCVVVD 356
Db	92 DKKVERRNGGIGHKCPTCPTCHKCPVPELLGGPSVFIFPPKPKDILLISQNAKVTICVVVD 151
QY	357 VSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCVSN 416
Db	152 VSEEPDVQFSWFVNNEVHTAQTPREEQYNSTFRVSALPIQHODWMSGKEFKCKVNN 211
QY	417 KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG 476
Db	212 KALPSPIEKTISKPKGLVRKPKQVYVMGPPTEQLTEQVSLTCLTSGFLPNDIGVEWTSNG 271
QY	477 QPENNYKTTTPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSP 536
Db	272 HIEKNYKNTPEVMDSDGSFFMYSKLNVERSRWDSRAPFVCSVVHEGLHNHHVEKISRPP 331
QY	537 GK 538
Db	332 GK 333
RESULT 10	
GC3M_MOUSE	
ID	GC3M_MOUSE STANDARD; PRT; 398 AA.
AC	P03987;
DT	23-OCT-1986 (Rel. 02, Created)
DT	01-AUG-1991 (Rel. 19, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	Ig gamma-3 chain C region, membrane-bound form.
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=85027161; PubMed=6092053;
RA	Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA	Tucker P.W., Blattner F.R.;
RT	"Structural analysis of the murine IgG3 constant region gene.";
RL	EMBO J. 3:2041-2046(1984).
RN	[2]
RP	SEQUENCE OF 328-398 FROM N.A.
RX	MEDLINE=84041483; PubMed=6314258;
RA	Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA	Wall R.;
RT	"The structure of the mouse immunoglobulin in gamma 3 membrane gene
RT	segment.";
RL	Nucleic Acids Res. 11:6775-6785(1983).
CC	-----
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; J00451; AAB59655.1; -.
DR	EMBL; V01526; CAA24767.1; ALT_SEQ.
DR	PIR; A02156; G3MSM.
DR	HSSP; P01857; 1FC1.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	Pfam; PF00047; Ig; 3.
DR	SMART; SM00407; IGcl; 2.
DR	PROSITE; PS50835; IG LIKE; 3.
DR	PROSITE; PS00290; IG_MHC; 1.


```
QY 253 QWPDGLASDNTLHFVHPLTFN---YSGVYICKVTNSLQGRSDQKVYIISDVPPKQTSSR 309
Db 41 KWSGALTSG-----VH--TFPAVLQSGLY--SLTSMVTVPSSQKATCNVAHP----ASST 88
QY 310 SCDKT-----HTCPCPAPEAEGAPSVFLFPPKPKDTLMSRTPEVTCVVVDVS 358
Db 89 KVDKTVPIRTPZBPBCTCKPCPPENLGGPSVFIFPPKPKDTLMSLTSPRVTCTVVVDVS 148
QY 359 HEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 418
Db 149 QDEPEVQFTWFVDNKPVGNAETKPRVEQYNTTFRVESVLPQHODWLRGKEFKCKVYNKA 208
QY 419 LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP 478
Db 209 LPAPIEKTISKTKGAPRMPDVTYTLPPSRDELSSKVSVCCLIINFFPADIHVEWASNRVP 268
QY 479 --ENNYKTTPPVLDSGDFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 536
Db 269 VSEKEYKNTPIEDADGSYFLYSKLTVDKSAWDQGTIVYTCVSMHEALHNHYTQKALSRS 328
QY 537 G 537
Db 329 G 329
```

```
RESULT 7
GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR HSSP; P01857; 1FC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
SQ SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;
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Query Match 29.3%; Score 845; DB 1; Length 329;

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Best Local Similarity 54.6%; Pred. No. 1.9e-52;
Matches 165; Conservative 43; Mismatches 62; Indels 32; Gaps 6;
QY 266 HFVHPLT--FNY-----SGVYICKVTNSLQGRSDQKVYIISDVPPKQTSSRS--CDKTH-- 315
Db 31 YFPEPVTKWNYGALSSGV--RTVSSVLQSGFYSLSSLVTVPSSTWPSQTVICNVARPA 87
QY 316 -----TCPP---CPAPEAEGAPSVFLFPPKPKDTLMSRTPEVTCVVVD 356
Db 88 SKTELIKRIEPRIPKSTPPGSSCPPGNILGGPSVFIFPPKPKDALMISLTTPKVTCTVVVD 147
QY 357 VSHEDPEVKFNWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSN 416
Db 148 VSEDDPDVHVSFWVDNKEVHTAWTPREAQYNSTFRVVSALPIQHODWMRGKEFKCKVNN 207
QY 417 KALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNG 476
Db 208 KALPAPIERTISKPKGRAQTPQVYTIPPPREQMSKKVSLTCLVTNFFSEALSVEWERN 267
QY 477 QPENNYKTTPPVLDSGDFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSP 536
Db 268 ELEQDYKNTPPILDSGTYFLYSKLTVDTDSWLQGRIFTCSVVHEALHNHHTQKNLSRSP 327
QY 537 GK 538
Db 328 GK 329
```

```
RESULT 8
GC1_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102
FT DISULFID 106 106
FT DISULFID 109 109
FT DISULFID 111 111
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EF49B9DA CRC64;
N-LINKED (GLCNAC...) (POTENTIAL).
```

Query Match 29.1%; Score 840.5; DB 1; Length 326;
Best Local Similarity 52.4%; Pred. No. 3.9e-52;

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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; M16426; AAA31289.1; -.
DR PIR; A91749; GHRB.
DR HSSP; P01857; 1PC1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON TER 1 1 IG-LIKE 1.
FT DOMAIN 6 96 IG-LIKE 2.
FT DOMAIN 114 213 IG-LIKE 3.
FT DOMAIN 222 318 T -> M (IN D11 MARKER).
FT VARIANT 104 104 T -> A (IN E15 MARKER).
FT VARIANT 185 185 N -> E (IN REF. 2).
FT CONFLICT 48 48 V -> VPV (IN REF. 2).
FT CONFLICT 71 71 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 144 144 N -> D (IN REF. 5).
FT CONFLICT 173 173 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 187 187 N -> D (IN REF. 5).
FT CONFLICT 201 201 Q -> E (IN REF. 5).
FT CONFLICT 218 218 E -> Q (IN REF. 5).
FT CONFLICT 233 233 N -> D (IN REF. 5).
FT CONFLICT 246 246 E -> G (IN REF. 5).
FT CONFLICT 256 256 N -> D (IN REF. 5).
FT CONFLICT 260 260 Y -> W (IN REF. 5).
FT CONFLICT 266 266 N -> S (IN REF. 5).
FT CONFLICT 280 280 N -> S (IN REF. 5).
FT CONFLICT 284 284
SQ SEQUENCE 323 AA; 35404 MW; 69E8AA118D579A8B CRC64;

Query Match 31.4%; Score 906.5; DB 1; Length 323;
Best Local Similarity 58.4%; Pred. No. 8.5e-57;
Matches 180; Conservative 38; Mismatches 63; Indels 27; Gaps 8;

QY 240 PPPFKSVWSRLDQWPDGLLASDNTLHFVHLPTFNYSGVY----ICKVTNSLQGRSDQKV 295
Db 34 PEPVTVTNW--SGTLTNGVR-----TFPSVRQSSGLYSLSSVSVTS-----SSQPV 78
QY 296 IYISDVFPKQTSRSCDKT---HTC--PPCPAPEAEGAPSVFLFPKPKDITLMISRTPEV 350
Db 79 --TCNVVAPATNTK-VDKTVAPSTCSKPTCPPPELLGPPSVFIFPPKPKDITLMISRTPEV 135
QY 351 TCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEY 410
Db 136 TCVVVDVSDQDDPEVFQFTWYINNEQVETARPPLRQQFNSTIRVSTLPIHQDWLNGKEY 195
QY 411 KCKVSNKALPAPIEKTISKAKGQPREPPQVYITLPPSREEMTKNQVSLTCLVKGFYPSDIAV 470
Db 196 KCKVSNKALPAPIEKTISKARGQPLEPKVYTMGPPREELSSRSVSLTCMINGFYPSDISV 255
QY 471 EWESNGQPENNYKTTTPVLDSDGSPFLYSLKLTVDKSRWQQGVFSCSVMEALHNYHTQK 530
Db 256 EWEKNGKAEDNYKTTTPAVLSDGSGFYLYNKLSVPTSEWQRGDVFTCSVMHEALHNYHTQK 315
QY 531 SLSLSPGK 538
Db 316 SISRSPGK 323

RESULT 6
GC2_CAVPO STANDARD; PRT; 329 AA.
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-2 chain C region.
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystriognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE OF 1-3.
RA Trischmann T.M.;
RL Submitted (APR-1975) to the PIR data bank.
RN [2]
RP SEQUENCE OF 4-68.
RX MEDLINE=71058471; PubMed=5538606;
RA Birshtein B.K., Hussain Q.Z., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
RT half-cysteine joining heavy and light chains.";
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE=71058486; PubMed=5538616;
RA Turner K.J., Cebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
RT and hinge region cyanogen bromide fragments.";
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE=75036072; PubMed=4429665;
RA Tracey D.E., Cebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE=75036073; PubMed=4609467;
RA Trischmann T.M., Cebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
RT antibodies.";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -!- MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC 13 inbred guinea pigs.
DR PIR; A94553; G2GP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164DIFBA9 CRC64;

Query Match 30.7%; Score 886; DB 1; Length 329;
Best Local Similarity 59.5%; Pred. No. 2.4e-55;
Matches 179; Conservative 31; Mismatches 63; Indels 28; Gaps 7;

CC of the CH1 region, and part of the hinge compared with normal
CC gamma-3 heavy chains.
CC -!- MISCELLANEOUS: Disease protein OMM may represent an allelic form
CC or another gamma chain subclass.
CC -!- MISCELLANEOUS: The hinge region in gamma-3 chains is about four
CC times as long as in other gamma chains and contains three
CC identical 15-residue segments preceded by a similar 17-residue
CC segment (12-28).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00231; AAA52805.1; ALT_SEQ.
CC HSP; P01857; 1FC1.
CC Genew; HGNC:5527; IGHG3.
CC MIM; 147120; -.
CC GO; GO:0005624; C:membrane fraction; NAS.
CC GO; GO:0003823; F:antigen binding; TAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig_cl.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; ig; 2.
CC SMART; SM00407; IGC1; 1.
CC PROSITE; PS50835; IG_LIKE; 2.
CC PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein; Repeat;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 12 73 HINGE.
FT DOMAIN 74 183 CH2.
FT DOMAIN 184 289 CH3.
FT REPEAT 29 43
FT REPEAT 44 58
FT REPEAT 59 73
FT MOD_RES 1 1
FT CARBOHYD 6 6
FT DISULFID 7 7
FT DISULFID 24 24
FT DISULFID 27 27
FT DISULFID 33 33
FT DISULFID 39 39
FT DISULFID 42 42
FT DISULFID 48 48
FT DISULFID 54 54
FT DISULFID 57 57
FT DISULFID 63 63
FT DISULFID 69 69
FT DISULFID 72 72
FT CARBOHYD 140 140
FT MOD_RES 290 290
FT VARIANT 126 127
FT VARIANT 134 134
FT VARIANT 139 139
FT VARIANT 182 182
FT VARIANT 227 227
FT VARIANT 227 227
FT VARIANT 279 279
FT SEQUENCE 290 AA; 32331 MW; E69CBC95705B2F46 CRC64;
Query Match 39.1%; Score 1129; DB 1; Length 290;
Best Local Similarity 89.6%; Pred. No. 1.5e-72;

Matches 206; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
QY 309 RSCDKTHTCPPCPAPEAGAPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFNW 368
Db 61 KSCDTPPPCPCRCAPPELLGGPSVFLPPPKDKTLMISRTPEVTCVVVDVSHEDPEVKFW 120
QY 369 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 428
Db 121 YVDGVQVHNAKTPREEQFNSTFRVSVLTVLHQNWLDGKEYKCKVSNKALPAPIEKTIS 180
QY 429 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTPPV 488
Db 181 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGYFSPDIAVEWESSGQPENNYNTTPPM 240
QY 489 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 538
Db 241 LDSGGSFFLYSKLTVDKSRWQQGNIFSCVMHEALHNRFTQKSLSLSPGK 290
RESULT 5
GC_RABIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
RT F-I haplotype.";
RL Immunogenetics 18:387-397(1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype.";
RL Biochem. J. 151:337-349(1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=83299917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G.";
RL Biochem. J. 116:249-259(1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -!- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,
CC 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
CC markers and Ref.5 the E15 marker.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC -----
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QY 486 PPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 538
Db 274 PPMLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 326

RESULT 3
GC4 HUMAN STANDARD; PRT; 327 AA.
AC P01861;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18 (1981).
RN [2]
RP SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
RT "Human immunoglobulin subclasses: Partial amino acid sequence of the constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47 (1970).
CC -----
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CC -----

DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; 1ADQ; 16-SEP-98.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; --
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; IG_MHC.
DR pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98 CH1.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 39.8%; Score 1150; DB 1; Length 327;
Best Local Similarity 75.4%; Pred. No. 5.8e-74;
Matches 224; Conservative 19; Mismatches 32; Indels 22; Gaps 5;

QY 254 WPDGLLASDNTLHFVH--PLTFNYSGVY-----ICKVTNSLQSRSDQKVIYISDVPEKQT 306
Db 41 WNSGALTSG-----VHTFPAVLQSSGLYSLSSVTVTPSSSLGTKT-----YTCNVVDHKPS 90
QY 307 SSRSCKDTHT-----CPPCPAPEAEGAPSVFLPPPKDKDTLMISRTPEVTCVVVDVSHED 361
Db 91 NTKVDRVESKYGPPCPCPAPFELGGPSVFLPPPKDKDTLMISRTPEVTCVVVDVSDQED 150
QY 362 PEVKFNWYVDGVEVHNNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKALPA 421
Db 151 PEVQFNWYVDGVEVHNNAKTPREEQNSTYRVSVLTVLHQDWLNGKEYCKVSNKGLPS 210
QY 422 PIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 481
Db 211 SIEKTIKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENN 270
QY 482 YKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSPGK 538
Db 271 YKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLGK 327

RESULT 4
GC3 HUMAN STANDARD; PRT; 290 AA.
ID GC3 HUMAN
AC P01860;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-3 chain C region (Heavy chain disease protein) (HDC).
GN IGHG3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (DISEASE PROTEIN WIS).
RX MEDLINE=81021548; PubMed=6774747;
RA Frangione B., Rosenwasser E., Prelli F., Franklin E.C.;
RT "Primary structure of human gamma 3 immunoglobulin deletion mutant: gamma 3 heavy-chain disease protein Wis.";
RL Biochemistry 19:4304-4308 (1980).
RN [2]
RP REVISIONS TO 12-97 (PROTEIN WIS).
RX MEDLINE=77118561; PubMed=402363;
RA Michaelson T.E., Frangione B., Franklin E.C.;
RT "Primary structure of the 'hinge' region of human IgG3. Probable quadruplication of a 15-amino acid residue basic unit.";
RL J. Biol. Chem. 252:883-889 (1977).
RN [3]
RP REVISIONS TO 59-289 (PROTEIN WIS/DISEASE PROTEIN ZUC).
RX MEDLINE=77021516; PubMed=823945;
RA Wolfenstein-Todel C., Frangione B., Prelli F., Franklin E.C.;
RT "The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the Fc fragment of immunoglobulin G3.";
RL Biochem. Biophys. Res. Commun. 71:907-914 (1976).
RN [4]
RP SEQUENCE FROM N.A. (DISEASE PROTEIN OMM).
RX MEDLINE=82247835; PubMed=6808505;
RA Alexander A., Steinmetz M., Barritault D., Frangione B., Franklin E.C., Hood L., Buxbaum J.N.;
RT "Gamma Heavy chain disease in man: cDNA sequence supports partial gene deletion model.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:3260-3264 (1982).
CC -!- SUBUNIT: Dimer linked by 12 disulfide bonds; it has an extra interchain disulfide bond at position 7 in addition to the 11 normally present in the hinge region.
CC -!- MISCELLANEOUS: The heavy chain disease protein WIS is shown.
CC -!- MISCELLANEOUS: The sequence of residues 42-76 was taken from the Ref.2.
CC -!- MISCELLANEOUS: Disease protein WIS is lacking most of the V region and all of the CH1 region.
CC -!- MISCELLANEOUS: Disease protein ZUC lack most of the V region, all

RT Intrachain disulfide bonds.";

RL Biochemistry 9:3188-3196(1970).

RN [7]

RP DISULFIDE BONDS.

RX MEDLINE=77070267; PubMed=1002129;

RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal

RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and

RT characterization of the protein, the L- and H-chains, the

RT cyanogen bromide cleavage products, and the disulfide bridges.";

RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).

RX MEDLINE=81208100; PubMed=7236608;

RA Deisenhofer J.;

RT "Crystallographic refinement and atomic models of a human Fc fragment

RT and its complex with fragment B of protein A from Staphylococcus

RT aureus at 2.9- and 2.8-A resolution.";

RL Biochemistry 20:2361-2370(1981).

CC -!- MISCELLANEOUS: Nie has the Glm(17) allotypic marker, 97-K, and the

CC Glm(1) markers, 239-D and 241-L. KOL and EU sequences have the

CC Glm(3) marker and the Glm (non-1) markers.

CC -!- MISCELLANEOUS: Nie also differs in the amidation states of

CC 35, 116, 198, 269 and 272.

CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues

CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues

CC 268-272.

CC -!- MISCELLANEOUS: KOL also differs in the amidation states of

CC residues 198, 267 and 272.

CC -----

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CC -----

DR EMBL; J00228; AAC82527.1; ALT_INIT.

DR PIR; A93433; GHU.

DR PDB; 1FC1; 15-JUL-92.

DR PDB; 1FC2; 15-JUL-92.

DR PDB; 1AJ7; 12-NOV-97.

DR PDB; 1DSB; 09-FEB-00.

DR PDB; 1DS1; 09-FEB-00.

DR PDB; 1D6V; 04-OCT-00.

DR PDB; 1DN2; 17-MAY-00.

DR PDB; 1E4K; 06-JUN-01.

DR PDB; 1FCC; 20-JUL-95.

DR PDB; 1HZH; 12-JUN-02.

DR PDB; 1I7Z; 08-AUG-01.

DR PDB; 1IIS; 16-MAY-01.

DR PDB; 1IIX; 16-MAY-01.

DR PDB; 1L6X; 10-APR-02.

DR PDB; 2RCS; 12-NOV-97.

DR Genew; HGNC:5525; IGHG1.

DR MIM; 147100; --.

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0003823; F:antigen binding; TAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; ig; 3.

DR SMART; SM00407; IGc1; 2.

DR PROSITE; PS00835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_MHC; 2.

KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

KW 3D-structure.

FT NON TER 1 1

FT DOMAIN 1 98 CH1.

FT DOMAIN 99 110 HINGE.

FT DOMAIN 111 223 CH2.

FT	DOMAIN	224	330	CH3.
FT	DISULFID	27	83	
FT	DISULFID	103	103	INTERCHAIN (WITH LIGHT CHAIN).
FT	DISULFID	109	109	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	112	112	INTERCHAIN (WITH HEAVY CHAIN).
FT	DISULFID	144	204	
FT	DISULFID	250	308	
FT	CARBCHYD	180	180	N-LINKED (GLCNAC. . .).
FT	MOD RES	330	330	REMOVED POST-TRANSLATIONALLY.
FT	VARIANT	97	97	K -> R (IN GLM(3) MARKER).
FT				/FTID=VAR_003886.
FT	VARIANT	239	239	D -> E (IN GLM(NON-1) MARKER).
FT				/FTID=VAR_003887.
FT	VARIANT	241	241	L -> M (IN GLM(NON-1) MARKER).
FT				/FTID=VAR_003888.
FT	STRAND	122	126	
FT	HELIX	130	134	
FT	TURN	136	137	
FT	STRAND	141	147	
FT	STRAND	157	162	
FT	TURN	163	164	
FT	STRAND	165	166	
FT	TURN	168	171	
FT	STRAND	176	179	
FT	TURN	180	181	
FT	STRAND	182	190	
FT	HELIX	193	197	
FT	TURN	198	199	
FT	STRAND	202	207	
FT	TURN	209	210	
FT	STRAND	215	219	
FT	STRAND	227	227	
FT	STRAND	230	234	
FT	HELIX	238	242	
FT	STRAND	245	256	
FT	STRAND	260	265	
FT	STRAND	270	270	
FT	STRAND	274	276	
FT	STRAND	280	281	
FT	TURN	283	284	
FT	STRAND	287	296	
FT	HELIX	297	301	
FT	TURN	302	303	
FT	STRAND	305	312	
FT	TURN	313	314	
FT	TURN	316	317	
FT	STRAND	320	325	
SQ	SEQUENCE	330 AA;	36106 MW;	3770EE106C2FA33D CRC64;
Query Match 43.3%; Score 1250.5; DB 1; Length 330;				
Best Local Similarity 80.3%; Pred.No. 4.9e-81;				
Matches 241; Conservative 13; Mismatches 21; Indels 25; Gaps 5;				
QY	254	WPDGLLASDNTLHFVH--PLTFNYSGVY-----ICKVTNSLQQRSDQKVIYISDVPEKQT	306	
Db	41	WNSGALTSG-----VHTFPAVLQSSGLYSLSSVTVTPSSSLGTQT-----YICNVNHPKS	90	
QY	307	SS-----RSCDKTHTCPPCPAPEAEAGAPSVFLFPPPKDITLMISRTPEVTCVVVDVS	358	
Db	91	NTKVDKKVEPKSCDKTHTCPPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVS	150	
QY	359	HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVHLQDNLNGKEYCKVSNKA	418	
Db	151	HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVSVLTVHLQDNLNGKEYCKVSNKA	210	
QY	419	LPAPIETISKAKGQPREPVVTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP	478	
Db	211	LPAPIETISKAKGQPREPVVTLPPSREDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP	270	
QY	479	ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK	538	
Db	271	ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK	330	

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 8.59785 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-14_COPY_58_595
Perfect score: 2886
Sequence: 1 GPIIIEPHVTAVGKNVSLK.....MHEALHNHYTQKSLSPGK 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1250.5	43.3	330	1 GC1_HUMAN	P01857 homo sapien
2	1165.5	40.4	326	1 GC2_HUMAN	P01859 homo sapien
3	1150	39.8	327	1 GC4_HUMAN	P01861 homo sapien
4	1129	39.1	290	1 GC3_HUMAN	P01860 homo sapien
5	906.5	31.4	323	1 GC_RABIT	P01870 oryctolagus
6	886	30.7	329	1 GC2_CAVPO	P01862 cavia porce
7	845	29.3	329	1 GC3_MOUSE	P22436 mus musculus
8	840.5	29.1	326	1 GC1_RAT	P20759 rattus norv
9	836	29.0	333	1 GCB_RAT	P20761 rattus norv
10	834	28.9	398	1 GC3M_MOUSE	P03987 mus musculus
11	830.5	28.8	324	1 GC1_MOUSE	P01868 mus musculus
12	825.5	28.6	393	1 GC1M_MOUSE	P01869 mus musculus
13	819	28.4	329	1 GCC_RAT	P20762 rattus norv
14	811.5	28.1	322	1 GCA_RAT	P20760 rattus norv
15	801	27.8	330	1 GCAA_MOUSE	P01863 mus musculus
16	801	27.8	335	1 GCAB_MOUSE	P01864 mus musculus
17	796	27.6	399	1 GCAM_MOUSE	P01865 mus musculus
18	780.5	27.0	336	1 GCB_MOUSE	P01866 mus musculus
19	775.5	26.9	405	1 GCBM_MOUSE	P01867 mus musculus
20	552.5	19.1	515	1 PVR1_MOUSE	Q9jkk6 mus musculus
21	542.5	18.8	517	1 PVR1_HUMAN	Q15223 homo sapien
22	537.5	18.6	515	1 PVR1_PIG	Q9gl76 sus scrofa
23	430	14.9	454	1 MUC_HUMAN	P01871 homo sapien
24	427	14.8	530	1 PVR2_MOUSE	P32507 mus musculus
25	416.5	14.4	458	1 MUC_RABIT	P03988 oryctolagus
26	406.5	14.1	479	1 MUCM_RABIT	P04221 oryctolagus
27	402	13.9	428	1 EPC_HUMAN	P01854 homo sapien
28	399.5	13.8	417	1 PVR_CERAE	P32506 cercopithec
29	399	13.8	538	1 PVR2_HUMAN	Q92692 homo sapien
30	398	13.8	391	1 MUCB_HUMAN	P04220 homo sapien
31	387	13.4	454	1 MUC_MESAU	P06337 mesocricetu
32	384.5	13.3	421	1 EPC_MOUSE	P06336 mus musculus
33	383.5	13.3	417	1 PVR_HUMAN	P15151 homo sapien

RESULT 1				
GC1_HUMAN				
ID	GC1_HUMAN	STANDARD;	PRT;	330 AA.
AC	P01857;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Ig gamma-1 chain C region.			
GN	IGHG1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino			
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a			
RT	monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The			
RT	chymotryptic peptides of the H-chain, alignment of the tryptic			
RT	peptides and discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=6884994;			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary			
RT	structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X.			

P01872 mus musculus
P01874 canis famil
P01855 rattus norv
P01873 mus musculus
P20768 suncus muri
P23085 heterodontu
P01879 oryctolagus
P23087 heterodontu
P23088 heterodontu
P01875 gallus gall
P23086 heterodontu
P23084 heterodontu

Db 208 YVDGVEVHNAKTPREEQYNSTFRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 267

QY 429 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 488

Db 268 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPM 327

QY 489 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGK 538

Db 328 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGK 377

RESULT 9

A60764

Ig gamma-3 chain C region, form LAT - human

C;Species: Homo sapiens (man)

C;Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999

C;Accession: A60764

R;Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A;Title: A human immunoglobulin IGHG3 allele (Gmb0, b1, c3, c5, u) with an IGHG4 conversion

A;Reference number: A60764; MUID:90007613; PMID:2571587

A;Accession: A60764

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-377 <HUC>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 39.7%; Score 1147; DB 2; Length 377;

Best Local Similarity 91.7%; Pred. No. 4.4e-65;

Matches 211; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 309 RSCDKTHTCPPCPAPEAGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 368

Db 148 KSCDTPPPCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFW 207

QY 369 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 428

Db 208 YVDGVEVHNAKTPREEQYNSTFRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 267

QY 429 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 488

Db 268 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 327

QY 489 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGK 538

Db 328 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPGK 377

RESULT 10

G3HUWI

Ig gamma-3 heavy chain disease proteins - human

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1979 #sequence_revision 23-Oct-1981 #text_change 16-Jul-1999

C;Accession: A90442; A92219; A93915; A02149

R;Frangione, B.; Rosenwasser, E.; Prelli, F.; Franklin, E.C.

Biochemistry 19, 4304-4308, 1980

A;Title: Primary structure of human gamma3 immunoglobulin deletion mutant: gamma3 heavy-

A;Reference number: A90442; MUID:81021548; PMID:6774747

A;Contents: heavy chain disease protein Wis

A;Accession: A90442

A;Molecule type: protein

A;Residues: 1-289 <FRA>

A;Note: this molecule is a dimer linked by 12 disulfide bonds; it has an extra interchain

A;Note: this protein lacks most of the V region and all of the CH1 region. Residue 12 co

A;Note: the sequence of residues 42-76 was taken from the reference that follows

R;Michaelson, T.E.; Frangione, B.; Franklin, E.C.

J. Biol. Chem. 252, 883-889, 1977

A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication

A;Reference number: A92219; MUID:77118561; PMID:402363

A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W

A;Accession: A92219

A;Molecule type: protein

A;Residues: 12-97 <MIC>

A;Note: the hinge region in gamma-3 chains is about four times as long as in other gamma

A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inte

R;Wolfenstein-Todel, C.; Frangione, B.; Prelli, F.; Franklin, E.C.

Biochem. Biophys. Res. Commun. 71, 907-914, 1976

A;Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of the

A;Reference number: A90198; MUID:77021516; PMID:823945

A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues

A;Accession: A90198

A;Molecule type: protein

A;Residues: 59-125, 'EB', 128-226, 228-289 <WOL>

A;Note: this protein lacks most of the V region, all of the CH1 region, and part of the

R;Alexander, A.; Steinmetz, M.; Barritault, D.; Frangione, B.; Franklin, E.C.; Hood, L.

Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982

A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion

A;Reference number: A93915; MUID:82247835; PMID:6808505

A;Contents: heavy chain disease protein Omm

A;Accession: A93915

A;Molecule type: mRNA

A;Residues: 12-70; 72-114; 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-15

A;Note: a carboxyl-terminal Lys is removed posttranslationally

A;Note: this sequence may represent an allelic form or another gamma chain subclass

C;Comment: The heavy chain disease protein Wis is shown.

C;Genetics:

A;Gene: GDB:IGHG3

A;Cross-references: GDB:119339; OMIM:147120

A;Map position: 14q32.33-14q32.33

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid

F;203-270/Domain: immunoglobulin homology <IMM>

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 38.9%; Score 1124; DB 1; Length 289;

Best Local Similarity 89.5%; Pred. No. 8.9e-64;

Matches 205; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 309 RSCDKTHTCPPCPAPEAGAPSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 368

Db 61 KSCDTPPPCPCPAPPELLGGPSVFLFPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFW 120

QY 369 YVDGVEVHNAKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 428

Db 121 YVDGVQVHNAKTPREEQFNSTFRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTIS 180

QY 429 KAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 488

Db 181 KTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPM 240

QY 489 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 537

Db 241 LDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYTQKSLSPG 289

RESULT 11

I47159

Ig gamma 2a chain constant region - pig (fragment)

C;Species: Sus scrofa domestica (domestic pig)

C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C;Accession: I47159

R;Kacskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A;Reference number: I47158; MUID:95015845; PMID:7930579

A;Accession: I47159

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-328 <KAC>

A;Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124

C;Genetics:

A;Gene: IGG2a

Db 274 PPMLDSDGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYTQKSLSPGK 326

RESULT 6

T08732

hypothetical protein DKFP566B0846.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C;Accession: T08732

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S. submitted to the Protein Sequence Database, May 1999

A;Reference number: Z16474

A;Accession: T08732

A;Molecule type: mRNA

A;Residues: 1-407 <OTT>

A;Cross-references: EMBL:AL050071

A;Experimental source: fetal kidney; clone DKFP566B0846

C;Genetics:

A;Note: DKFP566B0846.1

Query Match 40.1%; Score 1158; DB 2; Length 407;

Best Local Similarity 67.1%; Pred. No. 9.7e-66;

Matches 241; Conservative 16; Mismatches 70; Indels 32; Gaps 5;

QY 86 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGDDSLIDGGNETVAAICIAATGKPVA 145

Db 1 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGDDSLIDGGNETVAAICIAATGKPVA 60

QY 146 HIDWEGDLGEMESTTSPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI 205

Db 61 HIDWEGDLGEMESTTSPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFI 120

QY 206 LDIQYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPDGLLASDNTL 265

Db 121 LDIQYAPEVSVTGYDGNWFVGRKGVNLKNADANPPPFKSVWSRLDGQWPDGLLASDNTL 180

QY 266 HFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVPPKQTSRRSCDKTHTCPPCPAPEA 325

Db 181 HFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVPPPTTLQ-----PTI 226

QY 326 EGAPSV-----FLFPPK----PKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 376

Db 227 QWHPSTADIEDLATEPKLPPPLSTLTIKDDTIATIASVVGALFIVLSVLAGIFCY 286

QY 377 NAKTKPREEQNSTY-----RVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKITISK 429

Db 287 RRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDPYPDSVKKENK---NPVNNLIRK 342

RESULT 7

G4HU

Ig gamma-4 chain C region - human

C;Species: Homo sapiens (man)

C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999

C;Accession: A90933; A90249; A02150

R;Ellison, J.; Buxbaum, J.; Hood, L. DNA 1, 11-18, 1981

A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.

A;Reference number: A90933; MUID:83157104; PMID:6299662

A;Accession: A90933

A;Molecule type: DNA

A;Residues: 1-327 <ELL>

A;Note: the sequence was determined from the germline gene

R;Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C. Biochem. J. 117, 33-47, 1970

A;Title: Human immunoglobulin sublcasses. Partial amino acid sequence of the constant r

A;Reference number: A90249; MUID:70207560; PMID:4192699

A;Accession: A90249

A;Molecule type: protein

A;Residues: 1-30;81-326 <PIN>

C;Genetics:

A;Gene: GDB:IGHG4

A;Cross-references: GDB:119340; OMIM:147130

A;Map position: 14q32.33-14q32.33

A;Introns: 99/1; 111/1; 221/1

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F;20-85/Domain: immunoglobulin homology <IM1>

F;99-110/Region: hinge

F;134-203/Domain: immunoglobulin homology <IM2>

F;240-307/Domain: immunoglobulin homology <IM3>

F;14/Disulfide bonds: interchain (to light chain) #status experimental

F;27-83,141-201,247-305/Disulfide bonds: #status predicted

F;106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 39.8%; Score 1150; DB 1; Length 327;

Best Local Similarity 75.4%; Pred. No. 2.4e-65;

Matches 224; Conservative 19; Mismatches 32; Indels 22; Gaps 5;

QY 254 WPDGLLASDNTLHFVH--PLTFNYSGVY-----ICKVTNSLQSRSDQKVIYISDVPPKQT 306

Db 41 WNSGALTSG-----VHTFPAVLQSSGLYSLSSVTVTPSSSLGTKT-----YTCNVDPHKPS 90

QY 307 SSRSCDKTHT-----CPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED 361

Db 91 NTKVDKRVESKYGPPCPSCPAPEFLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSQED 150

QY 362 PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA 421

Db 151 PEVQFNWYVDGVEVHNAKTKPREEQFNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKGLPS 210

QY 422 PIEKTISKAKGQPREPPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENY 481

Db 211 SIEKTISKAKGQPREPPQVYTLPPSQEEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENY 270

QY 482 YKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYTQKSLSPGK 538

Db 271 YKTTTPVLDSDGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYTQKSLSLGK 327

RESULT 8

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C;Species: Homo sapiens (man)

C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999

C;Accession: A23511

R;Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G. Nucleic Acids Res. 14, 1779-1789, 1986

A;Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene: c

A;Reference number: A23511; MUID:86148507; PMID:3081877

A;Accession: A23511

A;Molecule type: DNA

A;Residues: 1-377 <HUC>

A;Cross-references: GB:X03604; GB:M12958; NID:G33070; PIDN:CAA27268.1; PID:G577056

C;Genetics:

A;Gene: GDB:IGHG3

A;Cross-references: GDB:119339; OMIM:147120

A;Map position: 14q32.33-14q32.33

A;Introns: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: immunoglobulin

F;20-85/Domain: immunoglobulin homology <IMM>

Query Match 39.8%; Score 1149; DB 2; Length 377;

Best Local Similarity 91.7%; Pred. No. 3.3e-65;

Matches 211; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 309 RSCDKTHTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 368

Db 148 KSCDTPPPCPRCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVQFKW 207

QY 369 YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTIS 428

QY 368 WYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTII 427
Db 85 WYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTII 144
QY 428 SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP 487
Db 145 SKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP 204
QY 488 VLDSGSGFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 538
Db 205 VLDSGSGFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 255
RESULT 4
PT0207
Ig gamma chain C region - chimpanzee
C:Species: Pan troglodytes (chimpanzee)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999
C:Accession: PT0207
R:Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.
Mol. Immunol. 28, 319-322, 1991
A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.
A:Reference number: PT0207; MUID:91287716; PMID:2062315
A:Accession: PT0207
A:Molecule type: mRNA
A:Residues: 1-234 <EHR>
C:Superfamily: immunoglobulin
C:Keywords: immunoglobulin
F;48-117/Domain: immunoglobulin homology <IMM>
Query Match 40.7%; Score 1176; DB 2; Length 234;
Best Local Similarity 94.3%; Pred. No. 3.6e-67;
Matches 215; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 304 KQTSSRSCKTHTCPPCAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE 363
Db 7 KKVEPKSCDTHTCPCCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPE 66
QY 364 VKFNWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 423
Db 67 VKFNWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI 126
QY 424 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 483
Db 127 EKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYK 186
QY 484 TTPPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKS 531
Db 187 TTPPVLDSDGSFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKS 234
RESULT 5
G2HU
Ig gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 21-Jul-2000
C:Accession: A93906; A92809; A90752; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A:Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A:Reference number: A93906; MUID:82197621; PMID:6804948
A:Accession: A93906
A:Molecule type: DNA
A:Residues: 1-326 <ELL>
A:Cross-references: GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; PID:g6066056
A:Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A:Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A:Reference number: A92809; MUID:81007873; PMID:6774012
A:Contents: myeloma protein Til
A:Accession: A92809
A:Molecule type: protein

A:Residues: 1-19,'Q',21-57,'Z',59,'A',61-193,'D',195-325 <WAN>
A:Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A:Title: The amino acid sequences of the three heavy chain constant region domains of a
A:Reference number: A90752; MUID:80001357; PMID:113060
A:Contents: myeloma protein Zie
A:Accession: A90752
A:Molecule type: protein
A:Residues: 1-24,'E',26-57,'EV',60-85;132-171,'ZZZ',175,'B',177-193,'D',195-196,'Q',198
A:Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A:Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A:Reference number: A93132; MUID:80114419; PMID:118920
A:Contents: Zie
A:Accession: A93132
A:Molecule type: protein
A:Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A:Reference number: A94591
A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A:Reference number: A90253; MUID:72033500; PMID:4940472
A:Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A:Title: Structural studies of immunoglobulin G.
A:Reference number: A93157; MUID:69064124; PMID:5782707
A:Contents: annotation; Sa, disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG2
A:Cross-references: GDB:119338; OMIM:147110
A:Map position: 14q32.33-14q32.33
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;133-202/Domain: immunoglobulin homology <IM2>
F;239-306/Domain: immunoglobulin homology <IM3>
F;14/Disulfide bonds: interchain (to light chain) #status experimental
F;27-83,140-200,246-304/Disulfide bonds: #status experimental
F;102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.4%; Score 1165.5; DB 1; Length 326;
Best Local Similarity 77.5%; Pred. No. 2.5e-66;
Matches 227; Conservative 14; Mismatches 37; Indels 15; Gaps 5;
QY 254 WPDGLLASDNTLHFVH--PLTFNYSGVYICKVTNSLQSRSDQKVIYISDVPFKQTSRRSC 311
Db 41 WNSGALISG-----VHTFPAVLQSSGLYSLSSVVTVPSSNFGTQTYTCNVDHKPSNTK-V 94
QY 312 DKT-----HTCPPCPAPEAEGAPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVK 365
Db 95 DKTVERKCCVECPPCAPPVAG-PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVQ 153
QY 366 FNWYVDGVEVHNAKTKPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEK 425
Db 154 FNWYVDGVEVHNAKTKPREEQNSTFRVSVLTVVHQDWLNGKEYKCKVSNKGLPAPIEK 213
QY 426 TISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 485
Db 214 TISKTKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT 273
QY 486 PPVLDSGSGFFLYSKLTVDKSRWQGNVFSCSVMEALHNHYTQKSLSLSPGK 538
||:|||||

igen Primaerstruktur.
A;Reference number: A91668; MUID:77070269; PMID:826475
A;Contents: myeloma protein Nie
A;Accession: B91668
A;Molecule type: protein
A;Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27
A;Note: this sequence has the G1m(17) and G1m(1) markers
R;Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A;Title: Die Primaerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOL
A;Reference number: A91723; MUID:83289131; PMID:6884994
A;Contents: myeloma protein KOL; disulfide bonds
A;Accession: A91723
A;Molecule type: protein
A;Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A;Note: this sequence has the G1m(3) and G1m(non-1) markers
R;Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A;Reference number: A90565; MUID:71064027; PMID:4923144
A;Contents: annotation; disulfide bonds
R;Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A;Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbromide cleavage products, and the disulfide bridges.
A;Reference number: A91667; MUID:77070267; PMID:1002129
A;Contents: annotation; disulfide bonds
C;Genetics:
A;Gene: GDB:IGHG1
A;Cross-references: GDB:120085; OMIM:147100
A;Map position: 14q32.33-14q32.33
A;Introns: 99/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F;20-85/Domain: immunoglobulin homology <IM1>
F;137-206/Domain: immunoglobulin homology <IM2>
F;243-310/Domain: immunoglobulin homology <IM3>
F;27-83, 144-204, 250-308/Disulfide bonds: #status experimental
F;103/Disulfide bonds: interchain (to light chain) #status experimental
F;109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 43.3%; Score 1250.5; DB 1; Length 330;
Best Local Similarity 80.3%; Pred. No. 1.1e-71;
Matches 241; Conservative 13; Mismatches 21; Indels 25; Gaps 5;

Qy 254 WPDGLLASDNTLHFVH--PLTFNYSGVY----ICKVTNSLQSRSDQKVIYISDVPFKQT 306
Db 41 WNSGALTSG----VHTFPAVLQSSGLYSLSSVTVPSSSLGQT-----YICNVNKKPS 90
Qy 307 SS-----RSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 358
Db 91 NTKVDKKEPKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVS 150
Qy 359 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 418
Db 151 HEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA 210
Qy 419 LPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQP 478
Db 211 LPAPIEKTISKAKGQPREPQVYTLPPSREELTKNQVSLTCLVKGFYPSDIAVEWESNGQP 270
Qy 479 ENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 538
Db 271 ENNYKTTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKSLSLSPGK 330

RESULT 2
S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 42.7%; Score 1232.5; DB 2; Length 374;
Best Local Similarity 90.9%; Pred. No. 1.8e-70;
Matches 231; Conservative 6; Mismatches 8; Indels 9; Gaps 2;

Qy 285 NSLQSRSDQKVIYISDVPFKQTSSRSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMI 344
Db 130 HSWGQGT--LVTVSSEP-----KSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMI 180
Qy 345 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 404
Db 181 SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDW 240
Qy 405 LNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY 464
Db 241 LNKKEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFY 300
Qy 465 PS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALH 524
Db 301 PS DIAVEWESNGQPENNYKTTPVLDSDGSFFLYSLKLTVDKSRWQQGNVFCSCVMHEALH 360
Qy 525 NHYTQKSLSLSPGK 538
Db 361 NHYTQKSLSLSPGK 374

RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C;Species: synthetic
A;Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C;Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C;Accession: S31866
R;Filpula, D.
submitted to the EMBL Data Library, February 1993
A;Description: Screening method for protein-protein interactions of cloned gene products
A;Reference number: S31866
A;Accession: S31866
A;Molecule type: mRNA
A;Residues: 1-255 <FIL>
A;Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C;Keywords: immunoglobulin
F;1-22/Region: Escherichia coli outer membrane protein A precursor
F;23-255/Region: human Ig gamma-1 chain C region

Query Match 42.6%; Score 1228; DB 4; Length 255;
Best Local Similarity 97.4%; Pred. No. 2.1e-70;
Matches 225; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 308 SRSCDKTHTCPPCPAPEAGAPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 367
Db 25 SKSCDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN 84

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 14.2358 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-14_COPY_58_595
Perfect score: 2886
Sequence: 1 GPIIIEPHVTAVWGKNVSLK.....MHEALHNHYTQKSLSLSPGX 538

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1250.5	43.3	330	1 GHU	Ig gamma-1 chain C
2	1232.5	42.7	374	2 S69339	Ig heavy chain V r
3	1228	42.6	255	4 S31866	Ig gamma-1 chain C
4	1176	40.7	234	2 PT0207	Ig gamma chain C r
5	1165.5	40.4	326	1 G2HU	Ig gamma-2 chain C
6	1158	40.1	407	2 T08732	hypothetical prote
7	1150	39.8	327	1 G4HU	Ig gamma-4 chain C
8	1149	39.8	377	2 A23511	Ig gamma-3 chain C
9	1147	39.7	377	2 A60764	Ig gamma-3 chain C
10	1124	38.9	289	1 G3HUWI	Ig gamma-3 heavy c
11	931.5	32.3	328	2 I47159	Ig gamma 2a chain
12	930.5	32.2	328	2 I47160	Ig gamma 2b chain
13	917	31.8	277	2 I47162	Ig gamma 4 chain c
14	906.5	31.4	323	1 GHRB	Ig gamma chain C r
15	903.5	31.3	328	2 I47158	Ig gamma 1 chain c
16	899.5	31.2	328	2 I47161	Ig gamma 3 chain c
17	886	30.7	329	1 G2GP	Ig gamma-2 chain C
18	872	30.2	470	2 S22080	Ig heavy chain pre
19	859.5	29.8	472	2 S31459	Ig gamma-1 chain -
20	853	29.6	308	2 C30554	Ig heavy chain C r
21	845.5	29.3	444	2 PC4436	monoclonal antibod
22	845	29.3	329	1 G3MSC	Ig gamma-3 chain C
23	840.5	29.1	325	2 PS0017	Ig gamma-1 chain C
24	836	29.0	333	2 PS0018	Ig gamma-2b chain
25	834	28.9	398	1 G3MSM	Ig gamma-3 chain C
26	830.5	28.8	324	1 G1MS	Ig gamma-1 chain C
27	829.5	28.7	469	2 S37483	Ig gamma-2a chain
28	825.5	28.6	393	1 G1MSM	Ig gamma-1 chain C
29	819	28.4	329	2 S00847	Ig gamma-2c chain

30	812	28.1	446	2 S40295	Ig gamma-2a chain
31	811.5	28.1	322	2 PS0019	Ig gamma-2a chain
32	801	27.8	330	1 G2MSA	Ig gamma-2a chain
33	801	27.8	335	1 G2MSAB	Ig gamma-2a chain
34	798	27.7	474	1 G2MS11	Ig gamma-2b chain
35	796	27.6	399	1 G2MSAM	Ig gamma-2a chain C
36	787	27.3	327	2 S06611	Ig gamma-2 chain C
37	784.5	27.2	475	2 S01321	Ig gamma-2b chain
38	775.5	26.9	405	1 G2MSBM	Ig gamma-2b chain
39	708	24.5	180	2 I46732	Ig gamma heavy cha
40	583.5	20.2	249	2 S69340	Ig gamma chain VHI
41	577	20.0	152	2 S14236	Ig gamma-1 chain C
42	568.5	19.7	218	2 A36040	Ig heavy chain V-I
43	520	18.0	518	2 JC4024	poliovirus recepto
44	470	16.3	572	2 B46529	Ig Y heavy chain (
45	447	15.5	627	2 S14683	Ig mu chain precur

ALIGNMENTS

RESULT 1

GHU

Ig gamma-1 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 16-Jul-1999
C;Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146
R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A;Reference number: A93433; MUID:82274238; PMID:6287432
A;Accession: A93433
A;Molecule type: DNA
A;Residues: 1-330 <ELL>
A;Cross-references: EMBL:Z17370
A;Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers,
A;Note: Lys-330 is removed after translation
R;Harris, L.J.
submitted to the EMBL Data Library, October 1992
A;Reference number: S33904
A;Accession: S36861
A;Molecule type: DNA
A;Residues: 2-330 <HAR>
A;Cross-references: EMBL:Z17370
R;Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A;Reference number: S33887; MUID:83001943; PMID:6811139
A;Accession: S33887
A;Molecule type: DNA
A;Residues: 88-113;235-330 <TAK>
A;Cross-references: EMBL:Z17370
R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequer
A;Reference number: A90563; MUID:71064024; PMID:5489771
A;Contents: myeloma protein Eu
A;Accession: B90563
A;Molecule type: protein
A;Residues: 1-96,'R',98-135 <CUN>
A;Note: this sequence has the G1m(3) marker, 97-Arg
R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer
A;Reference number: A90564; MUID:71064025; PMID:5530842
A;Contents: Eu
A;Accession: A90564
A;Molecule type: protein
A;Residues: 136-154,'Q',156-165,'Q',167-176,'Q',178-194,'N',196-197,'D',199-238,'E',240,
A;Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met
R;Ponatingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A;Title: Die Primaerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/905,125A
PRIOR FILING DATE: 2001-07-12
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-905-125A-84
Query Match 9.9%; Score 238.5; DB 4; Length 398;
Best Local Similarity 26.1%; Pred. No. 4.1e-15;
Matches 86; Conservative 61; Mismatches 159; Indels 23; Gaps 13;
QY 10 TAVNGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOQYGFVSQGEYQGRVLFKNY 69
Db 39 TVVAGGFVVLKQVQKHED-SSLQWS---NPAQQTLD-----YFGKRALRDNRIQLVTS 88
QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDGN 129
Db 89 TPHELISISNVALADEGEYTCISIFMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145
QY 130 ETVAATCIAATGKPAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTTRFARGR 185
Db 146 DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVTSSSVTFQVTRDDGA 205
QY 186 RITCVVVKHPALE-KDIRYSFILDIQVAPEVSVTYGDGNFVGRKGVNLCNADANPPPFK 244
Db 206 SIVCSVNHESLKGADRTSQRIEVLVYPTAMIRPDPPHREGQK-LLLHCEGRGNFVPPQ 264
QY 245 SVNSRLDQWPDGLLASDNTLHFVHBLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPPK 304
Db 265 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYKAYTYTLNVND-PSP 321
QY 305 QTSSIAVAGAVIGAVLALFIIAIFVTVLL 333

Db 322 VPSSSTYHAIGGIVA-FIVFLLLLMLI 349
RESULT 14
US-09-902-775A-84
Sequence 84, Application US/09902775A
Patent No. 6686451
GENERAL INFORMATION:
APPLICANT: Genentech, Inc.
APPLICANT: Ashkenazi, Avi
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, A.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth, J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Mather, Jennie P.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/23089
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: PCT/US99/28214
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05


```
RESULT 9
US-09-778-510-22
; Sequence 22, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 423
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-22

Query Match 11.5%; Score 279; DB 4; Length 423;
Best Local Similarity 25.1%; Pred. No. 4.1e-19;
Matches 92; Conservative 69; Mismatches 147; Indels 58; Gaps 13;

QY 9 VTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVVHHPQYGFVSQGEYQGRVLFKN 68
Db 34 VTVIEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YFRDRPLKDSRFQLLN 83

QY 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIK-GPDSLIDG 127
Db 84 FSSSELKVSILTNVSIISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMDIQKDTAVEG 141

QY 128 GNETVAAICIAATGKPVAHIDW-EGD-----LGEMESTTTSFPNETATIIISQYKLFPTRF 181
Db 142 --EEIEVNCTAMASKPATITIRWFKGNKELGKSEVEEWSDMY-----TVTSQLMLKVHKE 194

QY 182 ARGRRITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGKRG--VNLKCNADAN 239
Db 195 DDGVPVICQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTREGDAFELTCEAIGK 254

QY 240 PPPEKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLQSRSDQKVYIYS 299
Db 255 PQPVMTWVRVDDDEMPQHAVLSGPNL-FINNLNKTNDNGYRCEASNIVGKAHSDMYLVYV 313

QY 300 DVP-----FKQTSSI-----AVAGAVIGAVLALFIATFVT 330
Db 314 DPPTTIPPTTTTTTTTTTTTTTTTILTIITDSRAGEGTICAVDHAVIGVAVVVFAMLC 373

QY 331 VLLTPR 336
Db 374 LILGR 379

RESULT 10
US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
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; SEQ ID NO 4
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-4

Query Match 10.3%; Score 248.5; DB 4; Length 398;
Best Local Similarity 26.7%; Pred. No. 4.1e-16;
Matches 88; Conservative 61; Mismatches 157; Indels 23; Gaps 13;

QY 10 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVVHHPQYGFVSQGEYQGRVLFKNY 69
Db 39 TVVAGGTVVLKCVKDHED--SSLQWS---NPAQOTL-----YFGEKRALRDNRIQLVSS 88

QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGN 129
Db 89 TPHELISISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145

QY 130 ETVAAICIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTRFARGR 185
Db 146 ETATLNCQSSGSKPAAQLTWKGDQELHGDQTRIQEDENGKTFVSSSVSFQVTRDDGA 205

QY 186 RITCVVKKHPALE-KDIRYSFILDIQYAPEVSVTGYDGNWVFGKGNLKNADANPPPEK 244
Db 206 NIVCSVNHESLKGAADRSTQRIEVLVYPTAMIRPEPAHPREGQK-LLLHCEGRGNPVPOQ 264

QY 245 SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVYICKVTNSLQSRSDQKVYIYISDVPPFK 304
Db 265 YVMVK-EGSEPPKMTQESALIFPF-LNKSDSGTGTATSNMGSYTAYFTLNVD-PSP 321

QY 305 QTSSIAVAGAVIGAVLALFIATFVTLL 333
Db 322 VPSSSSTYHAIIGGIVA-FIVFLLILLI 349

RESULT 11
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 9.9%; Score 238.5; DB 4; Length 398;
Best Local Similarity 26.1%; Pred. No. 4.1e-15;
Matches 86; Conservative 61; Mismatches 159; Indels 23; Gaps 13;

QY 10 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVVHHPQYGFVSQGEYQGRVLFKNY 69
Db 39 TVVAGGTVVLKCVKDHED--SSLQWS---NPAQOTL-----YFGEKRALRDNRIQLVTS 88

QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGN 129
Db 89 TPHELISISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145

QY 130 ETVAAICIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTRFARGR 185
Db 146 DTATLNCQSSGSKPAAQLTWKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGA 205
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Db 491 Y---DPEQLDAENMVSNQDGSFISKKEWYV 518

RESULT 4

US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match 17.7%; Score 427.5; DB 4; Length 479;
Best Local Similarity 29.2%; Pred. No. 7.4e-34;
Matches 108; Conservative 64; Mismatches 151; Indels 47; Gaps 11;

QY 5 VEPHVTAVWGKNSLKLCLI---EVNETITQISWEKIHGKSS-QTAVVHHPOYGFVSQGEY 60
Db 38 VLPEVRGQLGGTVLPPVGLYISLVTWQRPDAPANHQNVAAAFHKMGSPFPSPK 97
QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108
Db 98 PGSERLSFVSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFATFPKGSVRGMTWLR 157
QY 109 VLVEP-----TVSLIKGPDSLIDGNETVAAICIAATGKPVAAHI-----DWEGLGE 155
Db 158 VIAKPKQNAEAKVTFSSQDP-----TTVALCISKEGRPPARISWLSLSDWEAKETQ 208
QY 156 MESITTSFPNETATILISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPEVS 215
Db 209 VSGTLG----TVVTSRFTLVPSGRADGVTVTCVKEHESFEPEPALIPVTLVSRYPPEVS 264
QY 216 VTGYDGNWVGRKGNLKNADANPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNY 275
Db 265 ISGYDDNWYLGRDATALSCDVRNPEPTGYDWSSTSGTFTPTSAVAQSQL-VIHAVDSLF 323
QY 276 SGVYICKVTNSLQSRSDQKVIYISDVFPFKQTSSIA--VAGAVIGAVLALFIIA--IFVTV 331
Db 324 NTTFCVCTVNAVGMGRAEQVIFVRETPRASPRDVGPLVWGAVGGLLVLLLAGGSLAFI 383

QY 332 LLTPRKKRPS 341
Db 384 LLRVRRRRKS 393

RESULT 5
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:

; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62

Query Match 16.1%; Score 390; DB 4; Length 408;
Best Local Similarity 30.8%; Pred. No. 3.2e-30;
Matches 108; Conservative 61; Mismatches 160; Indels 22; Gaps 10;

QY 3 IIVEPHVTAVWGKNSLKLCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPQYGFVSQGE 59
Db 32 VLVPYNSTGVLGGSTTLHCSLTSNENVTITQITWMKKDSSGSHALVAVFHPKKGPNKEP 91
QY 60 YQGRVLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSL 117
Db 92 ERVKFLAAQQDLRNASLAISNLSVEDEGIYECQIATFPRGSRSTNAWLKVQARPKNATAE 151
QY 118 IKGPDSLI--DGGNETVAAICIAATGKPVAAHIDW----EGDLGEMESTTTSFPNETATII 171
Db 152 LEPSPTLILQD-----VAKCISANGHEPGRISWPSNVNGSHREMKE-PGSQPG-TTIVT 203
QY 172 SQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTCYDGNWVGRKGV 230
Db 204 SYLSMVPSRQADGKNITCTVEHESLQELDQLLVTLISQYPPPENVSISGYDGNWYVGLTNL 263
QY 231 NLKCNADANPPPKS--VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 288
Db 264 TLTCEAHSKPAPDMAGYNWSTNTGDFPNSVKRQGNMLLISTVEDGLNNTVIVCEVTNALG 323
QY 289 QRSQDKVIVISDVFPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKR 339
Db 324 SGQGQVHIIIVKPKPENMQNTRLHLGYIFLIVFVLAIVVIAALYTIIRRCR 374

RESULT 6

US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper

Db 223 SLACIVNYHM--DRFKESLTNLVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEY 280
QY 246 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSDDQKVIYISDVPFKQ 305
Db 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYTP 340
QY 306 TS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRK--RPSYLDK----- 345
Db 341 SPPEHGRRAGPVPTAIIGGVAGSILLVLIIVGGIIVALRRRHTFKDGYSTKKHVGNGY 400
QY 346 -VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNLSRSDY 404
Db 401 SKAGIPQHH--PPMAQNLQYPDDSD-----EKKAGPLGGS-----SYEE 438
QY 405 EDENPVGEDGIQOM-----YPLYN-----QMCYQDRSPGKHHQNNDPKRV 444
Db 439 EEEEEGGGGERKVGPHPKYDEDAKRPYFTVDEAEARQDGYGDRILGYQY--DPEQL 495
QY 445 -----YIDPREHYV 453
Db 496 DLAEENVSQNDGSFISKKEWYV 517

RESULT 2
US-09-435-956A-1
; Sequence 1, Application US/09433956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: Hlgr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 24.2%; Score 584.5; DB 4; Length 458;
Best Local Similarity 35.5%; Pred. No. 1.5e-49;
Matches 137; Conservative 67; Mismatches 165; Indels 17; Gaps 9;
QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTSPFNETATIIISQYKLFPRFARGR 185
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGEAEYQETRNPNGTVTVISRYRLVPSREAHQ 222
QY 186 RITCVVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVRKGVNLKCNADANPPPFKS 245
Db 223 SLACIVNYHM--DRFKESLTNLVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEY 280
QY 246 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSDDQKVIYISDVPFKQ 305

Db 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEKPRPQ 340
QY 306 TSSIAVAGAVIGAVLALFIIAIFVTV--LLTPRKRPYSYLDKV-IDLPPTHKPPPLYEER 362
Db 341 RGLSAAARLLAGTVAVFLLIVAVLTVFFLYNRQOKSPPETDGAGTDQPLSQKPEPSPSRQ 400
QY 363 SPPLPQKDLFQPEHL-PLQTQPKERE 387
Db 401 SSLVPED--IQVVHLDPGRQQQEE 424

RESULT 3
US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20

Query Match 23.4%; Score 565.5; DB 4; Length 518;
Best Local Similarity 29.0%; Pred. No. 1.4e-47;
Matches 148; Conservative 85; Mismatches 171; Indels 107; Gaps 16;
QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDW-----GDLGEMESTTSPFNETATIIISQYKL 176
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGEARVPGDSGT-----PMAPVTVISRYRL 214
QY 177 FPTRFARGRRITCVVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVRKGVNLKCN 236
Db 215 VPSREAHQOQSLACIVNYHM--DRFKESLTNLVQYEPEVTIEGFDGNWYLQRMVDVKLTCK 272
QY 237 DANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQKVI 296
Db 273 DANPPATEYHWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332
QY 297 YISDVPFKQTS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRK--RPSYLD 344
Db 333 NITEFPYTPSPPEHGRRAGPVPTAIIGGVAGSILLVLIIVGGIIVALRRRHTFKGDYST 392
QY 345 K-----VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSN 395
Db 393 KKHVYNGYKAGIPQHH--PPMAQNLQYPDDSD-----EKKAGPLGGS- 435
QY 396 GLNSRSFDYEDENPVGEDGIQOM-----YPLYN-----QMCYQDRSPGKH 435
Db 436 -----SYEEEEEEGGGGERKVGPHPKYDEDAKRPYFTVDEAEARQDGYGDRITLGYQ 490
QY 436 HQNDPKRV-----YIDPREHYV 453

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 14.9536 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-12_COPY_58_510
Perfect score: 2417
Sequence: 1 GPIIIEPHVTAVWGKNVSLK.....KHHQNDPKRVYIDPREHYV 453

Scoring table: BLOSUM62
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	588	24.3	517	4	US-09-723-368-4
2	584.5	24.2	458	4	US-09-435-956A-1
3	565.5	23.4	518	4	US-09-919-172-20
4	427.5	17.7	479	4	US-09-723-368-2
5	390	16.1	408	4	US-09-724-864-62
6	283	11.7	440	4	US-09-866-028-61
7	283	11.7	442	4	US-09-778-510-20
8	283	11.7	442	4	US-09-930-803-1
9	279	11.5	423	4	US-09-778-510-22
10	248.5	10.3	398	4	US-09-778-510-4
11	238.5	9.9	398	4	US-09-778-510-6
12	238.5	9.9	398	4	US-09-907-794A-84
13	238.5	9.9	398	4	US-09-905-125A-84
14	238.5	9.9	398	4	US-09-902-775A-84
15	238.5	9.9	432	4	US-09-778-510-2
16	237	9.8	421	2	US-08-659-984A-1
17	237	9.8	421	3	US-08-660-531-1
18	237	9.8	444	2	US-08-659-984A-5
19	237	9.8	444	3	US-08-660-531-5
20	192.5	8.0	1101	3	US-08-660-485-2
21	190.5	7.9	227	4	US-09-205-258-947
22	187.5	7.8	274	4	US-09-570-367C-19
23	187.5	7.8	274	4	US-09-915-524-19
24	171	7.1	387	4	US-09-175-928-2
25	166.5	6.9	1091	3	US-08-986-485-5
26	166	6.9	467	3	US-09-046-736-2
27	163	6.7	365	3	US-08-928-383B-23

28	163	6.7	365	3	US-08-928-383B-24	Sequence 24, Appl
29	162.5	6.7	278	4	US-09-570-367C-2	Sequence 2, Appli
30	162.5	6.7	278	4	US-09-915-524-2	Sequence 2, Appli
31	162	6.7	365	2	US-08-979-424-3	Sequence 3, Appli
32	162	6.7	365	3	US-08-928-383B-2	Sequence 2, Appli
33	162	6.7	365	3	US-09-272-496-2	Sequence 2, Appli
34	161	6.7	365	3	US-08-928-383B-26	Sequence 26, Appl
35	160.5	6.6	642	1	US-08-217-299-1	Sequence 1, Appli
36	160.5	6.6	698	2	US-08-602-725-36	Sequence 36, Appl
37	160.5	6.6	734	2	US-08-389-459A-17	Sequence 17, Appl
38	160.5	6.6	734	3	US-08-987-867A-17	Sequence 17, Appl
39	160.5	6.6	1059	4	US-09-907-794A-290	Sequence 290, App
40	160.5	6.6	1059	4	US-09-905-125A-290	Sequence 290, App
41	160.5	6.6	1059	4	US-09-902-775A-290	Sequence 290, App
42	160.5	6.6	1119	4	US-09-907-794A-294	Sequence 294, App
43	160.5	6.6	1119	4	US-09-905-125A-294	Sequence 294, App
44	160.5	6.6	1119	4	US-09-902-775A-294	Sequence 294, App
45	159.5	6.6	278	4	US-09-570-367C-21	Sequence 21, Appl

ALIGNMENTS

RESULT 1
US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match	24.3%;	Score 588;	DB 4;	Length 517;
Best Local Similarity	30.1%;	Pred. No. 7.9e-50;		
Matches	151;	Conservative	85;	Mismatches 176; Indels 90; Gaps 15;
QY	14	GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSGVEYQGRVLFKNYS	70	
Db	44	GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSLAPYRVERVEFLRPS	103	
QY	71	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDG---	127	
Db	104	FTDGTIRLSRLELEDEGVYICEFATFPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG	162	
QY	128	-GNETVAAICIAATCKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTREARGR	185	
Db	163	QDDKVLVAICTSANGKPPSVSVSWETRLKGEABYQEI RNPNGT VVISRYRLVPSREAHQQ	222	
QY	186	RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFVGRKGVLNLCNADANPPPFKS	245	

Db 358 PPTTT-----LQPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIATRS CD 408
Qy 351 PTHKPPPLYEERSPPLPQKOLFQPE 375
Db 409 KTHTCPGCPAPEAEGAPSVFLFPPK 433

Search completed: April 12, 2004, 10:25:27
Job time : 38.8588 secs

QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VP-----FKQTSSIAVAGAVIGAVLALF 323
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFIV 417
QY 324 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP 364
Db 418 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYDPSVKKENKN 476
QY 365 PLPQKDLFQPEHL--PLQTFKEREVEGNLQHSNLSRSDYEDENPVGEDIQOMPLY 422
Db 477 PV--NNLIRKDYLEEPEKTQW-----NNVENLNRF-ERPMDYVEDLKMGMKFVSD----- 523
QY 423 NQMCYQDRSPGKHQNDPKRV-----YIDPREHYV 453
Db 524 -----EHDYDENEEDDLVSHVDGSGVISRREWYV 549

RESULT 14
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 67.5%; Score 1630.5; DB 14; Length 549;
Best Local Similarity 64.4%; Pred. No. 5.5e-133;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VP-----FKQTSSIAVAGAVIGAVLALF 323
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFIV 417
QY 324 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP 364
Db 418 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYDPSVKKENKN 476
QY 365 PLPQKDLFQPEHL--PLQTFKEREVEGNLQHSNLSRSDYEDENPVGEDIQOMPLY 422
Db 477 PV--NNLIRKDYLEEPEKTQW-----NNVENLNRF-ERPMDYVEDLKMGMKFVSD----- 523
QY 423 NQMCYQDRSPGKHQNDPKRV-----YIDPREHYV 453
Db 524 -----EHDYDENEEDDLVSHVDGSGVISRREWYV 549

RESULT 15
US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13
Query Match 66.6%; Score 1609.5; DB 10; Length 634;
Best Local Similarity 82.1%; Pred. No. 4.5e-131;
Matches 316; Conservative 7; Mismatches 43; Indels 19; Gaps 2;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRKPSYLDKVIDL-----P 350

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 51 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 110
QY 61 QGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 111 QGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 170
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 171 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 230
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 231 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 290
QY 241 PPFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQSDQKVIYISD 300
Db 291 PPFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQSDQKVIYISD 350
QY 301 VP-----FKOTSSIAVAGAVIGAVLALF 323
Db 351 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIV 410
QY 324 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP 364
Db 411 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQOQDELDSYDPSVKKENKN 469
QY 365 PLPQKDLFQPEHL--PLQTFKEREVGNLQHSNRSFYEDENPVGEDGIQOMYPLY 422
Db 470 PV--NNLRKDYLEEPEKTQW-----NNVENLNRF-ERPMDYEDLKMGMKFVSD----- 516
QY 423 NQMCYQDRSPGKHHQNNDPKRV-----YIDPREHYV 453
Db 517 -----EHYDENEDDLVSHVDGSGVISRREWYV 542

RESULT 12
US-09-972-268-4
; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from
; OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match 67.5%; Score 1630.5; DB 10; Length 549;
Best Local Similarity 64.4%; Pred. No. 5.5e-133;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117

QY 61 QGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVMSRLDGOWPDGLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 VP-----FKOTSSIAVAGAVIGAVLALF 323
Db 358 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIV 417
QY 324 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP 364
Db 418 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQOQDELDSYDPSVKKENKN 476
QY 365 PLPQKDLFQPEHL--PLQTFKEREVGNLQHSNRSFYEDENPVGEDGIQOMYPLY 422
Db 477 PV--NNLRKDYLEEPEKTQW-----NNVENLNRF-ERPMDYEDLKMGMKFVSD----- 523
QY 423 NQMCYQDRSPGKHHQNNDPKRV-----YIDPREHYV 453
Db 524 -----EHYDENEDDLVSHVDGSGVISRREWYV 549

RESULT 13
US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-6

Query Match 67.5%; Score 1630.5; DB 10; Length 549;
Best Local Similarity 64.4%; Pred. No. 5.5e-133;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

QY 361 ERSPLPQKOL 371
Db 418 ERISLPQKOL 428

RESULT 9

US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match 67.8%; Score 1638; DB 10; Length 595;
Best Local Similarity 84.8%; Pred. No. 1.4e-133;
Matches 318; Conservative 3; Mismatches 16; Indels 38; Gaps 2;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 297
QY 241 PPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 300
Db 298 PPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPIYE 360
Db 358 VPFKQTSSRS-----CDK-----THTCPPCA 379

RESULT 10

US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

Query Match 67.7%; Score 1636; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.1e-133;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANP 297
QY 241 PPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 300
Db 298 PPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 357
QY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365

RESULT 11

US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match 67.5%; Score 1630.5; DB 10; Length 542;
Best Local Similarity 64.4%; Pred. No. 5.4e-133;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

; ORGANISM: homo sapiens
US-09-972-268-31

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Query Match      81.4%; Score 1967; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 2.le-162;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	1	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOXFVSQGEY	60
Db	58	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOXFVSQGEY	117
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR	180
Db	178	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR	237
QY	181	FARGRRITCVWKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFVGRKGVNLKCNADANP	240
Db	238	FARGRRITCVWKHPALEKDIRYSFILDIOYAPEVSVTYDGNWFVGRKGVNLKCNADANP	297
QY	241	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD	300
Db	298	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD	357
QY	301	VPFKQTSSIAVAGAVIGAVLALFIALFVTVLLTPRKRKRPYSYLDKVIDLPPTHKPPPLYE	360
Db	358	VPFKQTSSIAVAGAVIGAVLALFIALFVTVLLTPRKRKRPYSYLDKVIDLPPTHKPPPLYE	417
QY	361	ERSPPLPQKOLFQ	373
Db	418	ERSPPLPQKOLFQ	430

RESIST. 7

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US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshihimi TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-6

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Query Match	77.8%;	Score 1880;	DB 10;	Length 438;
Best Local Similarity	94.9%;	Pred. No. 7.9e-155;		
Matches 352; Conservative	11;	Mismatches 8;	Indels 0;	Gaps 0;

[illegible]

QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIISQYKLFPTR	180
Dd	178	PDSLIDGGNETVAACVVAATGKPVAQIDWEGDLGEMESSTSPFNETATIVSQYKLFPTR	237
QY	181	FARGRRITCVVKHPALEKDRIYSFILDIQYAPEVSVTGYDGNWFVGRKGWNLKNADANP	240
Dd	238	FARGRRITCVVKHPALEKDRIYSFILDIQYAPEVSVTGYDGNWFVGRKGWNLKNADANP	297
QY	241	PPFKSVWSRLDGOWPDGLLASDNTHLHFVHPLTFNYSGVYICKVTNSLGQRSDOKVIYISD	300
Dd	298	PPFKSVWSRLDGOWPDGLLASDNTHLHFVHPLTVNYSGVYVCVKSNSLGQRSDOKVIYISD	357
QY	301	VPEKOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYE	360
Dd	358	IPLTOTSSIAVAGAVIGAVLALFIITVFVTVLLTPRKRPSYLDKVIDLPPTHKPPPYVE	417
QY	361	ERSPPLPOKOL	371
Dd	418	ERIPSLPOKOL	428

RESULT 8

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US-09-972-268-19
; Sequence 19, Application US/09972368
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES,
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 438
; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-19

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Query Match 77.8%; Score 1880; DB 10; Length 438;
Best Local Similarity 94.9%; Pred. NO. 7.9e-155;
Matches 352; Conservative 11; Mismatches 8; Indels 0;
Gaps 0;

Qy	1	GPII	VEPHV	TAVWG	KNVSL	KCLIE	VNETI	TQIS	WEKIH	GSSTQ	TVA	VHHP	QYGF	SVQ	GEY	60	
Db	58	GSII	VEPHV	TAVWG	KNVSL	KCLIE	VNETI	TQIS	WEKIH	GSSTQ	TVA	VHHP	QYGF	SVQ	GDY	117	
Qy	61	QGRV	LFNYS	LNDAT	ITLHN	IGFSD	SGKYI	CKAV	TFPL	GNAQS	STTV	TLV	VEPT	VS	LKG	120	
Db	118	QGRV	LFNYS	LNDAT	ITLHN	IGFSD	SGKYI	CKAV	TFPL	GNAQS	STTV	TLV	VEPT	VS	LKG	177	
Qy	121	PD	SLIDG	GNET	VAAIC	IAATG	KPVA	HDW	EGDL	GEMES	TTTSP	FN	ETAT	II	SOY	180	
Db	178	PD	SLIDG	GNET	VAAIC	IAATG	KPVA	HDW	EGDL	GEMES	TTTSP	FN	ETAT	II	SOY	237	
Qy	181	FARG	RRITC	VVKHP	ALEKD	IRYS	FILDI	IQYA	PEVS	VTGY	DGNF	VGR	KGV	NLKN	CNAD	240	
Db	238	FARG	RRITC	VVKHP	ALEKD	IRYS	FILDI	IQYA	PEVS	VTGY	DGNF	VGR	KGV	NLKN	CNAD	297	
Qy	241	PP	FKSV	WSRLD	GQW	PDGL	LAS	DN	TLHF	VHPL	TNYS	GVV	ICK	VTNS	LQ	300	
Db	298	PP	FKSV	WSRLD	GQW	PDGL	LAS	DN	TLHF	VHPL	TNYS	GVV	ICK	VTNS	LQ	357	
Qy	301	VP	EKQ	TSSIA	VAGAV	IGAV	LALF	IIA	IFV	TLLT	TPR	KRP	PSY	L	DKV	360	
Db	358	IP	L	TQ	TSSIA	VAGAV	IGAV	LALF	IIA	IFV	TLLT	TPR	KRP	PSY	L	DKV	417

Db 172 PDSLIDGGNETVAAICIAATGKPAVAHIDWEGDLGEMESTTTSPNETATIISQYKLPFTR 231
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGYNLKCNDANP 240
Db 232 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGYNLKCNDANP 291
QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 292 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 351
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSPSYLDKVIDLPPTHKPPPLYE 360
Db 352 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSPSYLDKVIDLPPTHKPPPLYE 411
QY 361 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYP 420
Db 412 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYP 471
QY 421 LYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 453
Db 472 LYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 504

RESULT 2

US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10

Query Match 100.0%; Score 2417; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.9e-201;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPAVAHIDWEGDLGEMESTTTSPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPAVAHIDWEGDLGEMESTTTSPNETATIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGYNLKCNDANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGYNLKCNDANP 297
QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357

QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSPSYLDKVIDLPPTHKPPPLYE 360
Db 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYP 420
Db 418 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYP 477
QY 421 LYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 453
Db 478 LYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 510

RESULT 3

US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match 100.0%; Score 2417; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 1.9e-201;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPAVAHIDWEGDLGEMESTTTSPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPAVAHIDWEGDLGEMESTTTSPNETATIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGYNLKCNDANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGYNLKCNDANP 297
QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSPSYLDKVIDLPPTHKPPPLYE 360
Db 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYP 420
Db 418 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSFDYEDENPVGEDGIQQMYP 477
QY 421 LYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 453
Db 478 LYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 510

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 37.8588 Seconds
(without alignments)
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Sequence: 1 GPIIPEPHVTAVGKNVSLK.....KHHQNDPKRVYIDPREHYV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
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9: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2417	100.0	504	10	US-09-972-268-8
2	2417	100.0	510	10	US-09-972-268-10
3	2417	100.0	510	10	US-09-972-268-12
4	2161	89.4	510	10	US-09-959-845-4
5	2161	89.4	510	10	US-09-972-268-18
6	1967	81.4	437	10	US-09-972-268-31
7	1880	77.8	438	10	US-09-959-845-6
8	1880	77.8	438	10	US-09-972-268-19
9	1638	67.8	595	10	US-09-972-268-14
10	1636	67.7	387	10	US-09-972-268-16
11	1630.5	67.5	542	10	US-09-972-268-2
12	1630.5	67.5	549	10	US-09-972-268-4
13	1630.5	67.5	549	10	US-09-972-268-6
14	1630.5	67.5	549	14	US-10-161-572-45
15	1609.5	66.6	634	10	US-09-972-268-13

16	1604	66.4	426	10	US-09-972-268-15	Sequence 15, Appl
17	1592.5	65.9	549	10	US-09-959-845-2	Sequence 2, Appli
18	1592.5	65.9	549	10	US-09-972-268-17	Sequence 17, Appl
19	588	24.3	514	14	US-10-161-572-60	Sequence 60, Appl
20	588	24.3	517	10	US-09-972-268-20	Sequence 20, Appl
21	537.5	24.3	458	10	US-09-972-268-21	Sequence 21, Appl
22	565.5	23.4	518	9	US-09-919-172-20	Sequence 20, Appl
23	518.5	21.5	497	10	US-09-972-268-37	Sequence 37, Appl
24	517	21.4	498	10	US-09-972-268-39	Sequence 39, Appl
25	503.5	20.8	479	10	US-09-766-511B-35	Sequence 35, Appl
26	503.5	20.8	510	10	US-09-766-511B-33	Sequence 33, Appl
27	503.5	20.8	510	12	US-10-058-270A-54	Sequence 54, Appl
28	503.5	20.8	510	14	US-10-161-572-55	Sequence 55, Appl
29	503.5	20.8	510	14	US-10-241-220-94	Sequence 94, Appl
30	503.5	20.8	510	15	US-10-295-027-66	Sequence 66, Appl
31	503.5	20.8	510	15	US-10-173-999-76	Sequence 76, Appl
32	502	20.8	511	10	US-09-972-268-34	Sequence 34, Appl
33	501.5	20.7	510	10	US-09-972-268-24	Sequence 24, Appl
34	501.5	20.7	510	14	US-10-161-572-54	Sequence 54, Appl
35	496	20.5	538	10	US-09-972-268-23	Sequence 23, Appl
36	496	20.5	538	10	US-09-984-130-138	Sequence 138, App
37	496	20.5	538	10	US-09-836-353A-138	Sequence 138, App
38	496	20.5	538	14	US-10-161-572-61	Sequence 61, Appl
39	496	20.5	538	15	US-10-411-010-17	Sequence 17, Appl
40	477.5	19.8	580	10	US-09-972-268-36	Sequence 36, Appl
41	471.5	19.5	458	12	US-10-296-115-1150	Sequence 1150, Ap
42	469.5	19.4	314	10	US-09-766-511B-36	Sequence 36, Appl
43	427.5	17.7	479	10	US-09-972-268-22	Sequence 22, Appl
44	427.5	17.7	479	14	US-10-161-572-62	Sequence 62, Appl
45	425.5	17.6	522	15	US-10-264-049-2969	Sequence 2969, Ap

ALIGNMENTS

RESULT 1
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

Query Match 100.0%; Score 2417; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 1.9e-201;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY	60
Db	52	GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY	111
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120
Db	112	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	171
QY	121	PDSLIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR	180


```
Db      298 PPFKSVSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
Qy      301 VP-----FKQTSSIAVAGAVIGAVLALF 323
Db      358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVWGGALFIV 417
Qy      324 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP 364
Db      418 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSPDSVKKENKN 476
Qy      365 PLPQKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVGEDGIQQMYPLY 422
Db      477 PV--NNLIRKDYLEEPEKTQW-----NNVENLNRFP-ERPMDYVEDLKMGMKFVSD----- 523
Qy      423 NQMCYQDRSPGKHQNDPKRV-----YIDPREHYV 453
Db      524 -----EHYDENEDDLVSHVDGVSISRREWYV 549
```

Search completed: April 12, 2004, 09:38:34
Job time : 55.7113 secs

FT	Domain	189. .250	
FT	/note= "Extracellular Ig domain"		
FT	Modified-site	222	
FT	/note= "N-glycosylated"		
FT	Domain	287. .342	
FT	/note= "Extracellular Ig domain"		
FT	Modified-site	331	
FT	/note= "N-glycosylated"		
FT	Domain	405. .424	
FT	/note= "Transmembrane domain"		
FT	Domain	425. .549	
FT	/note= "C-terminal domain"		
XX			
PN	WO200228902-A2.		
XX			
PD	11-APR-2002.		
XX			
PF	05-OCT-2001; 2001WO-US031392.		
XX			
PR	05-OCT-2000; 2000US-0238557P.		
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
PI	Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;		
XX			
DR	WPI; 2002-426103/45.		
DR	N-PSDB; AAD37442.		
XX			
PT	Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,		
PT	useful for treating or preventing heart failure, malaria,		
PT	glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,		
PT	sepsis, stroke.		
XX			
PS	Claim 1; Page 89-91; 141pp; English.		
XX			
CC	The invention relates to a substantially purified nectin3alpha, beta,		
CC	gamma and nectin-4 polypeptides and their corresponding polynucleotides.		
CC	Nectin DNA and protein are useful for treating a disease associated with		
CC	cell adhesion activity, adherens junction formation activity, epithelial		
CC	or endothelial barrier function activity, endothelial proliferation or		
CC	migration activity, viral polypeptide binding activity. The epithelial or		
CC	endothelial barrier function disorder which is treated by the above		
CC	mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,		
CC	asthma, allergy, allograft rejection, metastasis of cancer cells,		
CC	paracellular transport disorders such as magnesium transport defects in		
CC	the kidney or inflammatory bowel disease. Nectin DNA is also useful for		
CC	inhibiting angiogenesis in a mammal and treating endothelial migration,		
CC	proliferation or angiogenic condition of a tissue or a subject, such as		
CC	ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,		
CC	stroke, restenosis, tumour growth and treating herpesvirus infection.		
CC	Nectin is also useful for modulating proliferation or migration of an		
CC	endothelial cell, an epithelial cell or a smooth muscle cell (vascular		
CC	smooth muscle cell). The present sequence is human nectin-3alpha DNA.		
CC	Human nectin-3alpha gene is located on chromosome 3		
XX			
SQ	Sequence 549 AA;		
	Query Match	67.5%;	Score 1630.5; DB 5; Length 549;
	Best Local Similarity	64.4%;	Pred. No. 1.4e-126;
	Matches 333; Conservative	33;	Mismatches 62; Indels 89; Gaps 10
QY	1	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY	60
DB	58	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY	117
QY	61	QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG	120
DB	118	QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTFFNETATIIISOYKLFPTTR	180
DB	178	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTFFNETATIIISOYKLFPTTR	237

QY	181	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFEVGRKGVNLKCNADANP	241
Db	238	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFEVGRKGVNLKCNADANP	297
QY	241	PPFKSVWSRLDGQWEDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISD	300
Db	298	PPFKSVWSRLDGQWEDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISD	357
QY	301	VP-----FKQTSSIAVAGAVIGAVLALF	323
Db	358	PPTTTTLOPTIQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFIV	417
QY	324	IIAIFVTVLLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSP	364
Db	418	LVSVLAGIFCYRRRRFRGDFYFAKNY-IPPSDMQKESQIDVLQQDELDSYPDSVKKENKN	476
QY	365	PLPOKDLFQPEHL--PLQTQFKEREVENLQHSNGLNSRSEFYEDENPVGEDGIQQMYPLY	422
Db	477	PV--NNLIRKDYLEEPEKTQW-----NNVENLNRF-ERPMDYEDLKMGMKFVSD-----	523
QY	423	NOMCYQDRSPGKHQNNDPKRV-----YIDPREHYV	453
Db	524	-----EHYDENEDDLVSHVDGVSISRREWYV	549
RESULT 14			
AAE23282			
ID	AAE23282 standard; protein; 549 AA.		
XX			
AC	AAE23282;		
XX			
DT	29-AUG-2003 (revised)		
DT	27-AUG-2002 (first entry)		
XX			
DE	Mouse nectin-3-human nectin 3alpha fusion protein.		
XX			
KW	Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;		
KW	paracellular transport disorder; kidney; diabetic retinopathy; allergy;		
KW	allograft rejection; metastasis; restenosis; inflammatory bowel disease;		
KW	oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;		
KW	stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;		
KW	chromosome 3.		
XX			
OS	Homo sapiens.		
OS	Mus musculus.		
OS	Chimeric.		
XX			
FH	Key		
FT	Region		
FT	1..7		
FT	/note= "Mouse nectin-3 protein"		
FT	8..549		
FT	/note= "Human nectin-3alpha protein"		
XX			
PN	WO200228902-A2.		
XX			
PD	11-APR-2002.		
XX			
PF	05-OCT-2001; 2001WO-US031392.		
XX			
PR	05-OCT-2000; 2000US-0238557P.		
XX			
PA	(IMMV) IMMUNEX CORP.		
XX			
PI	Baum PR, Fanglow WC, Lofton TE, Sorensen EA, Youakim A;		
XX			
DR	WPI; 2002-426103/45.		
DR	N-PSDE; AAD37441.		
XX			
PT	Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,		
PT	useful for treating or preventing heart failure, malaria,		
PT	glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,		
PT	sepsis, stroke.		
XX			

CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta-
CC FLAGpolyHis fusion protein
XX
SQ Sequence 387 AA;

Query Match 67.7%; Score 1636; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. NO. 3e-127;
Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLPFTR 237
QY 181 FARRRITCVVKHPALEKDIRYFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSS 308
Db 358 VPFKQTSS 365

RESULT 11
AAM39143
ID AAM39143 standard; protein; 555 AA.
XX
AC AAM39143;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2288.
XX
KW Human; neutropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.
PF
XX 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
(HYSE-) HYSEQ INC.
Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI58299.

Novel nucleic acids and polypeptides, useful for treating disorders such
as central nervous system injuries.
Example 4; SEQ ID NO 2288; 10078pp; English.

The invention relates to human nucleic acids (AAI57798-AAI61369) and the
encoded polypeptides (AAM38642-AAM42213) with neutropic,
immunosuppressant and cytostatic activity. The polynucleotides are useful
in gene therapy. A composition containing a polypeptide or polynucleotide
of the invention may be used to treat diseases of the peripheral nervous
system, such as peripheral nervous injuries, peripheral neuropathy and
localised neuropathies and central nervous system diseases, such as
Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
utilisation of the activities such as: Immune system suppression,
Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
assays for receptor activity, arthritis and inflammation, leukaemias and
C.N.S disorders. Note: The sequence data for this patent did not form
part of the printed specification

Sequence 555 AA;

Query Match 67.5%; Score 1632.5; DB 4; Length 555;
Best Local Similarity 64.4%; Pred. No. 9.5e-127;
Matches 333; Conservative 34; Mismatches 61; Indels 89; Gaps 10;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 64 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 123
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 124 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 183
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLPFTR 180
Db 184 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLPFTR 243
QY 181 FARRRITCVVKHPALEKDIRYFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 244 FARRRITCVVKHPALEKDIRYFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 303
QY 241 PPFKSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 304 PPFKSVMSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 363
QY 301 VP-----FKQTSSIAVAGAVIGAVLALF 323
Db 364 PPTTTTLQPTTQWHPSTADIEDLATEPKKLPFPLSTLATIKODTTATIIASVWGALFIV 423

RESULT 9
AAE23288 ID AAE23288 standard; protein; 595 AA.
XX AC AAE23288;
XX DT 27-AUG-2002 (first entry)
XX DE Human nectin-3beta-IgG1Fc region fusion protein.
XX KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX PN WO200228902-A2.
XX PD 11-APR-2002.
XX PF 05-OCT-2001; 2001WO-US031392.
XX PR 05-OCT-2000; 2000US-0238557P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX DR WPI; 2002-426103/45.
XX KW Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX PS Claim 9; Page 102-104; 141pp; English.
XX CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX SQ Sequence 595 AA;
Query Match 67.8%; Score 1638; DB 5; Length 595;
Best Local Similarity 84.8%; Pred. No. 3.7e-127;
Matches 318; Conservative 3; Mismatches 16; Indels 38; Gaps 2;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTFPNETATIIISQYKLFPTTR 237
QY 181 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 240
Db 238 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 297
QY 241 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 VPFKQTSSRS-----CDK-----THTCPPCPA 379
QY 361 ERSPPLPQKDLFQPE 375
Db 380 PEAGAPSVLEFPKP 394
RESULT 10
AAE23290 ID AAE23290 standard; protein; 387 AA.
XX AC AAE23290;
XX DT 27-AUG-2002 (first entry)
XX DE Human nectin-3beta-FLAGpolyHis fusion protein.
XX KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX FH Key Location/Qualifiers
FT Region 1..365 /note= "Human nectin-3alpha protein"
FT Region 366..381 /note= "FLAG peptide"
FT Region 382..387 /note= "PolyHis tag"
XX WO200228902-A2.
XX PN 11-APR-2002.
XX PF 05-OCT-2001; 2001WO-US031392.
XX PR 05-OCT-2000; 2000US-0238557P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX DR WPI; 2002-426103/45.
XX KW Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX PS Claim 9; Page 105-107; 141pp; English.

XX WPI; 2001-570771/64.
DR N-PSDB; AAH78181.
XX
PT New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and
PT corresponding antibodies.
XX
PS Claim 3; Page 53-55; 64pp; Japanese.
XX
CC The present sequence represents a murine nectin-3 polypeptide. Nectin-3
CC is an immunoglobulin-like cell adhesion molecule that shows homophilic
CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
CC polynucleotides are useful for investigating the mechanisms of cell
CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
CC malignancies of various cancers, and the development of methods for the
CC treatment and prevention of cancer
XX
SQ Sequence 438 AA;
Query Match 77.8%; Score 1880; DB 4; Length 438;
Best Local Similarity 94.9%; Pred. No. 1.9e-147;
Matches 352; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAVCAATGKPVQAQIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLCNADANP 297
QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
Db 298 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
QY 301 VPFKOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFVTLLTPRKKRPSYLDKVIDLPPTHKPPPYE 417
QY 361 ERSPPLPQKDL 371
Db 418 ERIPSLPQKDL 428
RESULT 8
AAE23293
ID AAE23293 standard; protein; 438 AA.
XX
AC AAE23293;
XX
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3gamma protein.
XX
KW Mouse; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma.
XX
OS Mus musculus.
XX
PN WO200228902-A2.
XX

PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
PI WPI; 2002-426103/45.
DR
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Disclosure; Page 111-112; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is mouse nectin-3gamma protein
XX
SQ Sequence 438 AA;
Query Match 77.8%; Score 1880; DB 5; Length 438;
Best Local Similarity 94.9%; Pred. No. 1.9e-147;
Matches 352; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAVCAATGKPVQAQIDWEGDLGEMESSTTSFPNETATIVSQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLCNADANP 297
QY 241 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
Db 298 PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
QY 301 VPFKOTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFVTLLTPRKKRPSYLDKVIDLPPTHKPPPYE 417
QY 361 ERSPPLPQKDL 371
Db 418 ERIPSLPQKDL 428

QY 121 PDSLIDGGNETVAALCIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLPFTR 180
DB 178 PDSLIDGGNETVAACVAAATGKPVAAIDWEGDLGEMESTTSPFPNETATIVSQYKLPFTR 237
QY 181 FARGRRITCVVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
DB 238 FARGRRITCVVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
DB 298 PPFKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
DB 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKDLF-QPEHLPLQTFQKEREVENGLQHSNLSRSDYEDENPVCGDGIQOMY 419
DB 418 ERIPSLPQKDLGLQTEHLPLQTFQKEKGAGGLQPSNGPISRFRDYEDESTMQEDGTQMC 477
QY 420 PLYNQMCYQDRSPGKHQNDPKRVYIDPREHYV 453
DB 478 PLYSQMCHQDRSPRQHPRN-PERLYINPREHYV 510

RESULT 6
AAE23299
ID AAE23299 standard; protein; 437 AA.
XX
AC AAE23299;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3gamma protein.

XX Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

OS Homo sapiens.
XX
XX WO200228902-A2.
XX
XX 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI

XX WPI; 2002-426103/45.
DR N-PSDB; AAD37450.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX

PS Claim 1; Page 125-126; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3gamma protein.
CC Human nectin-3gamma gene is located on chromosome 3
XX

SQ Sequence 437 AA;
Query Match 81.4%; Score 1967; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 1.le-154;
Matches 373; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
DB 58 GPIIVEPHVTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
DB 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAALCIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLPFTR 180
DB 178 PDSLIDGGNETVAALCIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
DB 238 FARGRRITCVVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
DB 298 PPFKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
DB 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKDLFQ 373
DB 418 ERSPPLPQKDLFQ 430

RESULT 7
AAG63984
ID AAG63984 standard; protein; 438 AA.
XX
AC AAG63984;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of murine nectin-3.
XX
KW Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
OS Mus sp.
XX
PN WO200166736-A1.
XX
PD 13-SEP-2001.
XX

PF 09-MAR-2001; 2001WO-JP001871.
XX
PR 09-MAR-2000; 2000JP-00065595.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.
XX
PI Takahashi K, Takai Y, Nakanishi H, Sato K;

XX Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
XX Mus sp.
OS WO200166736-A1.
XX 13-SEP-2001.
PD 09-MAR-2001; 2001WO-JP001871.
PF 09-MAR-2000; 2000JP-00065595.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.
XX Takahashi K, Takai Y, Nakanishi H, Sato K;
PI WPI; 2001-570771/64.
XX N-PSDB; AAH78180.
DR
DR
XX New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and
PT corresponding antibodies.
XX Claim 2; Page 45-48; 64pp; Japanese.
PS
PS The present sequence represents a murine nectin-3 polypeptide. Nectin-3
XX is an immunoglobulin-like cell adhesion molecule that shows homophilic
CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
CC polynucleotides are useful for investigating the mechanisms of cell
CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
CC malignancies of various cancers, and the development of methods for the
CC treatment and prevention of cancer
XX
SQ Sequence 510 AA;
Query Match 89.4%; Score 2161; DB 4; Length 510;
Best Local Similarity 89.6%; Pred. No. 1e-170;
Matches 407; Conservative 21; Mismatches 24; Indels 2; Gaps 2;
QY 1 GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 60
Db 58 GSIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTAVVHHPOYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLFPT 180
Db 178 PDSLIDGGNETVAAVCVATGKPVQAIDWEGDLGEMESSTTSFPNETATISQYKLFPT 237
QY 181 FARGRRITCVVKHPALEKDRIYSFILDIOYAPEVSVTGYDGNWVFGKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDRIYSFILDIOYAPEVSVTGYDGNWVFGKGVNLCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGALALFIIAIFVTVLLTPRKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGALALFIIITVFTVLLTPRKRPSYLDKVIDLPPTHKPPPYE 417
QY 361 ERSPLPQKOLF-QPEHLPLOTQFKEREVGNLQHSNLSRSDYEDENPVGEDGIQQMY 419
Db 418 ERIPSLPQKDLGQTEHLPLOTQFKEKGAGGLQPSNGPIISRRFDYEDESTMQEDGTQMC 477
QY 420 PLYNQMCYQDRSPGKHQNDPKRVYIDPREHYV 453
Db 478 PLYSQMCHQDRSPRQHPRN-PERLYINPREHYV 510

RESULT 5
AAE23292
ID AAE23292 standard; protein; 510 AA.
XX
AC AAE23292;
XX 27-AUG-2002 (first entry)
XX Mouse nectin-3beta protein.
KW Mouse; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma.
XX
OS Mus musculus.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Disclosure; Page 109-110; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is mouse nectin-3beta protein
XX
SQ Sequence 510 AA;
Query Match 89.4%; Score 2161; DB 5; Length 510;
Best Local Similarity 89.6%; Pred. No. 1e-170;
Matches 407; Conservative 21; Mismatches 24; Indels 2; Gaps 2;
QY 1 GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEY 60
Db 58 GSIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTAVVHHPOYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

Db 298 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQQMYP 420
Db 418 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQQMYP 477
QY 421 LYNQMCYQDRSPGKHQNDPKRVYIDPREHYV 453
Db 478 LYNQMCYQDRSPGKHQNDPKRVYIDPREHYV 510

RESULT 3
AAE23286
ID AAE23286 standard; protein; 510 AA.
XX
AC AAE23286;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta protein.

XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX Homo sapiens.
OS
XX
FH Key Location/Qualifiers
FT Modified-site 73 /note= "N-glycosylated"
FT Domain 74. .152 /note= "Extracellular Ig domain"
FT Modified-site 83 /note= "N-glycosylated"
FT Modified-site 125 /note= "N-glycosylated"
FT Modified-site 186 /note= "N-glycosylated"
FT Domain 189. .250 /note= "Extracellular Ig domain"
FT Modified-site 222 /note= "N-glycosylated"
FT Domain 287. .342 /note= "Extracellular Ig domain"
FT Modified-site 331 /note= "N-glycosylated"
FT Domain 386. .510 /note= "Intracellular C-terminal domain"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37445.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,

PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 98-99; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein.
CC Human nectin-3beta gene is located on chromosome 3
XX
SQ Sequence 510 AA;

Query Match 100.0%; Score 2417; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.5e-192;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGSVQGEY 60
Db 58 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 417
QY 361 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQQMYP 420
Db 418 ERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSDYEDENPVGEDGIQQMYP 477
QY 421 LYNQMCYQDRSPGKHQNDPKRVYIDPREHYV 453
Db 478 LYNQMCYQDRSPGKHQNDPKRVYIDPREHYV 510

RESULT 4
AAG63983
ID AAG63983 standard; protein; 510 AA.
XX
AC AAG63983;
XX
DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of murine nectin-3.

CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX
SQ Sequence 504 AA;

Query Match 100.0%; Score 2417; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. No. 5.4e-192;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db |||||
QY 52 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 111
Db |||||
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
QY 112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171
Db |||||
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db |||||
QY 172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 231
Db |||||
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLCNADANP 240
Db |||||
QY 232 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLCNADANP 291
Db |||||
QY 241 PPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db |||||
QY 292 PPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 351
Db |||||
QY 301 VPKQTSSIAVAGAVIGAVLALFIAFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db |||||
QY 352 VPKQTSSIAVAGAVIGAVLALFIAFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 411
Db |||||
QY 361 ERSPPLPKDLFQPEHLPLQTPKREVGNLQHSNGLNSRFDYEDENPVGEDGIQWYP 420
Db |||||
QY 412 ERSPPLPKDLFQPEHLPLQTPKREVGNLQHSNGLNSRFDYEDENPVGEDGIQWYP 471
Db |||||
QY 421 LYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 453
Db |||||
QY 472 LYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 504
Db |||||

RESULT 2
AAE23285
ID AAE23285 standard; protein; 510 AA.
XX
AC AAE23285;
XX
XX 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin-3beta fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX

FH Key Location/Qualifiers
FT Region 1. .6
FT /note= "Mouse nectin-3 pprotein"
FT Region 7. .510
FT /note= "Human nectin-3beta protein"
XX
PN WO200228902-A2.
XX
XX 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX WPI; 2002-426103/45.
XX
XX N-PSDB; AAD37444.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
XX Claim 1; Page 94-95; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 510 AA;

Query Match 100.0%; Score 2417; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. No. 5.5e-192;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db |||||
QY 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
Db |||||
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db |||||
QY 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
Db |||||
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db |||||
QY 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237
Db |||||
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLCNADANP 240
Db |||||
QY 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLCNADANP 297
Db |||||
QY 241 PPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
Db |||||

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 54.7113 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-12_COPY_58_510
Perfect score: 2417
Sequence: 1 GPIVPEPHVTAVGKNVSLK.....KHHQNDPKRVYIDPREHYV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	2417	100.0 504 5	Aae23284 Human del
2	2417	100.0 510 5	Aae23285 Mouse nec
3	2417	100.0 510 5	Aae23286 Human nec
4	2161	89.4 510 4	Aag63983 Amino aci
5	2161	89.4 510 5	Aae23292 Mouse nec
6	1967	81.4 437 5	Aae23299 Human nec
7	1880	77.8 438 4	Aag63984 Amino aci
8	1880	77.8 438 5	Aae23293 Mouse nec
9	1638	67.8 595 5	Aae23288 Human nec
10	1636	67.7 387 5	Aae23290 Human nec
11	1632.5	67.5 555 4	Aam39143 Human pol
12	1630.5	67.5 542 5	Aae23281 Human del
13	1630.5	67.5 549 5	Aae23283 Human nec
14	1630.5	67.5 549 5	Aae23282 Mouse nec
15	1630.5	67.5 549 6	Abj20222 Human IG
16	1609.5	66.6 634 5	Aae23287 Human nec
17	1604	66.4 426 5	Aae23289 Human nec
18	1592.5	65.9 549 4	Aag63982 Amino aci
19	1592.5	65.9 549 4	Aag63985 Amino aci
20	1592.5	65.9 549 5	Aae23291 Mouse nec
21	1543	63.8 559 4	AAM40929 Human pol
22	1218	50.4 267 4	AAM93536 Human pol
23	588	24.3 514 6	Abj20237 Human IG
24	588	24.3 517 3	Aay32390 Herpesvir
25	588	24.3 517 5	Aae23294 Human nec

26	587.5	24.3	458	5	AAE23295	Aae23295 Human nec
27	565.5	23.4	518	5	ABG77170	Abg77170 Prostate
28	518.5	21.5	497	5	AAE23303	Aae23303 Human nec
29	517	21.4	498	5	AAE23305	Aae23305 Human nec
30	503.5	20.8	510	4	AAE23365	Aab93365 Human pro
31	503.5	20.8	510	4	AAU00471	Aau00471 Human TAN
32	503.5	20.8	510	5	ABJ05562	Abj05562 Breast ca
33	503.5	20.8	510	6	ABJ20232	Abj20232 Human IG
34	503.5	20.8	510	6	ABR48229	AbR48229 Human bla
35	503.5	20.8	510	6	ABU56613	Abu56613 Lung canc
36	503.5	20.8	510	6	ABP97212	Abp97212 Tumour-as
37	503.5	20.8	510	7	ADB80512	ADB80512 Ovarian c
38	502	20.8	511	5	AAE23301	Aae23301 Human nec
39	501.5	20.7	510	5	AAE23300	Aae23300 Human nec
40	501.5	20.7	510	6	ABJ20231	Abj20231 Human IG
41	496	20.5	538	5	AAE23297	Aae23297 Human nec
42	496	20.5	538	6	ABJ20238	Abj20238 Human IG
43	496	20.5	538	8	ADE86687	Ade86687 Human pol
44	477.5	19.8	580	5	AAE23302	Aae23302 Human nec
45	471.5	19.5	458	4	AAM25635	Aam25635 Human pro

ALIGNMENTS

RESULT 1
AAE23284
ID AAE23284 standard; protein; 504 AA.
XX
AC AAE23284;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3beta protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis; paracellular transport disorder; kidney; diabetic retinopathy; allergy; allograft rejection; metastasis; restenosis; inflammatory bowel disease; oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSD3; AAD37443.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 89-91; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

Db 38 VLPEVRGLGCTVELPCHLLPPTTERTVSQVWORLDG---TVVAAFHPSFGVDFPNSQFS 94
QY 61 QGRVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP- 113
Db 95 KDLRSFVRARPETNADRLDATLAFRGLRVEDEGNYTCEPATFNGTRRGVTLWRVIAQPE 154
QY 114 ----TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFN---E 166
Db 155 NHAEAQEVITGPQSV-----AVARCVSTGGRPPARITWISSLGG-EAKDTQEPGIGQAG 206
QY 167 TATISQYKLPPTRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGV 226
Db 207 TVTIIISRYSLVPVGRADGVKTCRVEHESFEPIILLPVTLVRYYPPEVSIISGYDDNWILG 266
QY 227 RKGYNLKNADANPPPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNS 286
Db 267 RSEAILTCDVRNPEPTDYDWTSGVFPASAVAQGSQ-L-LVHSVDRMNTTIFICTATNA 325
QY 287 LGQBSDQKVIYISDVPEFKQTSIAVAGAVIGAVLALFI-IAIFVTVLLTPRKKRPSYL-- 343
Db 326 VGTGRAEQVILVRESP--STAGAGATGGIIGGIIAIIATAVAGTGILICRQQRKEQLQ 383
QY 344 ----DKVIDLPPTHKPP-PLYBERSPPLPQK--DLFQPEHPLQTFP----- 383
Db 384 AADDEEELEGPPSYKPPTPKAKLEPEMPSQLFTLGASEHSPVKTYPYFDAGVSCADQEMP 443
QY 384 KEREVGNLQH-----SNGLN-----SRSPDYEDENPVGEDGIQQMYP 420
Db 444 RYHELPTLEWSGPLLGLGATGLGPSLLVPPGPNVVEGVSLSEDEEEDDEEEDFLDKINP 503
QY 421 LYNQMCYQDRSPGKHQNNND 440
Db 504 IYDALSYN--SPSDSYQSKD 521

RESULT 13

Q9DBP8
ID Q9DBP8 PRELIMINARY; PRT; 483 AA.
AC Q9DBP8;
DT 01-JUN-2001 (TremBLrel. 17, Created)
DT 01-JUN-2001 (TremBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE 1200017F15RIK protein.
GN PVRL4 OR 1200017F15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-P.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).

DR EMBL; AK004821; BAB23592.1; -.
DR MGD; MGI:1918990; Pvr14.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 483 AA; 53030 MW; F8F0466C000852E8 CRC64;

Query Match 21.0%; Score 507; DB 11; Length 483;
Best Local Similarity 29.6%; Pred. No. 1.5e-34;
Matches 141; Conservative 80; Mismatches 193; Indels 62; Gaps 16;

QY 9 VTAVWGKNVSLKCLI--EVNETITQISWEKIH-GKSSQTVAVHHPOYGFVSQGEYQGRV- 64
Db 39 VTVVLGQDAKLPCFYRGDPDEQVGVAVARVDPNEGIRELALLHSKYGLHVNPAVEDRVE 98
QY 65 -----LFXNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVS 116
Db 99 QPPPPRDPL-----DGSVLLRNAVQADEGEYECRVSTFPAGSFQARMRLRVLPPLPS 151
QY 117 LTKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKL 176
Db 152 LNPGP-PLIEGQGLTLAASC-TAEGSPAPSVTWDTEVKTQSSRSFTHPRSAAVTSEFHL 209
QY 177 FPTRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGN--WFGVGRKGVNLKC 234
Db 210 VPSRMNGQPLTCVSHPGLLQDRRIHTTLQVAFLEASVVRGLEDQNLWQVREGATLKC 269
QY 235 NADANPPPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQK 294
Db 270 LSEGQPPP-KYNWTRLDGRLPSGVVRKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQV 327
QY 295 VIYISDV--PFKQTSIAVAGAVIGAVLALFIIFVTVLLTPRKKR-----PSYLDKV 346
Db 328 TVEVLDPEDPGKQVLDVLSASVIVGVIAALLFCLLVVVVVLMSRYHRRKAQQMTQKYEEE 387
QY 347 IDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSNGLNSRSPDYED 406
Db 388 LTLTRENSIRRLSHSHSDPRSQSE--EPEGRSYSTLTVTREI---ETQTELLSPGSGRTE 442
QY 407 ENPVGEDGIQOMYPLYNQMCYQDRSPGKH--QNNDPKR-----VYIDPREHYV 453
Db 443 EDDDDQDEGIKQ-----AMNHFVQENGTLRAKPTGNGIYINGRHLV 483

RESULT 14

Q96NY8
ID Q96NY8 PRELIMINARY; PRT; 510 AA.
AC Q96NY8;
DT 01-DEC-2001 (TremBLrel. 19, Created)
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Nectin 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.,
RT "Nectin4/PRR4: A new afadin-associated member of the nectin family
RT that trans-interacts with nectin1/PRR1 through V domain interaction."
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF426163; AAL23958.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 510 AA; 55454 MW; DCF5E1D794F227FA CRC64;


```
QY 347 IDLPPTH-----KPPPLYEERSPLPQKDLFQPEHL--PLQTQFKEREVG 389
      :||:
      :||:
Db 301 Y-IPPSDMQKESQIDVLQQDELDPYPDSVKKENKNPVNNLIRKDYLEEPEKTQW-----N 354
      :||:
      :||:
QY 390 NLQHSNGLNSRSFYEDENPVG 411
      :||:
      :||:
Db 355 NVENLNRF-ERPMDYEDLKMG 375

RESULT 8
Q9BVA9
ID Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Similar to nectin 3, DKFZP566B0846 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; IG-Like.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 26.8%; Score 648.5; DB 4; Length 304;
Best Local Similarity 44.1%; Pred. No. 6.5e-47;
Matches 145; Conservative 33; Mismatches 62; Indels 89; Gaps 10;

QY 189 CVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPFKSVM 248
      |||||
Db 1 CVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPFKSVM 60

QY 249 RLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVP----- 302
      |||||
Db 61 RLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPPTTTLQ 120

QY 303 -----FKQTSSIAVAGAVIGAVLALFIIAIFTV 331
      :||:
      :||:
Db 121 PTIQWHPSTADIEDLATEPKKLPFLSTLTIKDDTIATIASVVGALFIVLSVLAGI 180

QY 332 LLTPRK--RPSYLDKVIDLPPTHK-----PPPLYEERSPLPQKDLF 372
      :||:
      :||:
Db 181 FCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYDPSVKKENKNPV--NNLI 237

QY 373 QPEHL--PLQTQFKEREVGNLQHSNGLNSRSPDYEDENPVGEDGIQQMYPLYNQMCYQDR 430
      :||:
      :||:
Db 238 RKDYLEEPEKTQW-----NNVENLNRF-ERPMDYEDLKMGKMFVSD----- 278

QY 431 SPGKHQNNDPKRV-----YIDPREHYV 453
      :||:
      :||:
Db 279 ---EHYDENEDDLVSHVDGVSISRREWYV 304

RESULT 9
Q9ERF5
ID Q9ERF5 PRELIMINARY; PRT; 295 AA.
AC Q9ERF5;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
```

```
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308634; AAG30283.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
FT NON_TER 1
FT NON_TER 295
SQ SEQUENCE 295 AA; 33112 MW; 03E5C4DCB5032E7F CRC64;

Query Match 22.1%; Score 534.5; DB 11; Length 295;
Best Local Similarity 38.3%; Pred. No. 3.3e-37;
Matches 113; Conservative 58; Mismatches 113; Indels 11; Gaps 6;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQIVAVHHHPQYGFVSQGEYQGRVLEKNYS 70
      :||:
      :||:
Db 3 GTDVLHCSFANPLPSVKITQVTWQKATNGSKQNNMAYNPTMGVSVLPPEYKRVLELRPS 62

QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLDG--- 127
      |||||
Db 63 FIDGTIRLSHLEDEGMVICEFATFPTGNRESQLNLTVMKPT-NWIEGTQAVLRARKG 121

QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSPNETATIIISQYKLFPTRFARGR 185
      :||:
      :||:
Db 122 QDDKVVVATCTSANGKPPSVSVSWETRLKGEAEYQEIKNPNTVTVISRYRLVPSREAHQ 181

QY 186 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPFKS 245
      :||:
      :||:
Db 182 SLACIVNY-HLDR-FRESLTILNVQYEPEVTIEGFDGNWYLQRTDVKLTCKADANPPATEY 239

QY 246 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
      :||:
      :||:
Db 240 HWTTLNGSLPKGVEAQNRTLFFRGPINYSLAGTYICEATNPIGTRSGQVEVNITE 294

RESULT 10
Q9GL74
ID Q9GL74 PRELIMINARY; PRT; 298 AA.
AC Q9GL74;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor.";
RL Virology 281:315-328(2001).
DR EMBL; AF308635; AAG30284.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
```


Db	238	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP	297
QY	241	PPFKSVWSRLDGOWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	300
Db	298	PPFKSVWSRLDGOWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	357
QY	301	VP-----FKOTSSIAVAGAVIGAVLALF	323
Db	358	PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIV	417
QY	324	IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP	364
Db	418	LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQOQDELDSYDPSVKKENKN	476
QY	365	PLPQKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVGEDGIQOMPLY	422
Db	477	PV--NNLIRKOYLEEPEKTQW-----NNVENLNR-ERPMDYIEDLKMGKMFVSD-----	523
QY	423	NQMCYQDRSPGKHQNDPKRV-----YIDPREHYV	453
Db	524	-----EHYDENEDDLVSHVDGVSISRREWYV	549
RESULT 4			
Q9JLB9			
ID	Q9JLB9	PRELIMINARY;	PRT; 549 AA.
AC	Q9JLB9;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Cell adhesion molecule nectin-3 alpha.		
GN	PVRL3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20209403; PubMed=10744716;		
RA	SatoH-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,		
RA	Tachibana K., Mizoguchi A., Takai Y.;		
RT	"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules		
RT	that shows homophilic and heterophilic cell-cell adhesion		
RT	activities.";		
RL	J. Biol. Chem. 275:10291-10299(2000).		
DR	EMBL; AF195833; AAF63685.1; --		
DR	MGD; MGI:1930171; Pvr13.		
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.		
DR	GO; GO:0005194; F:cell adhesion molecule activity; IDA.		
DR	GO; GO:0005515; F:protein binding; IPI.		
DR	GO; GO:0007155; P:cell adhesion; IDA.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	Pfam; PF00047; ig; 2.		
DR	SMART; SM00409; IG; 1.		
DR	PROSITE; PS50835; IG LIKE; 3.		
SQ	SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;		
Query Match 65.9%; Score 1592.5; DB 11; Length 549;			
Best Local Similarity 66.5%; Pred. No. 4.5e-127;			
Matches 322; Conservative 34; Mismatches 51; Indels 77; Gaps 9;			
QY	1	GPIIIEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	60
Db	58	GSIIEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY	117
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLPFTR	180
Db	178	PDSLIDGGNETVAAVCVAATGKPVQIDWEGDLGEMESSTTSFPNETATISQYKLPFTR	237

QY	181	FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP	240
Db	238	FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP	297
QY	241	PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD	300
Db	298	PPFKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISD	357
QY	301	VPEKQT-----SSIA-----VAGAVIGAVLALF	323
Db	358	PPTTTTLOPTVQWSSPADVQDIATEHKLPFPLSTLATLKDDTIGTIIASVVGALFLV	417
QY	324	IIAIFVTVLLTPRKKR-----PSYLDKVIDLPPTHK-----PPPLYEERSPP	365
Db	418	LVSILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSYDPSVKKENKNP	477
QY	366	LPQKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVG-----	411
Db	478	V--NNLIRKDYLEEPEKTQW--NNVENLTRF----ERPMDYYEDLKMGKMFVSDERYNES	529
QY	412	EDGI 415	
Db	530	EDGL 533	
RESULT 5			
Q9D006			
ID	Q9D006	PRELIMINARY;	PRT; 549 AA.
AC	Q9D006;		
DT	01-JUN-2001 (TrEMBLrel. 17, Created)		
DT	01-JUN-2001 (TrEMBLrel. 17, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	2610301B19Rik protein.		
GN	PVRL3 OR 2610301B19RIK.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=C57BL/6J; TISSUE=Embryo;		
RX	MEDLINE=21085660; PubMed=11217851;		
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,		
RA	Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,		
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,		
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,		
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,		
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,		
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,		
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,		
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,		
RA	Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,		
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,		
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,		
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,		
RA	Nordene P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,		
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,		
RA	Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,		
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,		
RA	Hayashizaki Y.;		
RT	"Functional annotation of a full-length mouse cDNA collection.";		
RL	Nature 409:685-690(2001).		
DR	EMBL; AK011949; BAB27933.1; --		
DR	MGD; MGI:1930171; Pvrl3.		
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.		
DR	GO; GO:0005194; F:cell adhesion molecule activity; IDA.		
DR	GO; GO:0005515; F:protein binding; IPI.		
DR	GO; GO:0007155; P:cell adhesion; IDA.		
DR	InterPro; IPR003599; IG.		
DR	InterPro; IPR007110; IG-like.		
DR	Pfam; PF00047; ig; 2.		
DR	SMART; SM00409; IG; 1.		

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVWSRLDQOWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQOWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYE 417
QY 361 ERSPPLPQKDLF-QPEHLPLQTOFKEREVGNLQHNGSLNRSFDEYEDENPVGEDGIQMY 419
Db 418 ERIPSLPQKDLLGQTEHLPLQTOFKKEGAGGLQPSNGPISRFDYEDESTMQEDGTQRM 477
QY 420 PLYNQMCYQDRSPGKHQNNDPKRVYIDPREHYV 453
Db 478 PLYSQMCHQDRSPRQHHPRN-PERLYINPREHYV 510
RESULT 2
Q9JLB7
ID Q9JLB7 PRELIMINARY; PRT; 438 AA.
AC Q9JLB7;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 gamma.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195835; AAF63687.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 438 AA; 47261 MW; 2ACA4416E5B02FEF CRC64;
Query Match 77.8%; Score 1880; DB 11; Length 438;
Best Local Similarity 94.9%; Pred. No. 9.7e-152;
Matches 352; Conservative 11; Mismatches 8; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60

Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVWSRLDQOWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQOWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 VPFKQTSSIAVAGAVIGAVLALFIIAIFVTVLLTPRKKRPSYLDKVIDLPPTHKPPPLYE 360
Db 358 IPLTQTSSIAVAGAVIGAVLALFIIITVFTVLLTPRKKRPSYLDKVIDLPPTHKPPPVYE 417
QY 361 ERSPPLPQKDL 371
Db 418 ERIPSLPQKDL 428
RESULT 3
Q9NQS3
ID Q9NQS3 PRELIMINARY; PRT; 549 AA.
AC Q9NQS3;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;
Query Match 67.5%; Score 1630.5; DB 4; Length 549;
Best Local Similarity 64.4%; Pred. No. 2.6e-130;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 36.7907 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-12_COPY_58_510
Perfect score: 2417
Sequence: 1 GPIIIEPHVTAVMGKNVSLK.....KHHQNNDPKRVYIDPREHYV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2161	89.4	510	11 Q9JLB8	Q9jlb8 mus musculu
2	1880	77.8	438	11 Q9JLB7	Q9jlb7 mus musculu
3	1630.5	67.5	549	4 Q9NQS3	Q9nqs3 homo sapien
4	1592.5	65.9	549	11 Q9JLB9	Q9jlb9 mus musculu
5	1548.5	64.1	549	11 Q9D006	Q9d006 mus musculu
6	1218	50.4	267	4 Q8NC05	Q8nc05 homo sapien
7	1173.5	48.6	407	4 Q9Y412	Q9y412 homo sapien
8	648.5	26.8	304	4 Q9BVA9	Q9bva9 homo sapien
9	534.5	22.1	295	11 Q9ERF5	Q9erf5 mesocricetu
10	528	21.8	298	6 Q9GL74	Q9gl74 cercopithec
11	526.5	21.8	295	6 Q9GL75	Q9gl75 bos taurus
12	516	21.3	530	11 Q8XJ35	Q8xj35 mus musculu
13	507	21.0	483	11 Q9DBP8	Q9dbp8 mus musculu
14	503.5	20.8	510	4 Q96NY8	Q96ny8 homo sapien
15	503.5	20.8	510	4 Q96K15	Q96k15 homo sapien
16	490.5	20.3	508	11 Q8R007	Q8r007 mus musculu

17	490.5	20.3	508	11 Q8CED8	Q8ced8 mus musculu
18	446	18.5	467	11 Q91VT9	Q91vt9 mus musculu
19	446	18.5	467	11 Q8C6F2	Q8c6f2 mus musculu
20	427.5	17.7	449	4 Q9UEI6	Q9uei6 homo sapien
21	400	16.5	412	11 Q9R1E1	Q9r1e1 rattus norv
22	398	16.5	417	4 Q96BJ1	Q96bj1 homo sapien
23	395	16.3	412	11 Q63611	Q63611 rattus norv
24	392	16.2	408	11 Q91WP1	Q91wp1 mus musculu
25	390	16.1	403	6 Q8HY15	Q8hy15 lemur catta
26	390	16.1	408	11 Q8K094	Q8k094 mus musculu
27	389	16.1	408	11 Q8BVF6	Q8bvf6 mus musculu
28	388.5	16.1	400	6 Q8HY16	Q8hy16 cebus apell
29	385	15.9	401	6 Q08835	Q08835 cercopithec
30	352	14.6	412	6 Q8HY14	Q8hy14 oryctolagus
31	348	14.4	415	11 Q60977	Q60977 mus musculu
32	289	12.0	417	11 Q7TNL1	Q7tnl1 mus musculu
33	286	11.8	394	13 Q7ZXX1	Q7zxx1 xenopus lae
34	282	11.7	442	4 Q9BY67	Q9by67 homo sapien
35	282	11.7	445	11 Q8K3T6	Q8k3t6 mus musculu
36	279	11.5	445	11 Q8R4L1	Q8r4l1 mus musculu
37	276.5	11.4	443	4 Q8N2F4	Q8n2f4 homo sapien
38	273.5	11.3	456	11 Q8R5M8	Q8r5m8 mus musculu
39	256.5	10.6	333	4 Q86WB8	Q86wb8 homo sapien
40	255	10.6	800	5 Q86LF9	Q86lf9 drosophila
41	255	10.6	801	5 Q86LF8	Q86lf8 drosophila
42	253.5	10.5	336	11 Q9D6E7	Q9d6e7 mus musculu
43	253.5	10.5	336	11 Q80VG4	Q80vg4 mus musculu
44	248.5	10.3	396	11 Q99N28	Q99n28 mus musculu
45	238.5	9.9	398	4 Q8N126	Q8n126 homo sapien

ALIGNMENTS

RESULT 1

Q9JLB8

ID Q9JLB8 PRELIMINARY; PRT; 510 AA.

AC Q9JLB8;

DT 01-OCT-2000 (TREMBlrel. 15, Created)

DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Cell adhesion molecule nectin-3 beta.

GN PVRL3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20209403; PubMed=10744716;

RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,

RA Tachibana K., Mizoguchi A., Takai Y.;

RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules

RT that shows homophilic and heterophilic cell-cell adhesion

RT activities.";

RL J. Biol. Chem. 275:10291-10299(2000).

DR EMBL; AF195834; AAF63686.1; -.

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005913; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS00835; IG_LIKE; 3.

SQ SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;

Query Match 89.4%; Score 2161; DB 11; Length 510;
Best Local Similarity 89.6%; Pred. No. 1.3e-175;
Matches 407; Conservative 21; Mismatches 24; Indels 2; Gaps 2;

CC or send an email to license@isb-sib.ch).

DR EMBL; M31811; AAA39487.1; --

DR EMBL; M74793; AAA91743.1; --

DR EMBL; M74783; AAA91743.1; JOINED.

DR EMBL; M74784; AAA91743.1; JOINED.

DR EMBL; M74785; AAA91743.1; JOINED.

DR EMBL; M74786; AAA91743.1; JOINED.

DR EMBL; M74787; AAA91743.1; JOINED.

DR EMBL; M74788; AAA91743.1; JOINED.

DR EMBL; M74790; AAA91743.1; JOINED.

DR EMBL; M74791; AAA91743.1; JOINED.

DR HSSP; Q62230; 1QFP.

DR MGD; MGI:96912; Mag.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00408; IgC2; 2.

DR PROSITE; PS50835; IG_LIKE; 2.

KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;

KW Immunoglobulin domain; Repeat; Palmitate; Lipoprotein;

KW Alternative splicing.

FT SIGNAL 1 19

FT CHAIN 20 626 MYELIN-ASSOCIATED GLYCOPROTEIN.

FT DOMAIN 20 516 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 517 536 POTENTIAL.

FT DOMAIN 537 626 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 22 120 IG-LIKE V-TYPE.

FT DOMAIN 139 237 IG-LIKE C2-TYPE 1.

FT DOMAIN 241 325 IG-LIKE C2-TYPE 2.

FT DOMAIN 327 412 IG-LIKE C2-TYPE 3.

FT DOMAIN 413 508 IG-LIKE C2-TYPE 4.

FT DISULFID 37 165 BY SIMILARITY.

FT DISULFID 42 100 BY SIMILARITY.

FT DISULFID 159 217 BY SIMILARITY.

FT DISULFID 261 305 BY SIMILARITY.

FT DISULFID 347 392 BY SIMILARITY.

FT DISULFID 421 430 BY SIMILARITY.

FT DISULFID 432 488 BY SIMILARITY.

FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT LIPID 531 531 S-palmitoyl cysteine (By similarity).

FT VARSPLIC 574 582 EKRLGSERR -> REVSTRDCH (in isoform S-MAG).

FT VARSPLIC 583 626 /FTid=VSP 002527.

FT VARSPLIC 583 626 Missing (in isoform S-MAG).

FT VARSPLIC 583 626 /FTid=VSP 002528.

SQ SEQUENCE 626 AA; 69259 MW; 9C797BD6B52B6057 CRC64;

Query Match 7.3%; Score 177; DB 1; Length 626;

Best Local Similarity 24.6%; Pred. No. 6.2e-06;

Matches 85; Conservative 50; Mismatches 142; Indels 68; Gaps 18;

QY 9 VTAVWGKNVSLKCLIEVNETITQISWEKIHGK-----SSQTVAVHHPQY 52

DB 30 ISAFEGTCVSI PCRFDPD---ELRPVAVGVVFN SPYKPNYPVVPVKSRQTQVVE--- 83

QY 53 GFSVQGEYQGRV-LFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLG--NAQSSTTVTV 109

DB 84 -----SFQGRSRLGLGLRNCITLLSTLSPELGGKYFRG---DLGGYNQYTFSEHSV 134

QY 110 L-VEPTVSLIKGPDSLIDGGNETVAAICIAATGKPV--AHIDWEGDLGEMESTTTSPNE 166

DB 135 LDI VNTPNIVVPPE--VVAGTE-VEVSCMVPDNCPELRPELSWLGHEGLGEPTVLGLRE 191

QY 167 ---TATII SQYKLFPTFRFARGRRITCVVKKHPALEKDIRYSFILDIOYAPEV-----SVTG 218

Db 192 DEGTWVQVSLHLHFVPTREANGHRLGCQAAPNTTLQFEGYASLDVKYPPVIVEMNSSVEA 251

QY 219 YDGNWFVGRKGVNLKCNADANPPPFKSVMSRLDQGWPDGLL---ASDNTLHF-VHPLTFN 274

Db 252 IEGS-----HVSLLCGADSNPPPLLT-WMR-----DGMVLREAVAKSLYLDLEEVTFG 298

QY 275 YSGVYICKVTNSLQGRSDQKVIYISDVPEKQT---SSIAVAGAVI 316

Db 299 EDGVYACLAENAYGQDNRTVELSVMYAPWKPTVNGTVVAVEGETV 343

Search completed: April 12, 2004, 09:39:49

Job time : 8.23946 secs

FT	DOMAIN	537	626	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	22	120	IG-LIKE V-TYPE.
FT	DOMAIN	139	237	IG-LIKE C2-TYPE 1.
FT	DOMAIN	241	325	IG-LIKE C2-TYPE 2.
FT	DOMAIN	327	412	IG-LIKE C2-TYPE 3.
FT	DOMAIN	413	508	IG-LIKE C2-TYPE 4.
FT	DISULFID	37	165	BY SIMILARITY.
FT	DISULFID	42	100	BY SIMILARITY.
FT	DISULFID	159	217	BY SIMILARITY.
FT	DISULFID	261	305	BY SIMILARITY.
FT	DISULFID	347	392	BY SIMILARITY.
FT	DISULFID	421	430	BY SIMILARITY.
FT	DISULFID	432	488	BY SIMILARITY.
FT	CARBOHYD	99	99	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	246	246	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	315	315	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	454	454	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID	531	531	S-palmitoyl cysteine (By similarity).
SQ	SEQUENCE	626 AA;	69068 MW;	ED2D3GB24F21CAA CRC64;
Query Match				
Best Local Similarity 7.3%; Score 177; DB 1; Length 626;				
Matches 83; Conservative 51; Mismatches 143; Indels 68; Gaps 17;				
Qy	9	VTAVWGKNSLKLIEVNETITQISWEKHGK-----SSQTVAVHHPQY 52		
Db	30	ISAFEGTCSIPCRDFPD---ELRPAVVGWYFNSPYKPNYPVVKSRQVWHE--- 83		
Qy	53	GFSVQGEYQGRV-LFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLG--NAQSSTTVTV 109		
Db	84	-----SFQGRSRLLDGLRNCITLLSNVSPELGGKYFRG---DLGGYNQYTFSEHSV 134		
Qy	110	L-VEPTVSLIKGPDSLIDGGNETVAAICIAATGKPV--AHIDWEGDLGEMESTTTSFPNE 166		
Db	135	LDIVNTPNIVVPE--VVAGTE-VEVSCMVDPNCPRLPELSWLGHGELGEPVGLRLRE 191		
Qy	167	---TATIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPEV-----SVTG 218		
Db	192	DEGTWQVSLHFPVTREANGHRLGCOQASFNTTLQFEGYASMDVKPPVIVEMNSSVEA 251		
Qy	219	YDGNWFVGRKGNLKNADANPPPFKSVSRDLGQWPDGLL-----ASDNTLHFVHPLTFN 274		
Db	252	IEGS-----HVSLLCGADSNPPPLLT-WMR-----DGTVLRREAVABSLLELEEVTPA 298		
Qy	275	YSGVYICKVNSLQGRSDQKVIYISDVPFKQT---SSIAVAGAVI 316		
Db	299	EDGVYACLAENAYQDNRTVGLSVMYAPKPTWGTMTVAVEGETV 343		

RESULT 15
MAG_MOUSE STANDARD; PRT; 626 AA.
AC P20917; P16880;
DT 01-AUG-1990 (Rel. 15, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-associated glycoprotein precursor (Siglec-4a).
GN MAG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS L-MAG AND S-MAG).
RX MEDLINE=90121220; PubMed=2482022;
RA Fujita N., Sato S., Kurihara T., Kuwano R., Sakimura K., Inuzuka T.,
RA Takahashi Y., Miyatake T.;
RT "cDNA cloning of mouse myelin-associated glycoprotein: a novel
RT alternative splicing pattern.";

Biochem. Biophys. Res. Commun. 165:1162-1169(1989).
[2]
SEQUENCE FROM N.A. (ISOFORM S-MAG).
TISSUE=Brain;
MEDLINE=91298961; PubMed=1712586;
Nakano R., Fujita N., Sato S., Inuzuka T., Sakimura K.,
RA Ishiguro H., Mishina M., Miyatake T.;
RT "Structure of mouse myelin-associated glycoprotein gene.";
Biochem. Biophys. Res. Commun. 178:282-290(1991).
[3]
TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
MEDLINE=91366725; PubMed=1716323;
Pedraza L., Frey A.B., Hempstead B.L., Colman D.R., Salzer J.L.;
RT "Differential expression of MAG isoforms during development.";
J. Neurosci. Res. 29:141-148(1991).
[4]
SIALIC ACID BINDING.
MEDLINE=95179521; PubMed=7533044;
Kelm S., Pelz A., Schauer R., Filbin M.T., Tang S., de Bellard M.E.,
RA Schnaar R.L., Mahoney J.A., Hartnell A., Bradfield P., Crocker P.R.;
RT "Sialoadhesin, myelin-associated glycoprotein and CD22 define a new
RT family of sialic acid-dependent adhesion molecules of the
RT immunoglobulin superfamily.";
Curr. Biol. 4:965-972(1994).
[5]
FUNCTION, AND TISSUE SPECIFICITY.
MEDLINE=20090811; PubMed=10625334;
Schachner M., Bartsch U.;
RT "Multiple functions of the myelin-associated glycoprotein MAG
RT (siglec-4a) in formation and maintenance of myelin.";
Glia 29:154-165(2000).
[6]
INTERACTION WITH RTN4R.
MEDLINE=22171378; PubMed=12089450;
Liu B.P., Fournier A., GrandPre T., Strittmatter S.M.;
RT "Myelin-associated glycoprotein as a functional ligand for the Nogo-66
RT receptor.";
Science 297:1190-1193(2002).
CC -!- FUNCTION: Adhesion molecule in postnatal neural development that
CC mediates sialic-acid dependent cell-cell interactions between
CC neuronal and myelinating cells. Preferentially binds to alpha2,3-
CC linked sialic acid. Isoform L-MAG is critical for the formation of
CC myelin in the CNS, whereas isoform S-MAG is sufficient to maintain
CC the integrity of myelin in PNS.
CC -!- SUBUNIT: Binds to RTN4R.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=L-MAG;
CC IsoId=P20917-1; Sequence=Displayed;
CC Name=S-MAG;
CC IsoId=P20917-2; Sequence=VSP 002527, VSP 002528;
CC -!- TISSUE SPECIFICITY: Expressed by myelinating glial cells in the
CC central and peripheral nervous system. Detected in oligodendrocyte
CC processes before formation of compact myelin. Restricted to the
CC periaxonal space after myelination. Isoform S-MAG is the
CC predominant isoform in CNS and PNS of the adult.
CC -!- DEVELOPMENTAL STAGE: In CNS isoform L-MAG is the major form
CC synthesized early in development, and it persists as a significant
CC proportion of the MAG present in the adult. In the PNS isoform L-
CC MAG is expressed at modest levels during development; it is absent
CC in the adult.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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FT	SIGNAL	1	19	NEURAL CELL ADHESION MOLECULE 1, 140 kDa
FT	CHAIN	20	853	ISOFORM.
FT				EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	20	719	POTENTIAL.
FT	TRANSMEM	720	737	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	738	853	IG-LIKE C2-TYPE 1.
FT	DOMAIN	20	111	IG-LIKE C2-TYPE 2.
FT	DOMAIN	116	205	IG-LIKE C2-TYPE 3.
FT	DOMAIN	212	300	IG-LIKE C2-TYPE 4.
FT	DOMAIN	307	412	IG-LIKE C2-TYPE 5.
FT	DOMAIN	415	500	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	527	604	FIBRONECTIN TYPE-III 2.
FT	DOMAIN	633	700	HEPARIN-BINDING (POTENTIAL).
FT	DOMAIN	152	156	HEPARIN-BINDING (POTENTIAL).
FT	DOMAIN	161	165	BY SIMILARITY.
FT	DISULFID	41	96	BY SIMILARITY.
FT	DISULFID	139	189	BY SIMILARITY.
FT	DISULFID	235	286	BY SIMILARITY.
FT	DISULFID	328	394	BY SIMILARITY.
FT	DISULFID	435	488	BY SIMILARITY.
FT	CARBOHYD	222	222	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	314	314	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	346	346	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	432	432	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	487	487	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	SEQUENCE	853 AA;	93893 MW;	E12FD49231A7A368 CRC64;
QY				Query Match 7.3%; Score 177.5; DB 1; Length 853;
Db				Best Local Similarity 23.7%; Pred. No. 8.7e-06;
QY				Matches 77; Conservative 54; Mismatches 127; Indels 67; Gaps 16;
QY	8	HVTAVWGKNVSLKCLIEVNETITQISWEKINGKSSQTVAVHHPQYGFVSQGEYQGRVLFK	67	
Db	222	NATANLGQSVTLVCNAEGFPEPT-VSWTK-----DGEQIENEDEKYLFS	265	
QY	68	NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG	127	
Db	266	D---DSSELTIRKVDKNDKDEAEYVCIAEN-KAGEQDASIHLLKVFAPKITYVENQTAM--E	319	
QY	128	GNETVAAICIAATGKPVAHIDWE---GDLGEMESTTTSFPNETATI-----ISQ	173	
Db	320	LEEQVTLTC-EASGDPIPSITWRTSTRNISSEKASWTRPEKQETLDGHMVVRSHARVSS	378	
QY	174	YKLPPTFRFARRRITCVVVKHPALEKDIRYSFILDIOYAPE---VSVTGYDGNWFFVGRKG	229	
Db	379	LTLKSIQYTDAGEYVCTASN-TIGQDSQ-SMYLEVQYAPKLQGPVAVYTWEGN-----Q	430	
QY	230	VNLKCNADANPPFKSVWSRLDGQWPDGLLASDNLHF-----VHPLTFNVSG	277	
Db	431	VNITCEVFAYPSATIS-WFR-DGQ----LLPSSNYSNIKIYNTPSASYLEVTPDSENDFG	484	
QY	278	VYICKVTNSLQGRSDQKVIYISDVP	302	
Db	485	NYNCTAVNRIGQESLEFVLVQADTP	509	
RESULT 14				
MAG_HUMAN				
ID	MAG_HUMAN	STANDARD;	PRT;	626 AA.
AC	P20916;			
DT	01-FEB-1991	(Rel. 17, Created)		
DT	01-FEB-1991	(Rel. 17, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Myelin-associated glycoprotein precursor (Siglec-4a).			
GN	MAG.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89392063; PubMed=2476987;			

RA	Sato S., Fujita N., Kurihara T., Kuwano R., Sakimura K., Takahashi Y.,
RA	Miyatake T.;
RT	"cDNA cloning and amino acid sequence for human myelin-associated
RT	glycoprotein.";
RL	Biochem. Biophys. Res. Commun. 163:1473-1480(1989).
RL	[2]
RN	SEQUENCE FROM N.A.
RP	Lamerdin J.E., McCready P.M., Adamson A.W., Burkhardt-Schultz K.,
RA	Kyle A., Ramirez M., Stillwagen S.A., Garnes J., Danganan L.,
RA	Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
RA	Carrano A.V.;
RL	Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RL	[3]
RN	SEQUENCE FROM N.A.
RP	TISSUE=Brain;
RC	MEDLINE=22388257; PubMed=12477932;
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length
RT	human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC	-!- FUNCTION: Adhesion molecule in postnatal neural development that
CC	mediates sialic-acid dependent cell-cell interactions between
CC	neuronal and myelinating cells. Preferentially binds to alpha2,3-
CC	linked sialic acid (By similarity).
CC	-!- SUBUNIT: Binds to RTN4R (By similarity).
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC	(sialic acid binding Ig-like lectin) family.
CC	-!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC	-----
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CC	-----
DR	EMBL; M29273; AAA59545.1; --
DR	EMBL; AC002132; AAB58805.1; --
DR	EMBL; BC053347; AAB53347.1; --
DR	PIR; A61084; A61084.
DR	HSSP; Q62230; IQFP.
DR	Genew; HGNC:6783; MAG.
DR	MIM; 159460; --
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003598; Ig_c2.
DR	Pfam; PF00047; ig; 2.
DR	SMART; SM00408; IGC2; 2.
DR	PROSITE; PS50835; IG_LIKE; 3.
KW	Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
KW	Immunoglobulin domain; Repeat; Palmitate; Lipoprotein.
FT	SIGNAL 1 19
FT	CHAIN 20 626
FT	DOMAIN 20 516
FT	TRANSMEM 517 536
FT	
FT	MYELIN-ASSOCIATED GLYCOPROTEIN.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.

FT	CARBOHYD	512	512	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	556	556	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	658	658	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	666	666	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	710	710	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	748	748	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	795	795	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	924	924	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	1142	1142	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	1160	1160	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	1250	1250	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	1271	1271	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	1341	1341	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	CARBOHYD	1488	1488	N-LINKED (GLCNAC. . .)	(POTENTIAL)	.
FT	VARSP LIC	1562	1571	NFATLNYDGS -> KEAARCKEFS (in isoform Short).		
FT				/FTID=VSP 002502.		
FT	VARSP LIC	1572	2012	Missing (in isoform Short).		
FT				/FTID=VSP 002503.		
FT	CONFLICT	1893	2012	HRPGDLHLPPYLRMDFLNRRGGPFTSRDLSLGQACLEPQK		
FT				SRTLKRPVLEPIPEAAASASTREGSQWGPQAVATLPQR		
FT				EGAELGQAAMSSQESLLDSRGHLKGNPNYAKSYTLV ->		
FT				IGQVTSYICLHTLEWTF (IN REF. 1).		
FT						
SQ	SEQUENCE	2012 AA;	222259 MW;	0E33CFB781A08334 CRC64;		
	Query Match		7.5%;	Score 181.5; DB 1; Length 2012;		
	Best Local Similarity		19.8%;	Pred. No. 1.4e-05;		
	Matches 108;	Conservative	83;	Mismatches 204; Indels 151; Gaps 26;		
QY	1	GPIIIEP--HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQG	58			
Db	503	GPASIRPMKNITAIAGRDYIHCVR-IGYPYYSIKWY----	554	KNSNLLPFNHRQVAFE---		
QY	59	EYQGRVLFKNYSLNDATITLHNIGFS-DSGKYICKAVTFPLGNAQSSTVTVLVEPTVSL	117			
Db	555	-----NNGTLKLSDVQKEVDEGYTCNVLVQPQLSTQSQVHVTVKVPFFIQP	601			
QY	118	IKGPDSLIDGNETVAACIAATGKPVAHIDWEGD---LGEMESTTSPNETATIISQ	173			
Db	602	FEFPRFSI---GQRFVPCVVVSGDLPTITWQDGRPIPSGLGVTIDNIDFTSSLRISN	658			
QY	174	YKLFFTRFARGRRITCVVHKPALEKDIRSFILDIQYAPEVSVTGDGNFVGRKGVLNK	233			
Db	659	LSLM-----HNGNYTCIARNEAAA--VEHQSLIVRPVKFVQPRDQGIYG-KAVILN	710			
QY	234	CNADANPPPKSVWSRLDQG-----WPDGL-----LASDNTLHFVHPLTFNYSGVYICKV	283			
Db	711	CSAEGYPVP-TIVWKFSKGAGVPQFQPIALNGRIQVLSNGSLLIKHHVVEED-SGYLCKV	768			
QY	284	TNSLGQRSDQKVIYISDVPPFKQTS-----SIAVAG-----AVI	316			
Db	769	SNDVGADVSKMYLTVKIPAMITSYPNTTLATQGGKEMSCSTAHEKPIIVRWEKEDRII	828			
QY	317	GAVLALFIIA-----IFVTVLLTPRKKRPSYL-----DK-VIDLPPTHKPPP	357			
Db	829	NPEMARYLVSTKEVEEVISTLIQILPTVREDSGFFSFCHAINSYGEDRGLIQLTVQEPDP	888			
QY	358	LYEERSPPLPKDLFQPEHLPLQTFQKEREVGNLQHSNGLNSRS-----FDYEDEN-----	408			
Db	889	-----PEIEIKDV-----KARTI-TLRWTMGFDGNSPITGYDIECKNKSWS	929			
QY	409	-----PVGEDGIQOMYP--LYNQMCYQDRSPGKHQND-----PK	442			
Db	930	DSAQRTKDVSPQLNSATIIDIHPSSTYSIRMYAKNRIGKSEPSNELTITADEAAPDPGPQ	989			
QY	443	RVYIDP	448			
Db	990	EVHLEP	995			
	RESULT 13					
	NCA1_BOVIN					
ID	NCA1_BOVIN	STANDARD;	PRT;	853 AA.		

AC	P31836;					
DT	01-JUL-1993 (Rel. 26, Created)					
DT	01-JUL-1993 (Rel. 26, Last sequence update)					
DT	10-OCT-2003 (Rel. 42, Last annotation update)					
DE	Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)					
DE	(NCAM-140).					
GN	NCAM1 OR NCAM.					
OS	Bos taurus (Bovine).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;					
OC	Bovidae; Bovinae; Bos.					
OX	NCBI_TaxID=9913;					
RN	[1]					
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.					
RC	TISSUE=Brain cortex;					
RX	MEDLINE=89378239; PubMed=2776887;					
RA	Lipkin V.M., Khrantsov N.V., Andreeva S.G., Moshnyakov M.V.,					
RA	Petukhova G.V., Rakitina T.V., Feshchenko E.A., Ishchenko K.A.,					
RA	Mirzoeva S.F., Chernova M.N., Dranytsyna S.M.;					
RT	"Calmodulin-independent bovine brain adenylate cyclase. Amino acid					
RT	sequence and nucleotide sequence of the corresponding cDNA.";					
RL	FEBS Lett. 254:69-73 (1989).					
RN	[2]					
RP	SEQUENCE OF 20-36.					
RX	MEDLINE=86140120; PubMed=3512556;					
RA	Rougon G., Marshak D.R.;					
RT	"Structural and immunological characterization of the amino-terminal					
RT	domain of mammalian neural cell adhesion molecules.";					
RL	J. Biol. Chem. 261:3396-3401 (1986).					
RN	[3]					
RP	IDENTIFICATION AS N-CAM.					
RX	MEDLINE=92111748; PubMed=1765159;					
RA	Premont R.T.;					
RT	"A bovine brain cDNA purported to encode calmodulin-insensitive					
RT	adenylate cyclase has extensive identity with neural cell adhesion					
RT	molecules (N-Cams).";					
RL	FEBS Lett. 295:230-231 (1991).					
CC	-!- FUNCTION: This protein is a cell adhesion molecule involved in					
CC	neuron-neuron adhesion, neurite fasciculation, outgrowth of					
CC	neurites, etc.					
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.					
CC	-!- ALTERNATIVE PRODUCTS:					
CC	Event=Alternative splicing; Named isoforms=1;					
CC	Comment=A number of isoforms are produced;					
CC	Name=1;					
CC	Isoid=P31836-1; Sequence=Displayed;					
CC	-!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.					
CC	-!- SIMILARITY: Contains 2 fibronectin type III domains.					
CC	-!- CAUTION: Was originally (Ref.1) thought to be a calmodulin-					
CC	independent adenylate cyclase.					
CC	-----					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration					
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -					
CC	the European Bioinformatics Institute. There are no restrictions on its					
CC	use by non-profit institutions as long as its content is in no way					
CC	modified and this statement is not removed. Usage by and for commercial					
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/					
CC	or send an email to license@isb-sib.ch).					
CC	-----					
DR	EMBL; X16451; CAA34470.1; -.					
DR	PIR; A32976; IJBONC.					
DR	HSSP; P40189; 1BQU.					
DR	InterPro; IPR008957; FN_III-like.					
DR	InterPro; IPR003961; FN_III.					
DR	InterPro; IPR007110; IG-like.					
DR	InterPro; IPR003598; IG_c2.					
DR	Pfam; PF00041; fn3; 2.					
DR	Pfam; PF00047; ig; 5.					
DR	SMART; SM00060; FN3; 2.					
DR	SMART; SM00408; IGc2; 5.					
DR	PROSITE; PS50835; IG_LIKE; 5.					
KW	Cell adhesion; Glycoprotein; Transmembrane; Repeat;					
KW	Immunoglobulin domain; Alternative splicing; Signal.					


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CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=P41217-1; Sequence=Displayed;
CC Name=2;
CC IsoId=P41217-2; Sequence=VSP 002613;
CC Note=No experimental confirmation available;
CC -|- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X05323; CAA28943.1; -.
CC EMBL; X05324; CAA28943.1; JOINED.
CC EMBL; X05325; CAA28943.1; JOINED.
CC EMBL; X05326; CAA28943.1; JOINED.
CC EMBL; AF063591; AAG43150.1; -.
CC EMBL; BC022522; AAH22522.1; -.
CC PIR; A47639; A47639.
CC Genew; HGNC:7203; MOX2.
CC MIM; 155970; -.
CC GO; GO:0005887; C: integral to plasma membrane; TAS.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR003596; IG_v.
CC Pfam; PF00047; ig; 2.
CC SMART; SM00409; IG; 1.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS50835; IG LIKE; 1.
CC Antigen; Neurone; T-cell; Signal; Transmembrane;
CC Immunoglobulin domain; Glycoprotein; Alternative splicing.
CC SIGNAL 1 30
CC CHAIN 31 278
CC DOMAIN 31 232
CC TRANSMEM 233 259
CC DOMAIN 260 278
CC DOMAIN 31 141
CC DOMAIN 142 232
CC DISULFID 51 121
CC DISULFID 160 214
CC CARBOHYD 95 95
CC CARBOHYD 103 103
CC CARBOHYD 110 110
CC CARBOHYD 157 157
CC CARBOHYD 181 181
CC CARBOHYD 190 190
CC VARSPLIC 268 278
CC /FTid=VSP 002613.
CC S -> C (IN REF. 3).
CC P -> T (IN REF. 1).
CC SEQUENCE 278 AA; 31264 MW; 38DF327B382CC970 CRC64;
Query Match 7.8%; Score 187.5; DB 1; Length 278;
Best Local Similarity 24.8%; Pred. No. 3.2e-07;
Matches 52; Conservative 36; Mismatches 97; Indels 25; Gaps 4;
QY 18 SLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDATIT 77
Db 48 SLKCSLQNAQEALIVTWQKKAVSPENMVTFSNHHGVVIOPAYKDKINITQLGLQNSTIT 107
QY 78 LHNIGFSDSGKYICKAVTFPLGNAQSSITTVTLVPEPTVSL-IKGPDSLIDGGNETVAAIC 136
Db 108 FWNITLEDGECYMCLENTFGFGKISGTACTLVVQPIVSLHYKFSEDHLN-----IT 159
QY 137 IAATGKPVAHIDWEGDLGEMESTTT--SFPNETATIISQYKLFPTFPFARGRRITCVVKHP 194
Db 160 CSATARPAPMFWKVPKRSGIENSTVTLSPNGTTSVTSILHIKDPKNQVGKEVICQVHL 219
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OY 195 ALEKDIRYSFILDIOYAPEVSVTGYDGNWF 224
Db 220 GTVTDFKQ-----TVNKGWYF 235

RESULT 11
PGSM_HUMAN
ID PGSM_HUMAN STANDARD; PRT; 4391 AA.
AC P98160; Q16287; Q9H3V5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basament membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basament membrane heparan sulfate proteoglycan core protein: a
RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Skin;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
RT basament membrane (HSPG2/perlecan). A chimeric molecule with multiple
RT domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
RX MEDLINE=20553141; PubMed=11101850;
RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
RA Hentati F., Fontaine B.;
RT "Perlecan, the major proteoglycan of basement membranes, is altered in
RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";
RL Nat. Genet. 26:480-483(2000).
RN [4]
RP SEQUENCE OF 1016-1470 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [5]
RP SEQUENCE OF 890-1396 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to lp36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [6]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
```



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RESULT 8
ICCR_DROME STANDARD; PRT; 764 AA.
AC Q08180;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Irregular chiasm C-roughest protein precursor (IRREC protein).
GN RST.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94102535; PubMed=7503814;
RA Ramos R.G., Igloi G.L., Lichte B., Baumann U., Maier D.,
RA Schneider T., Brandstaetter J.H., Froehlich A., Fischbach K.-F.;
RT "The irregular chiasm C-roughest locus of Drosophila, which affects
RT axonal projections and programmed cell death, encodes a novel
RT immunoglobulin-like protein.";
RL Genes Dev. 7:2533-2547(1993).
CC -!- FUNCTION: REQUIRED FOR CORRECT AXONAL PATHWAY FORMATION IN
CC THE OPTIC LOBE AND FOR PROGRAMMED CELL DEATH IN THE DEVELOPING
CC RETINA.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: POSTEMBRYONIC EXPRESSION IS STRONG IN THE
CC DEVELOPING OPTIC LOBE AND IN THE EYE IMAGINAL DISC.
CC -!- DEVELOPMENTAL STAGE: STRONGLY EXPRESSED IN EMBRYOS. ALSO FOUND
CC IN LATE LARVAL AND PUPAL STAGES.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z21641; CAA79756.1; -.
CC EMBL; L11040; AAA16632.1; -.
CC FIR; A49448; A49448.
CC FlyBase; FBgn0003285; rat.
CC GO; GO:0016202; P:regulation of myogenesis; IMP.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; ig; 4.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS50835; IG_LIKE; 5.
KW Transmembrane; Immunoglobulin domain; Glycoprotein; Signal; Repeat;
KW Cell adhesion.
FT SIGNAL 1 19
FT CHAIN 20 764
FT DOMAIN 20 533
FT TRANSMEM 534 556
FT DOMAIN 557 764
FT DOMAIN 21 123
FT DOMAIN 117 230
FT DOMAIN 245 261
FT DOMAIN 237 343
FT DOMAIN 346 419
FT DOMAIN 430 530
FT DOMAIN 637 660
FT CARBOHYD 211 211
FT CARBOHYD 313 313
FT CARBOHYD 393 393
FT CARBOHYD 400 400
FT CARBOHYD 507 507
FT SEQUENCE 764 AA; 82947 MW; 262225D2B2A1C181 CRC64;
SQ
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Query Match

9.4%; Score 227; DB 1; Length 764;

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Best Local Similarity 24.7%; Pred. No. 1.2e-09;
Matches 89; Conservative 60; Mismatches 142; Indels 70; Gaps 18;
QY 5 VEPH-VTAVMGKNVSLKCLIEVNETITQISWEKHKSSQTAVVHHPQYGFSGVEYQGR 63
Db 32 MEPQDQTAVVGARVTLPCRV-INKQT-LQWTK-----DDFGLGTSRDLSG- 75
QY 64 VLFKNYSL-----NDATITLHNIGFSDSGKYICKAVTFPLGNAQSST---VTVLVEPT 114
Db 76 --FERYAMVGSDEGDYSLDIYPVMLDDDDARYQCQVSPGPEGQPAIRSTFAGLTVLVPPE 133
QY 115 VSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGDLG-----EMESTTTSFPNETA- 168
Db 134 APKITQGDVIYATADRKVEIECVSVGGKPAEITWIDGLNVLTNDNIEYTVIPLDQRRF 193
QY 169 TIISQYKLFPTFRFARRRITCVVKKHPALEKDIRYSFI-LDIOYAPEVSVT-----GYD 220
Db 194 TAKSVLRLLTPKKEHHNTNFSCQAQNTA-DRTYRSAKIRVEVKYAPKVVNVMGSLPGGAG 252
QY 221 GNWFFVGRKG-----VNLKCNADANPPPKSVWSRLDGQWPDGGLLASDN 263
Db 253 GS--VGGAGGGSVHMSTGSRIVEHSQVRLECRADANPSDVRYRWFIND----EPIIGGQK 306
QY 264 TLHFVHPLTFNYSGVYI-CKVTNSLQSRSDQKVIYISDVP-FKQTSSIAVAGAVIGAVLA 321
Db 307 TEMVIRNVTRKFHDAIVKCEVQNSVGKSEDSSETLDISYAPSFQRQPQSMEAD--VGSVVS 364
QY 322 L 322
Db 365 L 365
RESULT 9
NCM2_MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (R4B12).
GN NCAM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
RX MEDLINE=97368238; PubMed=9221781;
RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA Kagamiyama H., Mori K.;
RT "OCAM: A new member of the neural cell adhesion molecule family
RT related to zone-to-zone projection of olfactory and vomeronasal
RT axons.";
RL J. Neurosci. 17:5830-5842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX MEDLINE=97476194; PubMed=9334170;
RA Alenius M., Bohm S.;
RT "Identification of a novel neural cell adhesion molecule-related gene
RT with a potential role in selective axonal projection.";
RL J. Biol. Chem. 272:26083-26086(1997).
CC -!- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
CC attached to the membrane by a GPI-anchor (short isoform).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O35136-1; Sequence=Displayed;
CC Name=Short;
```


GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 7.23946 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-12_COPY_58_510
Perfect score: 2417
Sequence: 1 GPIIIEPHVTAVWGKNVSLK.....KHHQNDPKRVIIDPREHYV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	602	24.9	515	1 PVR1_MOUSE	Q9jkf6 mus musculus
2	588	24.3	515	1 PVR1_PIG	Q9gl76 sus scrofa
3	588	24.3	517	1 PVR1_HUMAN	Q15223 homo sapien
4	519	21.5	530	1 PVR2_MOUSE	P32507 mus musculus
5	496	20.5	538	1 PVR2_HUMAN	Q92692 homo sapien
6	411	17.0	417	1 PVR_CERAE	P32506 cercopithec
7	401	16.6	417	1 PVR_HUMAN	P15151 homo sapien
8	227	9.4	764	1 ICCR_DROME	Q08180 drosophila
9	208.5	8.6	837	1 NCM2_MOUSE	O35136 mus musculus
10	187.5	7.8	278	1 OX2G_HUMAN	P41217 homo sapien
11	187	7.7	4391	1 PGBM_HUMAN	P98160 homo sapien
12	181.5	7.5	2012	1 DSCA_HUMAN	O60469 homo sapien
13	177.5	7.3	853	1 NCA1_BOVIN	P31836 bos taurus
14	177	7.3	626	1 MAG_HUMAN	P20916 homo sapien
15	177	7.3	626	1 MAG_MOUSE	P20917 mus musculus
16	175	7.2	626	1 MAG_RAT	P07722 rattus norv
17	175	7.2	837	1 NCM2_HUMAN	O15394 homo sapien
18	169.5	7.0	509	1 SHS1_RAT	P97710 r protein-t
19	166	6.9	588	1 C166_CHICK	P42292 gallus gall
20	162.5	6.7	278	1 OX2G_MOUSE	O54901 mus musculus
21	162.5	6.7	278	1 OX2G_RAT	P04218 rattus norv
22	162.5	6.7	858	1 NCA1_RAT	P13596 rattus norv
23	162	6.7	353	1 CEPU_CHICK	Q90773 gallus gall
24	162	6.7	365	1 CXAR_HUMAN	P78310 homo sapien
25	162	6.7	761	1 NCA2_HUMAN	P13592 homo sapien
26	162	6.7	848	1 NCA1_HUMAN	P13591 homo sapien
27	161.5	6.7	739	1 VCA1_MOUSE	P29533 mus musculus
28	161	6.7	365	1 CXAR_MOUSE	P97792 mus musculus
29	160.5	6.6	702	1 CEAS_HUMAN	P06731 homo sapien
30	160	6.6	725	1 NCA2_MOUSE	P13594 mus sapien
31	158	6.5	3707	1 PGBM_MOUSE	Q05793 mus musculus
32	157.5	6.5	595	1 SILL_HUMAN	Q96pql homo sapien
33	157	6.5	1091	1 NCA1_CHICK	P13590 gallus gall

34	156.5	6.5	597	1 SILL_PANTR	Q95lh0 pan troglod
35	156	6.5	337	1 OPCM_CHICK	Q98892 gallus gall
36	156	6.5	467	1 SILL_HUMAN	Q9y286 homo sapien
37	156	6.5	847	1 CD22_HUMAN	P20273 homo sapien
38	153.5	6.4	1115	1 NCA1_MOUSE	P13595 mus musculus
39	150	6.2	646	1 MUI8_HUMAN	P43121 homo sapien
40	149.5	6.2	467	1 SILL_MOUSE	Q91y57 mus musculus
41	149.5	6.2	1051	1 PTK7_CHICK	Q91048 gallus gall
42	149	6.2	344	1 NTRI_MOUSE	Q99pj0 mus musculus
43	149	6.2	344	1 NTRI_RAT	Q62718 rattus norv
44	149	6.2	345	1 OPCM_BOVIN	P11834 bos taurus
45	149	6.2	569	1 TACT_HUMAN	P40200 homo sapien

ALIGNMENTS

RESULT 1
PVR1_MOUSE STANDARD; PRT; 515 AA.
AC Q9JKF6; Q9ERL5; Q9JII7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Hvec) (Nectin 1).
GN PVR1 OR PRR1 OR HVEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubreuil P., Campadelli-Fiume G.;
RT "The murine homolog of human nectin1 delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-lalpha to human nectin-lalpha (Hvec) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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CC EMBL; AF239762; AAF60333.1; -.

Search completed: April 12, 2004, 09:47:05
Job time : 12.9866 secs

A;Title: Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein
A;Reference number: A47639; MUID:87192943; PMID:3032785
A;Accession: A47639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <MCC>
A;Cross-references: GB:X05323; NID:g34742; PIDN:CAA28943.1; PID:g1335216; GB:M17226; GB:
C;Superfamily: MRC OX-2 antigen; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein
F:40-119/Domain: immunoglobulin homology <IMM>

Qy	18	SLKCLIEVN	ETITQISWEK	IHGSSQTVA	VHHPQYGF	SVQGEYQ	GRVLFKN	YSLNDATIT	77
			:::		:::		:::		
Db	44	SLKCSLQNA	QEAALIVTWQ	KKKAVSPEN	MVTFSENH	GVVIQPAY	KDKINITQ	LGLQNSTIT	103
			:::		:::		:::		

QY 229 GVNLCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSG-VYICKVTNSL 287
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 267 NVNLTCEARSKPPPTNYSWSTATGPLPNSTHFQENGSHLLISTVDDLNTTFVCKAINAL 326
QY 288 GQRSDQKQVIVISDVVPFKQTSSI 309
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 327 GSGQGQVTLV-----KEASEI 343

RESULT 12
A49448
irregular chiasm C-roughest precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: irreC-roughest protein
C;Species: Drosophila melanogaster
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 07-May-1999
C;Accession: A49448; S34129
R;Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandst
Genes Dev. 7, 2533-2547, 1993
A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal proje
A;Reference number: A49448; PMID:94102535; PMID:7503814
A;Accession: A49448
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-764 <RAM>
A;Cross-references: GB:L11040; NID:G304790; PID:G304791; EMBL:Z21641; NID:G312985; PID:G
C;Genetics:
A;Gene: FlyBase:rst
A;Cross-references: FlyBase:FBgn0003285
C;Keywords: transmembrane protein

Query Match 9.4%; Score 227; DB 2; Length 764;
Best Local Similarity 24.7%; Pred. No. 7.2e-09;
Matches 89; Conservative 60; Mismatches 142; Indels 70; Gaps 18;
QY 5 VEPH-VTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGR 63
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 32 MEPQDQTAVVGARVTLPCRV-INKQGT-LQWTK-----DDFGLGTSRDLGS- 75
QY 64 VLFKNYSL-----NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSIT---VTVLVEPT 114
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 76 --FERYAMVGSDEGDYSLDIYPVMLDDDDARYQQQVSPGPEGQPAIRSTFAGLTVLVPPE 133
QY 115 VSLIKGPDSLDGGNETVAAICIAATGKPVAHIDWEGDLG-----EMESTTSPFNETA- 168
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 134 APKITQGDVIYATADRKVEIECVSVGGKPAEITWIDGLGNVLTDNIETVIPLEPDQRRF 193
QY 169 TIISQYKLFPTFARGRRITCVKHPALEKDIRYSFI-LDIQYAPEVSVT-----GYD 220
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 194 TAKSVLRLTPKKEHHTNFSCQAQNTA-DRTYRSAKIRVEVKYAPKVKVNVMSLPGGAG 252
QY 221 GNWVFGVRKG-----VNLKCNADANPPPFKSVWSRLDGQWPDGLLASDN 263
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 253 GS--VGGAGGSGVHMTSGSRIVEHSQVRLECRADANPSDVRYRWFIND---EPIIGGQK 306
QY 264 TLHFVHPLTFNYSGVYI-CKVTNSLGQRSDQKVIYISDVP-FKQTSSIAVAGAVIGAVLA 321
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 307 TEMVIRNVRKFKHDAIVKCEVQNSVGKSEDSSETLDSYAPSFQRQPQSMEAD--VGSVVS 364
QY 322 L 322
|
Db 365 L 365

RESULT 13
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T20992; T24733
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20992

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone F15G9
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24733
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: CESP:F15G9.4a
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077
Query Match 8.1%; Score 196.5; DB 2; Length 5175;
Best Local Similarity 26.4%; Pred. No. 1.7e-05;
Matches 88; Conservative 42; Mismatches 138; Indels 65; Gaps 19;
QY 2 PIIVE-PHVTAV-WGNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGE 59
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 793 PTIIESPHTRVNIERQVTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG- 847
QY 60 YQGRVLEFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSIT--VTVLVEPTVSL 117
| : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 848 -----NLLITDAQI-----EDQGQFTCIARN-TYQQQSOSTLMVTGLVSPVLGH 891
QY 118 IKGPDSLDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETAIIISQYKLF 177
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 892 VPPEEQLEGGQDLTSL--CVVVLGTFKPSIVWIKDDKPVEE-----GPTIKIEGGGSL 943
QY 178 PTRFARGR--RITCVKHPALEKDIRYSFIL----DIQYAPE-----VSVTGYDGNW- 223
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 944 RLRGGNPKDEGKYTCIAVSPAGNSTLHINVLIKKPEFVYKPEGGIVFKPTISGMDEKHV 1003
QY 224 -----FVGRKGVNLKCNADANPPPFKSVWSRLDGQWP-----DGLLASDNTLHFVH 269
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
Db 1004 AVVNSTHDVLDGEGFAIPCWSGTTPPI-ITW-YLDGR-PITPNRSRDFVTADNTL-IVR 1059
QY 270 PLTFNYSGVYICKVTNSLGQRSDQKVIYISDVP 302
: | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTP 1092

RESULT 14
T43290
hemicentir precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43290; T20993; T24734
R;Vogel, E.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ
A;Reference number: Z22396
A;Accession: T43290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
A;Cross-references: EMBL:AF074901; PIDN:AAC26792.1
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20993
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b

Db 27 GDVVVQAPTQVPGFLGDSVTLPCYLQVPMNEVTHVSQLTWTR-HGESGSMVAFHQIQGPS 85
QY 52 YGFSVQGEYQGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV 111
Db 86 YSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLFVTFFPQGSRSVDIWLRLVA 143
QY 112 EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTT--TSFPNET 167
Db 144 KPQNTAEVQKVLT---GEPVPMARCVSTGGRPPAQITWHSDLGMPNTSQVPGFLSGT 199
QY 168 ATIIISQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227
Db 200 VVTSLWILVPSSQVDGKNVTCKVEHSEFEKPQLLTVNLTVYYPPEVSISGYDNNWYLGQ 259
QY 228 KGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 260 NEATLTCDARSNPEPTGYNNWSTMGPPLPPFAVAQAQL-LIRPVDKPINTTLICNVTNAL 318
QY 288 QORSDDQKVIYISDVFPFKQTSIAVAGAVIGAVLALFIAIFVTV 331
Db 319 GARQAELTVQVKEGPPSEHSGMS-RNAIIFLVLGILVFLILLGI 361

RESULT 10
RWHUPA
poliovirus receptor splice form alpha precursor - human
N;Alternate names: poliovirus receptor H20A
N;Contains: poliovirus receptor beta
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: S12048; A31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take
EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A;Reference number: S12048; MUID:91006015; PMID:2170108
A;Accession: S12048
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: EMBL:X64116; NID:G35809; PIDN:CAA45478.1; PID:G825708
A;Note: 67-Ala was also found
A;Note: the gamma form has 331-Gly and lacks residues 332-384
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: A31496
A;Molecule type: mRNA
A;Residues: 1-66, 'A', 68-417 <MEN>
A;Cross-references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C;Genetics:
A;Gene: GDB:PVR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-417/Product: poliovirus receptor alpha #status predicted <EXT>
F;21-343/Domain: extracellular #status predicted <EXT>
F;21-339,385-417/Product: poliovirus receptor beta #status predicted <PVRB>
F;42-125/Domain: immunoglobulin homology <IMM1>
F;159-223/Domain: immunoglobulin homology <IMM2>
F;259-314/Domain: immunoglobulin homology <IMM3>
F;344-367/Domain: transmembrane #status predicted <TMN>
F;368-417/Domain: intracellular #status predicted <INT>
F;49-123,166-221,266-312/Disulfide bonds: #status predicted
F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 16.5%; Score 398; DB 1; Length 417;
Best Local Similarity 29.4%; Pred. No. 6.4e-22;
Matches 101; Conservative 64; Mismatches 157; Indels 22; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEVNET---ITQISWEKIHGKSSQTVAVHH---PQ 51
Db 27 GDVVVQAPTQVPGFLGDSVTLPCYLQVPMNEVTHVSQLTWTR-HGESGSMVAFHQIQGPS 85
QY 52 YGFSVQGEYQGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV 111
Db 86 YSESKRLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLFVTFFPQGSRSVDIWLRLVA 143
QY 112 EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTT--TSFPNET 167
Db 144 KPQNTAEVQKVLT---GEPVPMARCVSTGGRPPAQITWHSDLGMPNTSQVPGFLSGT 199
QY 168 ATIIISQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227
Db 200 VVTSLWILVPSSQVDGKNVTCKVEHSEFEKPQLLTVNLTVYYPPEVSISGYDNNWYLGQ 259
QY 228 KGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 260 NEATLTCDARSNPEPTGYNNWSTMGPPLPPFAVAQAQL-LIRPVDKPINTTLICNVTNAL 318
QY 288 QORSDDQKVIYISDVFPFKQTSIAVAGAVIGAVLALFIAIFVTV 331
Db 319 GARQAELTVQVKEGPPSEHSGMS-RNAIIFLVLGILVFLILLGI 361

RESULT 11
A54017
colon carcinoma-associated antigen pE4 precursor - rat
N;Alternate names: pE4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 01-Dec-1995
C;Accession: A54017; A61206
R;Chadeneau, C.; LeMouillac, B.; Denis, M.G.
J. Biol. Chem. 269, 15601-15605, 1994
A;Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcino
A;Reference number: A54017; MUID:94253144; PMID:8195207
A;Accession: A54017
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <CHA>
A;Cross-references: GB:L12025
R;Chadeneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K
Int. J. Cancer 47, 903-908, 1991
A;Title: Characterization, isolation and amino terminal sequencing of a rat colon carcin
A;Reference number: A61206; MUID:91184910; PMID:2010233
A;Accession: A61206
A;Molecule type: protein
A;Residues: 34-41, 'X', 43-53 <CH2>
A;Note: the residue at position 9 is suggested to be glycosylated asparagine
C;Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma ce.
C;Keywords: glycoprotein; membrane protein

Query Match 13.0%; Score 315; DB 2; Length 416;
Best Local Similarity 29.2%; Pred. No. 9.4e-16;
Matches 94; Conservative 49; Mismatches 155; Indels 24; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNVSLKCLII--EVNETITQISWEKIHGKSSQTVAVHHPOYGFVS 56
Db 33 GEIAVQVLSNSTGFLGSLVHLCSLASKDNVTITQLTWKMRDPDGSPPFRACLPPQEGPSI 92
QY 57 QGEYQGRVLF-KNY-SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP- 113
Db 93 SDPERVKFLVAKVYEDLRNASLAISNLRVEDEGIYEQIATFPTGSKSANVWLKVFARPK 152
QY 114 -TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTSPFPNETA 168
Db 153 NTBALEPSPITLMPQD----VAKCISADGHPGPRITWSSNVNGSYREMKETGSRAPPQL 208
QY 169 TIISQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRK 228
Db 209 SATSPWCLLARQMARISPAQWNMK--ASRSRTSRPLLSLPYPPEVSISGYEGNWIIGLT 266

Db 384 LRVRRRKS 392

RESULT 7

B44194

poliovirus receptor (clone AGM-delta-1) - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: B44194

R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A:Title: A second gene for the African green monkey poliovirus receptor that has no puta

A:Reference number: A44194; MUID:93059651; PMID:1331508

A:Accession: B44194

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <KOI>

A:Cross-references: GB:S48817

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 17.0%; Score 411; DB 2; Length 392;

Best Local Similarity 30.4%; Pred. No. 6.4e-23;

Matches 105; Conservative 64; Mismatches 152; Indels 24; Gaps 11;

QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51

Db 27 GDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGN 85

QY 52 YGFSVQGEYQGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 111

Db 86 YSEPKRLEFVAARL--GTELRDASLRMFGRLVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143

QY 112 EP--TVSLIKGPDSDLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTS--FPNET 167

Db 144 KPQNTAEVQKVQLT----GKVPVAVRCVSTGGRPPAHITWHSDLGGMPNTSQAPGFLSGT 199

QY 168 ATIISQYKLFPTRFARGRRITCVVKHPALEKDRIYSFILDIOYAPEVSVTGYDGNWVGR 227

Db 200 VTVTSWLILVPSSQVDGKSVTCKVEHSEFEKPOLLTVNLTVYYPPEVSISGYDNNWYLSQ 259

QY 228 KGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287

Db 260 NEATLTCDARSNPEPTGYNWSTTMGPLPPFAVAQGAQL-LIRPVDKPIINTTFCINVTNAL 318

QY 288 GQRSDQKVIYISDVPFKQTSSIA---VAGAVIGAVLALFIIAIFV 329

Db 319 GARQALTVQKEGPPSEPSGSMSSNIIIFILIGIVILLTLLIGIV 363

RESULT 8

A44194

poliovirus receptor (clone AGM-alpha-1) - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: A44194

R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A:Title: A second gene for the African green monkey poliovirus receptor that has no puta

A:Reference number: A44194; MUID:93059651; PMID:1331508

A:Accession: A44194

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-417 <KOI>

A:Cross-references: GB:S48777

C:Superfamily: poliovirus receptor; immunoglobulin homology

C:Keywords: transmembrane protein

F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 17.0%; Score 411; DB 2; Length 417;

Best Local Similarity 30.4%; Pred. No. 7e-23;

Matches 105; Conservative 64; Mismatches 152; Indels 24; Gaps 11;

QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51

Db 27 GDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGN 85

QY 52 YGFSVQGEYQGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 111

Db 86 YSEPKRLEFVAARL--GTELRDASLRMFGRLVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143

QY 112 EP--TVSLIKGPDSDLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTS--FPNET 167

Db 144 KPQNTAEVQKVQLT----GKVPVAVRCVSTGGRPPAHITWHSDLGGMPNTSQAPGFLSGT 199

QY 168 ATIISQYKLFPTRFARGRRITCVVKHPALEKDRIYSFILDIOYAPEVSVTGYDGNWVGR 227

Db 200 VTVTSWLILVPSSQVDGKSVTCKVEHSEFEKPOLLTVNLTVYYPPEVSISGYDNNWYLSQ 259

QY 228 KGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287

Db 260 NEATLTCDARSNPEPTGYNWSTTMGPLPPFAVAQGAQL-LIRPVDKPIINTTFCINVTNAL 318

QY 288 GQRSDQKVIYISDVPFKQTSSIA---VAGAVIGAVLALFIIAIFV 329

Db 319 GARQALTVQKEGPPSEPSGSMSSNIIIFILIGIVILLTLLIGIV 363

poliovirus receptor splice form delta precursor - human

N:Alternate names: poliovirus receptor H20B

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997

C:Accession: A43024; B31496

R:Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Tak

EMBO J. 9, 3217-3224, 1990

A:Title: The poliovirus receptor protein is produced both as membrane-bound and secrete

A:Reference number: S12048; MUID:9106015; PMID:2170108

A:Accession: A43024

A:Molecule type: DNA

A:Residues: 1-392 <KOI>

A:Cross-references: EMBL:X64116

A>Note: 67-Ala was also found

R:Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.

Cell 56, 855-865, 1989

A:Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and

A:Reference number: A90910; MUID:89168426; PMID:2538245

A:Accession: B31496

A:Molecule type: mRNA

A:Residues: 1-66, 'A', 68-392 <MEN>

A:Cross-references: GB:M24406

C:Comment: The normal function of this receptor is unknown. Membrane-bound and soluble

C:Genetics:

A:Gene: GDB:PVR; PVS

A:Cross-references: GDB:120324; OMIM:173850

A:Map position: 19q13.2-19q13.2

A:Introns: 27/1; 143/1; 242/1; 281/2; 331/1

C:Superfamily: poliovirus receptor; immunoglobulin homology

C:Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pr

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-392/Product: poliovirus receptor delta #status predicted <MAT>

F:21-343/Domain: extracellular #status predicted <EXT>

F:42-125/Domain: immunoglobulin homology <IMM1>

F:159-223/Domain: immunoglobulin homology <IMM2>

F:259-314/Domain: immunoglobulin homology <IMM3>

F:344-367/Domain: transmembrane #status predicted <TMN>

F:368-392/Domain: intracellular #status predicted <INT>

F:49-123,166-221,266-312/Disulfide bonds: #status predicted

F:105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status p

Query Match 16.5%; Score 398; DB 1; Length 392;

Best Local Similarity 29.4%; Pred. No. 5.9e-22;

Matches 101; Conservative 64; Mismatches 157; Indels 22; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEKIHGKSSQTVAVHH---PQ 51

Db	Best Local Similarity 26.4%; Pred. No. 4.8e-29; Matches 138; Conservative 92; Mismatches 197; Indels 96; Gaps 19;
Qy	5 VEPHVTAVWGKNSLKCII--EVNETITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEY 60
Db	38 VLPEVRGQLGGTVLPCHELLPPVGLYISLVTWQRPDAPANHQNVAAAFHPKMGSPSPK 97
Qy	61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108
Db	98 PGSERLSFVSAKQSTGQDTEAELQDATLALHGLTVEDEGNYTCEFATFPKGSVRGMTWLR 157
Qy	109 VLVEP-----TVSLIKGPDSLIDGNETVAAICIAATGKPVVAHI-----DWEGDLGE 155
Db	158 VIAKPNQAEAKVTFSDP-----TTVALCISKEGPPPARISLWSSLDWEAKETQ 208
Qy	156 MESTTTSFPNETATIIISQYKLPFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVS 215
Db	209 VSGTLAG---TVTTSRFTLVPSGRADGVTVTCVKEHESFEELPILPTLSVRYPPPEVS 264
Qy	216 VTGYDGNWFVGRKGNLKNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNY 275
Db	265 ISGYDDNWYLGRTDATALSCDVRSNPEPTGYDWSTTSGTFTPSAVAQGSQ--VIHAVDSL 323
Qy	276 SGVYICKVTNSLQSRSDQKVIYISDVPPFKQTSIIAVAGAVIGAVLALFI-IAIFVTVL 334
Db	324 NTTFCVTVTNAVGMGRAEQVIFVRETP--NTAGAGATGGIIGGIIAIIATAVAATGILI 381
Qy	335 PRKKRPSYL-----DKVIDLPPTHKPP-PLYEERSPPLPQK--DLFQPEHLPLQTF-- 383
Db	382 CRQORKEQTLQGAEEDEDELEGPPSYKPPTPKAKLEAQEMPSQLFTLGASEHSPLKTPYFD 441
Qy	384 -----KEREVGNLOHSNG-----LNSRSFDYED-ENPV 410
Db	442 AGASCTEQEMPRYHELPTELRSGPLHPGATSLGSPIPVPPGPPPAVEDVSLDLEDEEGEE 501
Qy	411 GEDGIQMYPLYNQMCYQDRSPGKHQNDPKRVIYIDPREHV 453
Db	502 BEEYLDKINPIYDALSYS--SPSDSYQG---KGFVMSRAMVY 538
RESULT 5	
HLMSP3	poliovirus receptor homolog precursor - mouse
C;Species:	Mus musculus domesticus (western European house mouse)
C;Date:	30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession:	A38211
R;Morrison, M.E.;	Racaniello, V.R.
J. Virol.	66, 2807-2813, 1992
A;Title:	Molecular cloning and expression of a murine homolog of the human poliovirus re
A;Reference number:	A38211; PMID:92219365; PMID:1560525
A;Accession:	A38211
A;Molecule type:	DNA
A;Residues:	1-467 <MOR>
A;Cross-references:	GB:M80206; NID:g199785; PIDN:AAA39734.1; PID:g199786
C;Superfamily:	poliovirus receptor; immunoglobulin homology
C;Keywords:	duplication; glycoprotein; transmembrane protein
F;1-25/Domain:	signal sequence #status predicted <SIG>
F;26-467/Product:	poliovirus receptor homolog #status predicted <MAT>
F;26-354/Domain:	extracellular #status predicted <EXT>
F;47-133/Domain:	immunoglobulin homology <IMM1>
F;167-231/Domain:	immunoglobulin homology <IMM2>
F;267-322/Domain:	immunoglobulin homology <IMM3>
F;355-374/Domain:	transmembrane #status predicted <TMN>
F;375-467/Domain:	intracellular #status predicted <INT>
F;54-131,174-229,274-320/Disulfide bonds:	#status predicted
F;128,138,315/Binding site:	carbohydrate (Asn) (covalent) #status predicted
Query Match	18.5%; Score 446; DB 1; Length 467;
Best Local Similarity	32.3%; Pred. No. 2e-25;
Matches	116; Conservative 54; Mismatches 153; Indels 36; Gaps 12;
Qy	5 VEPHVTAVWGKNSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY-- 60

Db	38 VLPEVRGRLGGTVLPCHELLPPTTERTVRSQVWQRLDG---TVVAAFHPSFGVDFPNSQFS 94
Qy	61 QGRVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEP- 113
Db	95 KDRLSFVRARPETNADRLATLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPE 154
Qy	114 ----TVSLIKGPDSLIDGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSEPN---E 166
Db	155 NHAAEQEVTIGPSV-----AVARCVSTGGRPPPARITWISSLGG-EAKDTQEPGQAG 206
Qy	167 TATIISQYKLPFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWPFV 226
Db	207 TVTIISRYSLVPVGRADGVKVTCTVVEHESFEELPILPTLSVRYPPPEVSIISGYDDNWYLG 266
Qy	227 RKGVNLCNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNS 286
Db	267 RSEAILTCDVRSNPEPTDYDWSTTSGVFPASAVAQGSQ--LVHSVDRMVNTTTFICTATNA 325
Qy	287 LQORSQDKVIYISDVPPFKQTS---SIAVAGAVIGAVLALFIIAIFVT-VLLTPRKKRPS 341
Db	326 VGTGRAEQVILVRDTP--QASRDVGPLVWGAVGGTLLVLLAGGFLALILLRGRRRRKS 382
RESULT 6	
I53960	PRR2 alpha - human
C;Species:	Homo sapiens (man)
C;Date:	02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession:	I53960
R;Eberle, F.;	Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.
Gene	159, 267-272, 1995
A;Title:	The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is t
A;Reference number:	I53960; PMID:95347610; PMID:7622062
A;Accession:	I53960
A;Status:	preliminary; translated from GB/EMBL/DBJ
A;Molecule type:	mRNA
A;Residues:	1-478 <RES>
A;Cross-references:	GB:S79171; NID:g1042202; PID:g1042203
C;Genetics:	
A;Gene:	PRR2alpha
C;Superfamily:	poliovirus receptor; immunoglobulin homology
F;276-331/Domain:	immunoglobulin homology <IMM>
Query Match	17.5%; Score 424; DB 2; Length 478;
Best Local Similarity	29.3%; Pred. No. 9e-24;
Matches	108; Conservative 65; Mismatches 150; Indels 46; Gaps 11;
Qy	5 VEPHVTAVWGKNSLKCII--EVNETITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEY 60
Db	38 VLPEVRGQLGGTVLPCHELLPPVGLYISLVTWQRPDAPANHQNVAAAFHPKMGSPSPK 97
Qy	61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108
Db	98 PGSERLSFVSAKQSTGQDTEAELQDATLALHGLTVEDEGNYTCEFATFPKGSVRGMTWLR 157
Qy	109 VLVEP-----TVSLIKGPDSLIDGNETVAAICIAATGKPVVAHI-----DWEGDLGE 155
Db	158 VIAKPNQAEAKVTFSDP-----TTVALCISKEGPPPARISLWSSLDWEAKETQ 208
Qy	156 MESTTTSFPNETATIIISQYKLPFRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVS 215
Db	209 VSGTLAG---TVTTSRFTLVPSGRADGVTVTCVKEHESFEELPILPTLSVRYPPPEVS 264
Qy	216 VTGYDGNWVGRKGNLKNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNY 275
Db	265 ISGYDDNWYLGRTDATALSCDVRSNPEPTGYDWSTTSGTFTPSAVAQGSQ--VIHAVDSL 323
Qy	276 SGVYICKVTNSLQSRSDQKVIYISDVPPF-KQTSIIAVAGAVIGAVLALFIIAIFVTVL 332
Db	324 NTTFCVTVTNAVGMGRAEQVIFVRETPRPRRDVGLVWGAVGGTLLVLLAGGSLAFIL 383
Qy	333 LTPRKKRPS 341

poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: J04024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubre
Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene
A;Reference number: J04024; MUID:95237621; PMID:7721102
A;Accession: J04024
A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
C;Genetics:
A;Gene: GDB:PVRR1
A;Cross-references: GDB:583951
A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;356-379/Domain: transmembrane #status predicted <TMM>
F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 23.4%; Score 565.5; DB 2; Length 518;
Best Local Similarity 29.0%; Pred. No. 3.1e-34;
Matches 148; Conservative 85; Mismatches 171; Indels 107; Gaps 16;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSLAPYRERVELRPS 103

QY 71 LNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICEFATFPTGNRESQNLITVMKPT-NWIEGTQAVLRAKKG 162

QY 128 -GNETVAAICIAATKCPVAHIDWE-----GDLGEMESTTTSFPNETATIIISQYKL 176
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGARVPGDSGT-----PMAPVTVISRYRL 214

QY 177 FPTRFARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCN 236
Db 215 VPSREAHQQSLACIVNYHM--DRFKESLTNLNQYEPVETIEGFDGNWYLQRMVDVKLTCKA 272

QY 237 DANPPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSILGQRSDQXVI 296
Db 273 DANPPATEYHWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332

QY 297 YISDVFPFKQTS-----SIAVAGAVIGAVLALFIIAIFVTVLLTPRKK--RPSYLD 344
Db 333 NITEFPYTPSPPEHGRAGVPVPTAIIGVAGSILLVIVGGIVVALRRRHTFKGDYST 392

QY 345 K-----VIDLPPTHKPPPLYEERSPPLPQKDLFQPEHLPLQTFKEREVGNLQHSN 395
Db 393 KKHVYNGYSGKAGIPQHH--PPMAQNLOYPDSDDD-----EKKAGPLGGS- 435

QY 396 GLNSRSFDYEDENPVGEDGIQOM-----YPLYN-----QMCYQDRSPGKH 435
Db 436 -----SYEEEEEEGGGGERKVGPHPKYDEDAKRPYFTVDEAEARQDGYGDRTLGYQ 490

QY 436 HQNDPKRV-----YIDPREHYV 453
Db 491 Y---DPEQLDLAENMVSNQDGSFISKKEWYV 518

RESULT 3
A53437
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A53437
R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with p

A;Reference number: A53437; MUID:94179228; PMID:8132569
A;Accession: A53437
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-530 <AOK>
A;Cross-references: GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g825507
A;Experimental source: C57/BL6, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIIP:146667)
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IMM>

Query Match 21.5%; Score 519; DB 2; Length 530;
Best Local Similarity 28.4%; Pred. No. 9.1e-31;
Matches 142; Conservative 82; Mismatches 196; Indels 80; Gaps 17;

QY 5 VEPHVTAVWGNVSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEY-- 60
Db 38 VLPEVRGRGLGTVLPCHELLPPTTERVSVQVTWQRLDG---TVVAAFHPSFGVDFPNSQFS 94

QY 61 QGRVLF-----KNYSLNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVEP- 113
Db 95 KDRLSFVRAARPETNADLRDATLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPE 154

QY 114 ----TVSLIKGPDSDLIDGNETVAAICIAATKCPVAHIDWEGLGEMESTTTSFPN---E 166
Db 155 NHAEAQEVITGPQSV-----AVARCVSTGGRPPARITWISSLGG-EAKDTQEPGIQAG 206

QY 167 TATIIISQYKLPPTRFARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFG 226
Db 207 TVTIIISRYSLVPVGRADGVKVTCTRVHESFEPIILLPVTLVSRYPPEVVISIGYDDNWYLG 266

QY 227 RKGVNLCNADANPPPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNS 286
Db 267 RSEAILTCDVRSNPEPTDYDWSITTSVGFPPASAVAQSQL-LVHSDRMVNTTTFICTATNA 325

QY 287 LGQRSDQKVIYISDVFPFKQTSIAVAGAVIGAVLALFI-IAIFVTVLLTPRKKRPSYL-- 343
Db 326 VGTGRAEQVILVRESP--STAGAGATGGIIGIIAAIATAVAGTGILICRQQRKEQRLQ 383

QY 344 ---DKVIDLPPTHKPP-PLYEERSPPLPQK--DLFQPEHLPLQTF----- 383
Db 384 AADEEELEGGPPSYKPTPKAKLEPEMPSQLFTLGASEHSPVKTPYFDAGVSCADQEMP 443

QY 384 -----KEREVGNLQHSNGLN-----SRSFYEDENPVGEDGIQQMYP 420
Db 444 RYHELPTLEERSGPLLLGATGLGPSLLVPPGNVVEGVSLSLEDEEDEDDEEDFLDKINP 503

QY 421 LYNQMCYQDRSPGKHQNNND 440
Db 504 IYDALSYP--SPSDSYQSKD 521

RESULT 4
I68093
PRR2 delta - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: I68093
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is t
A;Reference number: I53960; MUID:95347610; PMID:7622062
A;Accession: I68093
A;Status: preliminary; translated from GB/EMBL/DBDJ
A;Molecule type: mRNA
A;Residues: 1-538 <RES>
C;Genetics:
A;Gene: PRR2delta
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 20.5%; Score 496; DB 2; Length 538;

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 11.9866 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-12_COPY_58_510
Perfect score: 2417
Sequence: 1 GPIIIEPHVTAVGKNVSLK.....KHHQNDPKRVYIDPREHYV 453

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1173.5	48.6	407	2 T08732	hypothetical prote
2	565.5	23.4	518	2 JC4024	poliovirus recepto
3	519	21.5	530	2 A53437	poliovirus recepto
4	496	20.5	538	2 I68093	PRR2 delta - human
5	446	18.5	467	1 HLMSP3	poliovirus recepto
6	424	17.5	478	2 I53960	PRR2 alpha - human
7	411	17.0	392	2 B44194	poliovirus recepto
8	411	17.0	417	2 A44194	poliovirus recepto
9	398	16.5	392	1 RWHUPD	poliovirus recepto
10	398	16.5	417	1 RWHUPA	poliovirus recepto
11	315	13.0	416	2 A54017	colon carcinoma-as
12	227	9.4	764	2 A49448	irregular Chiasm C
13	196.5	8.1	5175	2 T20992	hypothetical prote
14	196.5	8.1	5198	2 T43290	hemacentin precurs
15	187.5	7.8	274	2 A47639	OX-2 membrane glyc
16	187	7.7	4391	2 A38096	perlecan precursor
17	181.5	7.5	1896	2 T08851	Down syndrome cell
18	177.5	7.3	853	1 IJBONC	neural cell adhesi
19	177	7.3	626	1 A61084	myelin-associated
20	177	7.3	637	2 B33785	myelin-associated
21	175	7.2	582	1 BNRT3S	myelin-associated
22	175	7.2	626	1 BNRT3	myelin-associated
23	166.5	6.9	1091	2 A58532	glial cell membran
24	166.5	6.9	7962	2 I38346	elastic titin - hu
25	166	6.9	588	2 JH0506	adhesion molecule
26	166	6.9	588	2 A45254	surface glycoprote
27	165	6.8	365	2 JC7780	coxsackie- and ade
28	162.5	6.7	278	1 TDRTOX	OX-2 membrane glyc
29	162.5	6.7	858	1 IJRTNC	neural cell adhesi

30	162	6.7	761	1 IJHUNG	neural cell adhesi
31	161.5	6.7	739	2 JN0581	vascular cell adhe
32	161	6.7	765	2 C42632	cell adhesion mole
33	161	6.7	812	2 B42632	cell adhesion mole
34	161	6.7	932	2 A42632	cell adhesion mole
35	160.5	6.6	702	2 A36319	carcinoembryonic a
36	160	6.6	725	1 IJMSNG	neural cell adhesi
37	158	6.5	3707	2 S18252	heparan sulfate pr
38	157	6.5	1091	1 IJCHNL	neural cell adhesi
39	156	6.5	847	2 JH0371	B-cell adhesion pr
40	154	6.4	587	2 JH0464	DM-GRASP precursor
41	153.5	6.4	1115	1 IJMSNL	neural cell adhesi
42	152.5	6.3	1612	2 T30805	dutt1 protein - mo
43	151	6.2	483	2 T17346	hypothetical prote
44	150	6.2	646	2 I38049	cell surface glyco
45	149.5	6.2	1051	2 A39712	kinase-like protei

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08732
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732
A;Molecule type: mRNA
A;Residues: 1-407 <OTT>
A;Cross-references: EMBL:AL050071
A;Experimental source: fetal kidney; clone DKFZp566B0846
C;Genetics:
A;Note: DKFZp566B0846.1

Query Match 48.6%; Score 1173.5; DB 2; Length 407;
Best Local Similarity 62.8%; Pred. No. 1.6e-79;
Matches 240; Conservative 28; Mismatches 51; Indels 63; Gaps 7;

Qy	86	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKPVA	145
Db	1	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKPVA	60
Qy	146	HIDWEGDLGEMESTTTFPNETATIISQYKLFPTFPARGRRITCVVKHPALEKDIRYSFI	205
Db	61	HIDWEGDLGEMESTTTFPNETATIISQYKLFPTFPARGRRITCVVKHPALEKDIRYSFI	120
Qy	206	LDIQYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPFKSVWSRLDGQWPDGLLASDNTL	265
Db	21	LDIQYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPFKSVWSRLDGQWPDGLLASDNTL	180
Qy	266	HFVHPLTFNYSGVYICKVTNSLGORSQSDQKVIYISDVP-----	302
Db	181	HFVHPLTFNYSGVYICKVTNSLGORSQSDQKVIYISDPPTTTTLQPTIQHHPSTADIEDLAT	240
Qy	303	-----FKQTSIAVAGAVIGAVLAFILAFIVTVLLTPRK--RPSYLDKV	346
Db	241	EPKKLPPLSTLATIKDDTIATIIASVVGALFIVLSVLAGIFCYRRRRTRFGDYFAKN	300
Qy	347	IDLPPTH-----KPPPLYEERSPLPKQDLFQPEHL--PLQTQFKEREVG	389
Db	301	Y-IPPSDMQKESQIDVLQQDELDPYDPSVKKNKNPNVNNLRKYDLEPEKPTQW-----N	354
Qy	390	NLQHSNGLNSRFDYEDENPVG	411
Db	355	NVENLNRF-ERPMDYEDLKMG	375

RESULT 2
JC4024

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 13.0186 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-6_COPY_58_549
Perfect score: 2611
Sequence: 1 GPIIIEPHVTAVMGKNVSLK.....EDDLVSHVDGVSISRREWYV 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2141	82.0	407	2 T08732	hypothetical prote
2	627	24.0	518	2 JC4024	poliovirus recepto
3	473	18.1	467	1 HLMSP3	poliovirus recepto
4	449	17.2	530	2 A53437	poliovirus recepto
5	432.5	16.6	478	2 I53960	PRR2 alpha - human
6	418.5	16.0	538	2 I68093	PRR2 delta - human
7	415.5	15.9	417	2 A44194	poliovirus recepto
8	408.5	15.6	392	2 B44194	poliovirus recepto
9	386.5	14.8	392	1 RWHUPD	poliovirus recepto
10	386.5	14.8	417	1 RWHUPA	poliovirus recepto
11	320	12.3	416	2 A54017	colon carcinoma-as
12	228	8.7	764	2 A49448	irregular chiasm C
13	201	7.7	5175	2 T20992	hypothetical prote
14	201	7.7	5198	2 T43290	hemicientin precurs
15	198	7.6	4391	2 A38096	perlecan precursor
16	189	7.2	853	1 IJBONC	neural cell adhesi
17	187.5	7.2	274	2 A47639	OX-2 membrane glyc
18	186	7.1	588	2 JH0506	adhesion molecule
19	182	7.0	588	2 A45254	surface glycoprote
20	181.5	7.0	1896	2 T08851	Down syndrome cell
21	178	6.8	7962	2 I38346	elastic titin - hu
22	174	6.7	587	2 JH0464	DM-GRASP precursor
23	174	6.7	858	1 IJRTNC	neural cell adhesi
24	173.5	6.6	761	1 IJHUNG	neural cell adhesi
25	173	6.6	637	2 B33785	myelin-associated
26	171	6.5	582	1 BNRT3S	myelin-associated
27	171	6.5	626	1 BNRT3	myelin-associated
28	170	6.5	847	2 JH0371	B-cell adhesion pr
29	169.5	6.5	1091	1 IJCHNL	neural cell adhesi

30	169	6.5	626	1 A61084	myelin-associated
31	167.5	6.4	3707	2 S18252	heparan sulfate pr
32	167	6.4	458	2 S23969	cell-adhesion mole
33	167	6.4	765	2 C42632	cell adhesion mole
34	167	6.4	812	2 B42632	cell adhesion mole
35	167	6.4	932	2 A42632	cell adhesion mole
36	166	6.4	739	2 JN0581	vascular cell adhe
37	165	6.3	725	1 IJMSNG	neural cell adhesi
38	165	6.3	1115	1 IJMSNL	neural cell adhesi
39	164.5	6.3	569	2 A46462	T cell activation
40	163	6.2	521	2 JC1508	biliary glycoprote
41	162.5	6.2	278	1 TDRTOX	OX-2 membrane glyc
42	162	6.2	458	1 WMSR1	biliary glycoprote
43	161	6.2	1259	2 A43425	Bravo/Nr-CAM cell
44	160.5	6.1	725	2 JE0099	neural cell adhesi
45	159.5	6.1	725	2 JE0100	neural cell adhesi

ALIGNMENTS

RESULT 1

T08732 hypothetical protein DKFZp566B0846.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C;Accession: T08732

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A;Reference number: Z16474

A;Accession: T08732

A;Molecule type: mRNA

A;Residues: 1-407 <OTT>

A;Cross-references: EMBL:AL050071

A;Experimental source: fetal kidney; clone DKFZp566B0846

C;Genetics:

A;Note: DKFZp566B0846.1

Query Match 82.0%; Score 2141; DB 2; Length 407;
Best Local Similarity 99.3%; Pred. No. 4.6e-147;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy	86	SGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPPVA	145
Db	1	SGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDSLIDGGNETVAAICIAATGKPPVA	60
Qy	146	HIDWEGDLGEMESTTTSFPNETATIIISQKLFPTFRFARRRITCVVKHPALEKDIRYSFI	205
Db	61	HIDWEGDLGEMESTTTSFPNETATIIISQKLFPTFRFARRRITCVVKHPALEKDIRYSFI	120
Qy	206	LDIQYAPEVSVTGYDGNWFVGRKGWNLKCNDANANPPPKSVWSRLDGQWPDGLLASDNTL	265
Db	121	LDIQYAPEVSVTGYDGNWFVGRKGWNLKCNDANANPPPKSVWSRLDGQWPDGLLASDNTL	180
Qy	266	HFVHPLTFNYSGVYICKVNSLQQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT	325
Db	181	HFVHPLTFNYSGVYICKVNSLQQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT	240
Qy	326	EPKILPFPPLSTLATIKDDTTIATIIASVVGALFIVLSVLGIFCYRRRRTRFRGDYFAKN	385
Db	241	EPKILPFPPLSTLATIKDDTTIATIIASVVGALFIVLSVLGIFCYRRRRTRFRGDYFAKN	300
Qy	386	YIPPSDMQKESQIDVLQDDELDPYDPSVKKENKPNVNNLRKDYLEEPEKTQWNNVENLN	445
Db	301	YIPPSDMQKESQIDVLQDDELDPYDPSVKKENKPNVNNLRKDYLEEPEKTQWNNVENLN	360
Qy	446	RFRPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGVSISRREWYV	492
Db	361	RFRPMDYYEDLKMGMRFVSDHYDENEDDLVSHVDGVSISRREWCVCV	407

RESULT 2
JC4024

A;Cross-references: GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g825507
A;Experimental source: C57/BL6, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IMM>

Query Match 17.2%; Score 449; DB 2; Length 530;
Best Local Similarity 24.2%; Pred. No. 1.3e-24;
Matches 129; Conservative 87; Mismatches 194; Indels 122; Gaps 18;

QY 5 VEPHVTAVWGKNSLKC--LIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY-- 60
DB 38 VLPEVRGRLGGTVLPCHELLPPTTERVSQVWQRLDG---TVVAAFHPSFGVDFPNSQFS 94

QY 61 QGRVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVLVEP- 113
DB 95 KDRLSFVRARPETNADLRDATLAFRLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPE 154

QY 114 ----TVSLIKGPDLSIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFN--E 166
DB 155 NHAEAQEVITIGQSV-----AVARCSTGGRPPARITWISSLGG-EAKDTQEPGIQAG 206

QY 167 TATIISOYKLPFTRFARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGV 226
DB 207 TVTIISRYSLVPVGRADGVKVCVEHESFEPEPILLPVTLVSRYPPEVSGYDDNWYLG 266

QY 227 RKGVNLCNADANPPPKSVMSRLDGQWPDGGLASDNTLHFVHPLTFNYSYGVICKVTNS 286
DB 267 RSEAILTCDVRSNPEPTDYDWSTTSGVFPPASAVAQGSQ-LVHSVDRMVNTTFFICTATNA 325

QY 287 LGQRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTTIA 346
DB 326 VGTGRAEQVILVRESPTAGAGAT----- 349

QY 347 TIIASVVGALFIVLVSVLG--IFCYRRRRRTF-----GDYFAKNYIPPSDM 392
DB 350 ---GGIIGGIIAIIATAVAGTGILICRQORKEQRLQAADDEELEG---PPSYKPTPK 403

QY 393 QKESQIDVLQDELDSPDSVKKNKNPNVNNLIRKDYLE-----EPEKTQWNNVENLNR 446
DB 404 AK-----LEPEMPSQLTLGASEHSPV---KTPYFDAGVSCADQEMPRYHELPTLEE 453

QY 447 FERPM-----DYEDLKMGKMFVSDHYDENEDDLVSHVD 481
DB 454 RSGPLLLGATGLPSLLVPPGPNVVEGVSLSE---DEEDDEEDFLDKIN 502

RESULT 5
I53960
PRR2 alpha - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
C;Accession: I53960
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A;Reference number: I53960; MUID:95347610; PMID:7622062
A;Accession: I53960
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-478 <RES>
A;Cross-references: GB:S79171; NID:g1042202; PID:g1042203
C;Genetics:
A;Gene: PRR2alpha
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 16.6%; Score 432.5; DB 2; Length 478;
Best Local Similarity 24.5%; Pred. No. 1.7e-23;
Matches 134; Conservative 74; Mismatches 175; Indels 163; Gaps 18;

QY 5 VEPHVTAVWGKNSLKCCLI---EVNETITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEY 60

DB 38 VLPEVRGQLGGTVLPCHELLPVPGLYISLVTWQRPDAPANHQNVAAFHPKMGSPFPSPK 97

QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108

DB 98 PGSERLSFVSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFATFPKGSVRGWTWLR 157

QY 109 VLVEP-----TVSLIKGPDLSIDGGNETVAAICIAATGKPVAHI-----DWEGLGE 155

DB 158 VIAKPKNOAEAKVTFSDP-----TTVALCISKEGRPPARISLWLLDWEAKETQ 208

QY 156 MESTTTSFPNETATILISOYKLPFTRFARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVS 215

DB 209 VSGTLAG---TVTVTSRFTLVPSGRADGVTVTCVKEHESFEPEPALIPVTLVSRYPPEVS 264

QY 216 VTGYDGNWFGVRKGNLKCNDANPPPKSVMSRLDGQWPDGGLASDNTLHFVHPLTFNY 275

DB 265 ISGYDDNWYLGRTDATLSCDVRSNPEPTGYDWSTTSGTFTPTSAVAQGSQ-L-VIHAVDSLF 323

QY 276 SGVYICKVTNSLQORSQDKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPPLS 335

DB 324 NTTFVCTVTNAVGMGRAEQVIFVRETP-----RPRR----- 354

QY 336 TLATIKDDTTIATIIASVVGALFIVLVSVLG--IFCYRRRRRTF----- 377

DB 355 -----DVGPLVWGA VGGTLLVLL--LLAGGSLAFILLRVRRRRKSPGGAGGASGDG 404

QY 378 -----RGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKNKNPNVNNLIR 426

DB 405 GFYDPKAQVLGNQDVPFWTPVPGPME-----PDG----- 434

QY 427 KDYLEEPEKQTQWNNVENLNRFERPMDYEDLKMGKMFVSDHYDENEDDLVSHVDGVSIS 486

DB 435 KDEEEEEEE-----EKAEGKGLMLPPPPAL---EDDMESQLDGSLSIS 472

QY 487 RREWYV 492

DB 473 RRAVYV 478

RESULT 6
I68093
PRR2 delta - human
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C;Accession: I68093
R;Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devillard, E.; Lopez, M.
Gene 159, 267-272, 1995
A;Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th
A;Reference number: I53960; MUID:95347610; PMID:7622062
A;Accession: I68093
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-538 <RES>
A;Cross-references: GB:S79172; NID:g1042204; PID:g1042205
C;Genetics:
A;Gene: PRR2delta
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;276-331/Domain: immunoglobulin homology <IMM>

Query Match 16.0%; Score 418.5; DB 2; Length 538;
Best Local Similarity 23.6%; Pred. No. 2.1e-22;
Matches 126; Conservative 89; Mismatches 191; Indels 129; Gaps 18;

QY 5 VEPHVTAVWGKNSLKCCLI---EVNETITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEY 60

DB 38 VLPEVRGQLGGTVLPCHELLPVPGLYISLVTWQRPDAPANHQNVAAFHPKMGSPFPSPK 97

QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108

DB 98 PGSERLSFVSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFATFPKGSVRGWTWLR 157

QY 109 VLVEP-----TVSLIKGPDLSIDGGNETVAAICIAATGKPVAHI-----DWEGLGE 155


```

158  VIAPKNQAEAQKVTFSQDP-----TTVALCISKEGRPPARISWLSLSDWEAKETQ 208
156  MESTTTSPNETATIIISQKLFPTFRFARGRRITCVWKHPALEKDIRYSFILDIQYAPEVS 215
209  VSGTLAG----TVTVTSRFTLVPSGRADGVTVTCVKEHESFEEPALIPVTLISVRYPPEVS 264
216  VTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGGLASDNLTILFVHPLTFNY 275
265  ISGYDDNWYLGRTDATLSCDVRSNPEPTGYDWSVTSGTFTPSAVAQSQL-VIHAVDSLF 323
276  SGVYICKVTNSLQORSQDKVIXISDPPTTTTLQPTIQWHPSTADIEDLATEPKLPFPLS 335
324  NTTFVCTVTNAVGMGRAEQVIFVRETPNTAGAGAT----- 358
336  TLATIKDDTIATIIASVVGGALFIVLVSULA--GIFCYRRRR---TFRGDYFAK----- 384
359  -----GGIIGGIIAAIATAVAATGILICRQQRKEQTLQAGAEDEDLGPP 404
385  NYIPPSDMQESQIDVLQQDELDSYPDSVKKENKNPVNNLIRKDYLE-----EPEKTQW 438
405  SYKPPTPKAK-----LEAQEMPSQLFTLGASEHSP----LKTPYFDAGASCTEQEMPRY 454
439  NNVENLNRFERPM-----DYEDLKMGMKFVSDEHYDENEDDL 476
455  HELPTLEERSGPLHPGATSLGSPFVPPGPPAVEDVSLDLE---DEEGEEEEYL 506

```

RESULT 7
A44194
poliovirus receptor (clone AGM-alpha-1) - green monkey
C:Species: Cercopithecus aethiops (green monkey, grivet)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C:Accession: A44194
R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A:Title: A second gene for the African green monkey poliovirus receptor that has no putative
A:Reference number: A44194; MUID:93059651; PMID:1331508
A:Accession: A44194
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-417 <KOI>
A:Cross-references: GB:S48777
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: transmembrane protein
F:259-314/Domain: immunoglobulin homology <IMM>

Query Match	15.9%	Score 415.5	DB 2	Length 417
Best Local Similarity	28.1%	Pred. No. 2.4e-22		
Matches 119	Conservative 68	Mismatches 165	Indels 71	Gaps 16
QY	1	GPIIVE--PHVTAVMGKNVSLKCLIEV--NET-ITQISWEKIHGKSSQTVAVHH--PQ	51	
Db	27	GDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGMAVFFHQTQGP	85	
QY	52	YGFSVQGEYQGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLV	111	
Db	86	YSEPKRLEFVAARL--GTELRDASLRMFLGRVEDEGNYTCLFVTFPGSRSVDIWLRLA	143	
QY	112	EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTIS--FPNET	167	
Db	144	KPQNTAEVQKVQLT---GKPVVARCVSTGGRPPAHITWHSDLGCMPTNSQAPFLSGT	199	
QY	168	ATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR	227	
Db	200	VTVTSLWILVPSSQVDGKSVTCKVEHESFEKPOLLTVNLTVTYYPPPEVSIISGYDNNWYLSQ	259	
QY	228	KGVLKCNADANPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL	287	
Db	260	NEATLTCDARSNPEPTGYNWSVTMGPLPPFFAVAQGAQL-LIRPVDKPINTTFCINVTNAL	318	
QY	288	QGRSDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKLPFPPLSTLATIKDDTIAT	347	
Db	319	GARQAEALTVOVKEGP-----PS-----EPGSMSSNI-----	344	

```

QY      348 IIASVVGALFIVLSVLGAGFCYRRR--RTF-----RGDYFAKNYIIPPSDMQ 393
         ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      345 IIFLILGIVILLTLGL--GVFYFRSRCREFFLWCHHLSPSSEEHASASANGYIISYDVS 402
                                         |::|::|::|::|::|::|::|::|::|
QY      394 KES 396
         :::
Db      403 REA 405

```

RESULT 8
B44194
poliovirus receptor (clone AGM-delta-1) - green monkey
C/Species: Cercopithecus aethiops (green monkey, grivet)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C/Accession: B44194
R/Kojke, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A/Title: A second gene for the African green monkey poliovirus receptor that has no put
A/Reference number: A44194; MUID:93059651; PMID:1331508
A/Accession: B44194
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-392 <KOI>
A/Cross-references: GB:S48817
C/Superfamily: poliovirus receptor; immunoglobulin homology
F:259-314/Domain: immunoglobulin homology <IMM>

Query Match	15.6%;	Score 408.5;	DB 2;	Length 392;
Best Local Similarity	27.9%;	Pred. No. 7e-22;		
Matches 114;	Conservative	72;	Mismatches 164;	Indels 59; Gaps 15;

QY	1	GPIIVE--PHYTAVMGKNVSLKCLIEV---NET-ITQISWEKIHGSSQTAVVH-----PQ	51
DB	27	GDIIQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQIQGN	85
QY	52	YGFSVQGEYQGRVLFFKNYSLNDATITLHNIGFSDGSKYICKAVTFPLGNAQSSTTVTLV	111
DB	86	YSEPKRLEFVAARL--GTELRDASLRMFGLRVEDEGNYTCLFVTFPQGRSVDIWLRLVA	143
QY	112	EP--TVSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTS--FPNET	167
DB	144	KPONTAEVQKQLT----GKPVVPVARCVSTGGRPPAHITWHSDDLGMPTNSQAPGFLSGT	199
QY	168	ATIISQYKLPETRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGR	227
DB	200	VTVTSLWILVPSSQVDGKSVTCCKVEHSEFEKPOLLTVNLTVYYPPEVVISIGYDNNWYLSQ	259
QY	228	KGVLKCNADANPPPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL	287
DB	260	NEATLTCDARSNEPTGYNWSTTMGPLPPFAVAQAQL-LIRPVDKPINTTFCINVTNAL	318
QY	288	QORSQKYVISDPPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT	347
DB	319	GARQAELTVQVKEGP-----PS-----EPSGMSSNI-----	344
QY	348	IIASVVGGLFIVLVSVLAGIFCYRRRRRTFRGDYFAKNYIPPSDMQKES	396
DB	345	IIFLIIGIVILLTLGI--GVYFYRSRCS--REFLWCHHLSPSSEHHQS	389

RESULT 9
RWHPD
poliovirus receptor splice form delta precursor - human
N/Alternate names: poliovirus receptor H20B
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 02-Sep-1997
C/Accession: A43024; B31496
R/Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, EMBO J. 9, 3217-3224, 1990
A/Title: The poliovirus receptor protein is produced both as membrane-bound and
A/Reference number: S12048; MUID:91006015; PMID:2170108
A/Accession: A43024

A;Molecule type: DNA
A;Residues: 1-392 <KOI>
A;Cross-references: EMBL:X64116
A;Note: 67-Ala was also found
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: B31496
A;Molecule type: mRNA
A;Residues: 1-66, 'A', 68-392 <MEN>
A;Cross-references: GB:M24406
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C;Genetics:
A;Gene: GDB:PVR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F;1-20/Delta: signal sequence #status predicted <SIG>
F;21-392/Product: poliovirus receptor delta #status predicted <MAT>
F;21-343/Delta: extracellular #status predicted <EXT>
F;42-125/Delta: immunoglobulin homology <IMM1>
F;159-223/Delta: immunoglobulin homology <IMM2>
F;259-314/Delta: immunoglobulin homology <IMM3>
F;344-367/Delta: transmembrane #status predicted <TMN>
F;368-392/Delta: intracellular #status predicted <INT>
F;49-123, 166-221, 266-312/Disulfide bonds: #status predicted
F;105, 120, 188, 218, 237, 278, 307, 313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 14.8%; Score 386.5; DB 1; Length 392;
Best Local Similarity 27.6%; Pred. No. 2.7e-20;
Matches 106; Conservative 65; Mismatches 156; Indels 57; Gaps 12;
QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEVNET---ITQISWEKIHGKSSQTVAVHH---PQ 51
DB 27 GDVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQLTWTR-HGESGSMVAFHQTOGPS 85
QY 52 YGFSVQGEYQGRVLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 111
DB 86 YSESKLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143
QY 112 EP--TVSLIKGPDSDLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTT--TSFPNET 167
DB 144 KPQNTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHSDLGMPNTSQVPGFLSGT 199
QY 168 ATIISQYKLFPTFRFARRRITCVVKHPALEKDRIYSFILDIOVAPEVSVTGYDGNWVGR 227
DB 200 VTVTSMLWILVPSSQVDGKNVTKVEHESFEKPKQLLTVNLTVYYPEVVISGYDNNWYLGQ 259
QY 228 KGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
DB 260 NEATLTCDARSNPEPTGYNWSSTMGLPPLPPFAVAQGAQL-LIRPVDKPIINTTLCNVTNAL 318
QY 288 QORSQDKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKLPPLSTLATIKDDTIAT 347
DB 319 GARQAELTVQVKEGP-----PSEHSGMSR-----NA 344
QY 348 IIASVVGALFIVLSVLAGIFCY 371
DB 345 IIFLVGLVFLILLGI--GIYFY 366

RESULT 10
RWHUPA
poliovirus receptor splice form alpha precursor - human
N;Alternate names: poliovirus receptor H20A
N;Contains: poliovirus receptor beta
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: S12048; A31496
R;Koike, S.; Horie, H.; Ise, I.; Okitsu, A.; Yoshida, M.; Iizuka, N.; Takeuchi, K.; Take

EMBO J. 9, 3217-3224, 1990
A;Title: The poliovirus receptor protein is produced both as membrane-bound and secreted
A;Reference number: S12048; MUID:91006015; PMID:2170108
A;Accession: S12048
A;Molecule type: DNA
A;Residues: 1-417 <KOI>
A;Cross-references: EMBL:X64116; NID:g35809; PIDN:CAA45478.1; PID:g825708
A;Note: 67-Ala was also found
A;Note: the gamma form has 331-Gly and lacks residues 332-384
R;Mendelsohn, C.L.; Wimmer, E.; Racaniello, V.R.
Cell 56, 855-865, 1989
A;Title: Cellular receptor for poliovirus: molecular cloning, nucleotide sequence, and e
A;Reference number: A90910; MUID:89168426; PMID:2538245
A;Accession: A31496
A;Molecule type: mRNA
A;Residues: 1-66, 'A', 68-417 <MEN>
A;Cross-references: GB:M29535
C;Comment: The normal function of this receptor is unknown. Membrane-bound and soluble f
C;Genetics:
A;Gene: GDB:PVR; PVS
A;Cross-references: GDB:120324; OMIM:173850
A;Map position: 19q13.2-19q13.2
A;Introns: 27/1; 143/1; 242/1; 281/2; 331/1; 384/1; 394/3
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; receptor; transmembrane pro
F;1-20/Delta: signal sequence #status predicted <SIG>
F;21-417/Product: poliovirus receptor alpha #status predicted <INT>
F;21-343/Delta: extracellular #status predicted <EXT>
F;21-339, 385-417/Product: poliovirus receptor beta #status predicted <PVRB>
F;42-125/Delta: immunoglobulin homology <IMM1>
F;159-223/Delta: immunoglobulin homology <IMM2>
F;259-314/Delta: immunoglobulin homology <IMM3>
F;344-367/Delta: transmembrane #status predicted <TMN>
F;368-417/Delta: intracellular #status predicted <INT>
F;49-123, 166-221, 266-312/Disulfide bonds: #status predicted
F;105, 120, 188, 218, 237, 278, 307, 313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 14.8%; Score 386.5; DB 1; Length 417;
Best Local Similarity 27.6%; Pred. No. 3e-20;
Matches 106; Conservative 65; Mismatches 156; Indels 57; Gaps 12;
QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEVNET---ITQISWEKIHGKSSQTVAVHH---PQ 51
DB 27 GDVVQAPTQVPGFLGDSVTLPCYLQVPNMEVTHVSQLTWTR-HGESGSMVAFHQTOGPS 85
QY 52 YGFSVQGEYQGRVLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 111
DB 86 YSESKLEFVAARL--GAELRNASLRMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143
QY 112 EP--TVSLIKGPDSDLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTT--TSFPNET 167
DB 144 KPQNTAEVQKVQLT----GEPVPMARCVSTGGRPPAQITWHSDLGMPNTSQVPGFLSGT 199
QY 168 ATIISQYKLFPTFRFARRRITCVVKHPALEKDRIYSFILDIOVAPEVSVTGYDGNWVGR 227
DB 200 VTVTSMLWILVPSSQVDGKNVTKVEHESFEKPKQLLTVNLTVYYPEVVISGYDNNWYLGQ 259
QY 228 KGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
DB 260 NEATLTCDARSNPEPTGYNWSSTMGLPPLPPFAVAQGAQL-LIRPVDKPIINTTLCNVTNAL 318
QY 288 QORSQDKVIYISDPPTTTTLQPTIQWHPSTADIEDLATEPKLPPLSTLATIKDDTIAT 347
DB 319 GARQAELTVQVKEGP-----PSEHSGMSR-----NA 344
QY 348 IIASVVGALFIVLSVLAGIFCY 371
DB 345 IIFLVGLVFLILLGI--GIYFY 366

RESULT 11
A54017
colon carcinoma-associated antigen pE4 precursor - rat

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 7.86272 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-6_COPY_58_549
Perfect score: 2611
Sequence: 1 GPIIIEPHVTAVMGKNVSLK.....EDDLVSHVDGVSIRREWYV 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	659.5	25.3	515	1 PVR1_MOUSE	Q9jkl6 mus musculus
2	649.5	24.9	517	1 PVR1_HUMAN	Q15223 homo sapien
3	640.5	24.5	515	1 PVR1_PIG	Q9gl76 sus scrofa
4	449	17.2	530	1 PVR2_MOUSE	P32507 mus musculus
5	418.5	16.0	538	1 PVR2_HUMAN	Q92692 homo sapien
6	415.5	15.9	417	1 PVR_CERAE	P32506 cercopithec
7	386.5	14.8	417	1 PVR_HUMAN	P15151 homo sapien
8	228	8.7	764	1 ICCR_DROME	Q08180 drosophila
9	225	8.6	837	1 NCM2_MOUSE	O35136 mus musculus
10	198	7.6	4391	1 PGBM_HUMAN	P98160 homo sapien
11	189.5	7.3	837	1 NCM2_HUMAN	O15394 homo sapien
12	189	7.2	853	1 NCAL_BOVIN	P31836 bos taurus
13	187.5	7.2	278	1 OX2G_HUMAN	P41217 homo sapien
14	186.5	7.1	509	1 SHS1_RAT	P97710 r protein-t
15	186	7.1	588	1 C166_CHICK	P42292 gallus gall
16	181.5	7.0	2012	1 DSCA_HUMAN	O60469 homo sapien
17	174	6.7	858	1 NCAL_RAT	P13596 rattus norv
18	173.5	6.6	353	1 CEPU_CHICK	Q90773 gallus gall
19	173.5	6.6	761	1 NCA2_HUMAN	P13592 homo sapien
20	173.5	6.6	848	1 NCAL_HUMAN	P13591 homo sapien
21	173	6.6	626	1 MAG_MOUSE	P20917 mus musculus
22	171	6.5	626	1 MAG_RAT	P07722 rattus norv
23	170	6.5	519	1 ECTO_RAT	P16573 rattus norv
24	170	6.5	847	1 CD22_HUMAN	P20273 homo sapien
25	169.5	6.5	1091	1 NCAL_CHICK	P13590 gallus gall
26	169	6.5	626	1 MAG_HUMAN	P20916 homo sapien
27	167.5	6.4	3707	1 PGBM_MOUSE	Q05793 mus musculus
28	166	6.4	739	1 VCA1_MOUSE	P29533 mus musculus
29	165	6.3	725	1 NCA2_MOUSE	P13594 mus musculus
30	165	6.3	1115	1 NCAL_MOUSE	P13595 mus musculus
31	164.5	6.3	569	1 TACT_HUMAN	P40200 homo sapien
32	163	6.2	467	1 SIL5_MOUSE	Q91y57 mus musculus
33	163	6.2	521	1 CEAL_MOUSE	P31809 mus musculus

34	162.5	6.2	278	1 OX2G_MOUSE	O54901 mus musculus
35	162.5	6.2	278	1 OX2G_RAT	P04218 rattus norv
36	158	6.1	702	1 CEAS_HUMAN	P06731 homo sapien
37	157.5	6.0	1088	1 NCAL_XENLA	P16170 xenopus lae
38	157.5	6.0	1092	1 NCA2_XENLA	P36335 xenopus lae
39	157.5	6.0	1709	1 SN_HUMAN	Q9bzz2 homo sapien
40	156.5	6.0	513	1 SHS1_MOUSE	P97797 m protein-t
41	154.5	5.9	1018	1 CONT_HUMAN	Q12860 homo sapien
42	154	5.9	1284	1 NRCA_CHICK	P35331 gallus gall
43	152.5	5.8	1256	1 NRCA_MOUSE	Q810u4 mus musculus
44	152	5.8	337	1 OPCM_CHICK	Q98892 gallus gall
45	151	5.8	569	1 SILF_MOUSE	Q920g3 mus musculus

ALIGNMENTS

RESULT 1
PVR1_MOUSE STANDARD; PRT; 515 AA.
AC Q9JKF6; Q9ERL5; Q9JII7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
DE mediator C) (Hvec) (Nectin 1).
GN PVRL1 OR PRR1 OR HVEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,
RA Lecocq E., Dubreuil P., Campadelli-Fiume G.;
RT "The murine homolog of human nectin1 delta serves as a species
RT nonspecific mediator for entry of human and animal alpha herpesviruses
RT in a pathway independent of detectable binding to gD.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-lalpha to human nectin-lalpha
RT (Hvec) in sequence and activity as a glycoprotein D receptor for
RT alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the
RT floor plate during embryogenesis, suggesting a role in neural
RT development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
CC ALPHAPERPEPVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF239762; AAF60333.1; -.

CC dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X76400; CAA53980.2; ALT_INIT.
DR EMBL; AF060231; AAC23798.1; -.
DR EMBL; AY029539; AAK33124.1; -.
DR EMBL; AF252867; AAG16648.1; -.
DR EMBL; AF196768; AAG16648.1; JOINED.
DR EMBL; AF196769; AAG16648.1; JOINED.
DR EMBL; AF196770; AAG16648.1; JOINED.
DR EMBL; AF196771; AAG16648.1; JOINED.
DR EMBL; AF196774; AAG16649.1; -.
DR EMBL; AF196768; AAG16649.1; JOINED.
DR EMBL; AF196769; AAG16649.1; JOINED.
DR EMBL; AF196770; AAG16649.1; JOINED.
DR EMBL; AF196771; AAG16649.1; JOINED.
DR EMBL; AF196772; AAG16649.1; JOINED.
DR EMBL; AF196773; AAG16649.1; JOINED.
DR Genew; HGNC:9706; PVRL1.
DR MIM; 600644; -.
DR MIM; 225000; -.
DR MIM; 225060; -.
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0004895; F:cell adhesion receptor activity; NAS.
DR GO; GO:0015026; F:coreceptor activity; TAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal; Alternative splicing.
FT SIGNAL 1 30
FT CHAIN 31 517 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 376 POTENTIAL.
FT DOMAIN 377 517 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 149 238 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 437 444 POLY-GLU.
FT DOMAIN 445 449 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 335 352 EFPYTPSPPEHGRAGPV -> AFCQLIYPGKGRTRAMF
/FTid=VSP 002624.
Missing (in isoform Gamma).
FT VARSPLIC 353 517
/FTid=VSP 002625.
FPTYTPSPPEHGRAGPVPTAIGGVAGSILLVLIVGGIVV
ALRRRHTFKGDYSTKKHVGNGYSKAGIPQHPPMAQNLO
YPDDSDDEKKAGPLGGSSYEETEEEEGGGGERKVGPH

FT -> KRPQRGLGSAARLLAGTVAVFLILVAULTVFFLYNRQ
FT QKSPETDAGTDQPLSQPEPSRQSSILVPEDIQVHLN
FT PGRQQQEEEDLQKLSLOPPYYDLGVSPSYHPSVRTTEPRG
FT ECP (in isoform Alpha).
FT /FTid=VSP 002626.
FT Missing (in isoform Alpha).
FT /FTid=VSP 002627.
SQ SEQUENCE 517 AA; 57158 MW; DF34C8AEC893EE6D CRC64;
Query Match 24.9%; Score 649.5; DB 1; Length 517;
Best Local Similarity 31.9%; Pred. No. 3.2e-41;
Matches 167; Conservative 80; Mismatches 182; Indels 95; Gaps 17;
QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTQKSTNGSKQNVAIYPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICEFATFPGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTRFARGR 185
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGEAYQEIERNPNGTVTVISRYRLVPSREAHQQ 222
QY 186 RITCVVKHFALEKDIRYSFILDIQYAPESVTVGYDGNWFWGRKGVNLCNADANPPFFKS 245
Db 223 SLACIVNYHM--DRFKESLTNLVQYEPEVTIEGFDGNWYLRQMDVKLTCKADANPPATEY 280
QY 246 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPTTT 305
Db 281 HWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYT- 339
QY 306 TLQPTIQWHPSTADIEDLATEPKKLPFLSTLATIKDDTIATIIASVVGALFIVLSVL 365
Db 340 ---PSPPEHGRAG-----PVP-----TAIIGGVAGSILLVLI-VV 371
QY 366 AGIF--CYRRRTFRGDYFAKNYI-----PPSDMQKESQIDVLQQDELDSY 409
Db 372 GGIVVALRRRRHTFKGDYSTKKHVGNGYSKAGIPQHPP--MAQNLO-----Y 418
QY 410 PDSVKKENK-NPVNNLIRKDYLEEPEKTQWNN-----VENLNRFEE 448
Db 419 PDDSDDEKKAGPLGG---SSYEEEEEEEEGGGGERKVGPHKPYDEDAKRPYFTVDEAE 475
QY 449 RPMDYVEDLKMGKMFVSDEHYDENEDDLVSHVDGVSISRREWYV 492
Db 476 ARQDGYGDRTLGYQY--DPEQLDLAENMVSNQDGSFISKKEWYV 517
RESULT 3
PVRL1_PIG
ID PVRL1_PIG STANDARD; PRT; 515 AA.
AC Q9GL76;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry
mediator C) (Hvec) (Nectin 1).
GN PVRL1 OR PRR1 OR HVEC.
OS Sus scrofa (Pig).
OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1] -
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine Hvec, a member of the highly conserved Hvec/nectin 1 family,
is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR

CC ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
CC CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gd) (By similarity).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF308632; AAG30281.1; -;
DR HSSP; P06907; 1NEU.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08315; IG_LIKE; 2.
KW Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;
KW Repeat; Glycoprotein; Signal.
FT SIGNAL 1 30 POTENTIAL.
FT CHAIN 31 515 POLIOVIRUS RECEPTOR RELATED PROTEIN 1.
FT DOMAIN 31 355 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 356 376 POTENTIAL.
FT DOMAIN 377 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 437 443 POLY-GLU.
FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BEAB00320DDE3785 CRC64;

Query Match 24.5%; Score 640.5; DB 1; Length 515;
Best Local Similarity 32.4%; Pred. No. 1.5e-40;
Matches 166; Conservative 83; Mismatches 189; Indels 75; Gaps 17;

Qy 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPGVKITQVTQKATNGSKQNVAIYNPAMGVSVLAPYRERVEFLRPS 103

Qy 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEPTVSLIKGPDSLIDG--- 127
Db 104 FTDGIRLSRLEDEGVYICEFATFPAGNRESQLNLTVMAKPT-NWIEGTQAVLRACKG 162

Qy 128 -GNETVAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATISQYKLFPTRFARGR 185
Db 163 KDDKVLVATCTSANGKPPSVSVSWETHLKGAEYQEIRNPNGTIVISRYLVPVSREDHRQ 222

Qy 186 RITCVVKGPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGKGVNLKCNADANPPPFKS 245
Db 223 SLACIVNYHM--DRFRESLTNVQVEEVTIEGFDGNWYLRQMDVKLTCKADANPPDATEY 280

Qy 246 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISDPPTTT 305
Db 281 HWTTLNGSLPKGVEAQNRTLFRGRPINYSMAGTYICEATNPICRSGQVEVNITEFPYT- 339

Qy 306 TLQPTIQWHPSTADIEDLATEPKKLPPPLSTLTIKDDTIATIIASVWGGALFIVLSVYL 365

RESULT 4

Db 340 ---PSPPEHGRRAG-----QVP-----TAIIGGVVGSILLVLF--VV 371
Qy 366 AGI---FCYRRRRTRFRGDYFAKNYI-----PPSDMQKESQIDVLQQDELDLS 408
Db 372 GGIWVLC-RRRHTFKGDYSTKGVYNGYSGAGIPQHPP--MAQNLQYPEDSDDEKKA 428
Qy 409 YP---DSVKENKNPNNLIRK-----DYLEEPEKTQWNVENLNRFRPMDYYEDLKM 459
Db 429 GPLGSSYEEEEEEGGGGERKVGPHPKYDEDAKRPYF---TVDEAEARQDGYGDRIL 484
Qy 460 GMKFVSDDEHYDENEDDLVSHVDGVSISRREWYV 492
Db 485 GYQY--DPEQLDLAENMVSNQDGSFISKWEYV 515

ID_PVR2_MOUSE STANDARD; PRT; 530 AA.
AC P32507; Q62096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
DE entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).
GN PVRL2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RT poliovirus receptor gene";
RL J. Virol. 66:2807-2813(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=CS7BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus";
RL J. Biol. Chem. 269:8431-8438(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Petersen K.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan G.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnurch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=9214397; PubMed=10196354;
RA Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB)

RP SEQUENCE FROM N.A.
RA Kodoyianni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
RA Shannon M., Brower A., Olsen A.S., Smith L.M.;
RT "Sequence analysis of a lmb region in 19ql3.2 containing a zinc finger
RT gene cluster";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS.
RX MEDLINE=91239515; PubMed=1851992;
RA Koike S., Ise I., Nomoto A.;
RT "Functional domains of the poliovirus receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N glycosylation of the virus binding domain is not essential for
RT function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P15151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P15151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC -!- MISCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
CC VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; M24407; AAA36461.1; -.
CC EMBL; M24406; AAA36462.1; -.
CC EMBL; X64116; CAA45478.1; -.
CC EMBL; X64117; CAA45478.1; JOINED.
CC EMBL; X64118; CAA45478.1; JOINED.
CC EMBL; X64119; CAA45478.1; JOINED.
CC EMBL; X64120; CAA45478.1; JOINED.
CC EMBL; X64121; CAA45478.1; JOINED.
CC EMBL; X64122; CAA45478.1; JOINED.
CC EMBL; X64123; CAA45478.1; JOINED.
CC EMBL; X64116; CAA45479.1; -.
CC EMBL; X64117; CAA45479.1; JOINED.
CC EMBL; X64118; CAA45479.1; JOINED.
CC EMBL; X64119; CAA45479.1; JOINED.
CC EMBL; X64120; CAA45479.1; JOINED.
CC EMBL; X64121; CAA45479.1; JOINED.
CC EMBL; X64122; CAA45479.1; JOINED.
CC EMBL; X64123; CAA45479.1; JOINED.
CC EMBL; X64116; CAA45480.1; -.
CC EMBL; X64117; CAA45480.1; JOINED.
CC EMBL; X64118; CAA45480.1; JOINED.
CC EMBL; X64119; CAA45480.1; JOINED.
CC EMBL; X64120; CAA45480.1; JOINED.
CC EMBL; X64121; CAA45480.1; JOINED.
CC EMBL; X64122; CAA45480.1; JOINED.
CC EMBL; X64123; CAA45480.1; JOINED.

DR EMBL; AC068948; AAF69803.1; -.
DR PIR; A43024; RWHUPD.
DR PIR; S12048; RWHUPA.
DR Genew; HGNC:9705; PVR.
DR MIM; 173850; -.
DR GO; GO:0005737; C:cytoplasm; TAS.
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0016021; C:integral to membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR GO; GO:0007125; P:invasive growth; TAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Antigen; Alternative splicing; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 105 105
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 218 218
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 307
FT CARBOHYD 313 313
FT VARSELIC 340 384
FT VARSELIC 331 331
FT VARSELIC 332 384
FT VARSELIC 385 392
FT VARSELIC 393 417
FT VARIANT 67 67
FT VARIANT 340 340
FT SEQUENCE 417 AA; 45302 MW; 45302 MM; DI5C012CE853169B CRC64;
SQ
Query Match 14.8%; Score 386.5; DB 1; Length 417;
Best Local Similarity 27.6%; Pred. No. 1.4e-21;
Matches 106; Conservative 65; Mismatches 156; Indels 57; Gaps 12;
QY 1 GPIIVE--PHVTAVWGKNVSLKCLIEVNET----ITQISWEKIHGKSSQTVAVHH---PQ 51
Db 27 GDVVVQAPTQVPGFLGDSVTLPCLYQVPMNEVTHVSQLTWAR-HGESGSMVAFHOTQGPS 85
QY 52 YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAGSSTTVTVLV 111
Db 86 YSESKRLEFFVAARL--GAELRNASLRMFLGRVEDEGNYTCLFVTFPQGSVDIWLRLVA 143
QY 112 EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTT--TSFPNET 167
Db 144 KPQNTAEVQKVQLT----GEPVPMARCVSTGGPPPAQITWHSDLGGMPTNSQVPGFLSGT 199
QY 168 ATIIISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTVGDNWFVGR 227
Db 200 VTVTSLWILVPSQVDGKNVTCKVEHSEFKEPQLLTVNLTVYPPPEVSIISYNNWYLGQ 259
QY 228 KGVNLKCNADANPPFPKSVWSRLDGQWPDGLLSDNTLHFVHPLTFNYSGVYICKVTNSL 287

Db 260 NEATLTCDARNPPTGYNWSTTMGLPFFFAVQAQL-LIRPVDKPIINTLICNTVAL 318
QY 288 QORSQKVIYISDPPTTTTLOPTIQWHPSTADIEDLATEPKLPLPSTLATIKDDTIAT 347
Db 319 GARQAEITVQKEGP-----PSEHSGISR-----NA 344
QY 348 IIAVVGALFVLVSVLAGIFY 371
Db 345 IIFVLGILVELILLGI--GIIFY 366

RESULT 8

ICCR DROME
ID ICCR DROME STANDARD; PRT; 764 AA.
AC Q08180;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Irregular chiasm C-roughest protein precursor (IRREC protein).
GN RST.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94102535; PubMed=7503814;
RA Ramos R.G., Igloi G.L., Lichte B., Baumann U., Maier D.,
RA Schneider T., Brandstaetter J.H., Froehlich A., Fischbach K.-F.;
RT "The irregular chiasm C-roughest locus of Drosophila, which affects
RT axonal projections and programmed cell death, encodes a novel
RT immunoglobulin-like protein.";
RL Genes Dev. 7:2533-2547(1993).
CC -!- FUNCTION: REQUIRED FOR CORRECT AXONAL PATHWAY FORMATION IN
CC THE OPTIC LOBE AND FOR PROGRAMMED CELL DEATH IN THE DEVELOPING
CC RETINA.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: POSTEMBRYONIC EXPRESSION IS STRONG IN THE
CC DEVELOPING OPTIC LOBE AND IN THE EYE IMAGINAL DISC.
CC -!- DEVELOPMENTAL STAGE: STRONGLY EXPRESSED IN EMBRYOS. ALSO FOUND
CC IN LATE LARVAL AND PUPAL STAGES.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC
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CC -----
DR EMBL; Z21641; CAA79756.1; -;
DR EMBL; L11040; AAA16632.1; -;
DR PIR; A49448; A49448.
DR FlyBase; FBgn0003285; rst.
DR GO; GO:0016202; P:regulation of myogenesis; IMP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG LIKE; 5.
KW Transmembrane; Immunoglobulin domain; Glycoprotein; Signal; Repeat;
KW Cell adhesion.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 764 IRREGULAR CHIASM C-ROUGHEST PROTEIN.
FT DOMAIN 20 533 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 534 556 POTENTIAL.
FT DOMAIN 557 764 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 21 123 IG-LIKE C2-TYPE 1.
FT DOMAIN 117 230 IG-LIKE C2-TYPE 2.
FT DOMAIN 245 261 GLY-RICH.

FT DOMAIN 237 343 IG-LIKE C2-TYPE 3.
FT DOMAIN 346 419 IG-LIKE C2-TYPE 4.
FT DOMAIN 430 530 IG-LIKE C2-TYPE 5.
FT DOMAIN 637 660 GLN-RICH (OPA-REPEAT).
FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 393 393 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 764 AA; 82947 MW; 262225D2B2A1C181 CRC64;

Query Match

Best Local Similarity 8.7%; Score 228; DB 1; Length 764;
Matches 112; Conservative 82; Mismatches 166; Indels 218; Gaps 24;

QY 5 VEPH-VTAVMGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGR 63
Db 32 MEPQDQAVVGARVTLPCRVLQTK-----DDFGLGTSRDLG- 75
QY 64 VLFKNYSL-----NDATITLHNIGFSDSGKYICKAVTFPLGNAGSSTT---VTVLVEPT 114
Db 76 --FERYAMVGSDEGDYSLDIYPVMLDDARYCQVSPGEGPAIRSTFAGLTVLVPPE 133
QY 115 VSLIKGPDSLIDGGNETVAAICIAATKPKVAHIDWEGDLG-----EMESTTTSFPNETA- 168
Db 134 APKITQGDVIYATADRKVEIECVSGKPAAEITWIDGLGNVLTDNIEYTVIPLDQRRF 193
QY 169 TIISQYKLEPTRFARGRRITCVVHKPALEKDIRYSFI-LDIQVAPEVSVT-----GYD 220
Db 194 TAKSVLRLLTPKKEHNTNFSCQAQNTA-DRYRSAKIRVEVKYAPKVKVNMVMSLPGGAG 252
QY 221 GNWFGVRKG-----VNLKCNADANPPPKSVMSRLDGQWPDGGLASDN 263
Db 253 GS--VGAGGGSVHMSTGSRIVHSQVRLECRADANPSDVRVRFIND---EPIIGGQK 306
QY 264 TLHFVHLPTFNYSGVYI-CKVTNSLQSRSDQKVIYISDPPT----- 303
Db 307 TEMVIRNVRKFHDAIVKCEVQNSVSKSEDSSETLDSYAPSRPQPSMEADVGSVSLT 366
QY 304 ---TTTLOPTIOW--HPS----- 316
Db 367 CEVDSNFPQFEIVWQHPSDRVVGTSNTLTFVSVNETAGRYCKANVPGYABISADAYVL 426
QY 317 -----TADIEDLATEPKK-----LP 331
Db 427 KGSPAIGSQRTQYGLVGDRTARIECFASSVPRARHVSWTENGQEISSSEGHDSILVDVAVP 486
QY 332 FPLSTLTIKDD-----TI-----ATIASVVG---ALFIV 360
Db 487 GGKSTLIIRDSQAYHYGKYNCTVVDYNDVDAEIQAKKSVSLMTIVGGISVAVALL 546
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQI 398
Db 547 VLTILVVVYIKCKRT-----KLPPADVISEHQI 575

RESULT 9

NCM2 MOUSE
ID NCM2 MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
DE adhesion molecule) (R4B12).
GN NCAM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/c; TISSUE=olfactory neuroepithelium;

RX MEDLINE=97368238; PubMed=9221781;
RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA Kagamiyama H., Mori K.;
RT "OCAM: A new member of the neural cell adhesion molecule family
RT related to zone-to-zone projection of olfactory and vomeronasal
RT axons.";
RL J. Neurosci. 17:5830-5842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=CS7BL/6J; TISSUE=Olfactory epithelium;
RX MEDLINE=97476194; PubMed=9334170;
RA Alenius M., Bohm S.;
RT "Identification of a novel neural cell adhesion molecule-related gene
RT with a potential role in selective axonal projection.";
RL J. Biol. Chem. 272:26083-26086(1997).
CC -!- FUNCTION: May play important roles in selective fasciculation and
CC zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
CC attached to the membrane by a GPI-anchor (short isoform).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O35136-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=O35136-2; Sequence=VSP_002590;
CC -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and
CC vomeronasal neurons in a zone-specific manner.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC -----
DR EMBL; AF001287; AAB69125.1; -
DR EMBL; AF001286; AAB69124.1; -
DR EMBL; AF016619; AAC53375.1; -
DR MGD; MGI:97282; Ncam2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS00835; IG_LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
FT SIGNAL 1 19
FT CHAIN 20 837
FT DOMAIN 20 697
FT TRANSMEM 698 718
FT DOMAIN 719 837
FT DOMAIN 21 108
FT DOMAIN 113 202
FT DOMAIN 208 297
FT DOMAIN 302 396
FT DOMAIN 401 491
FT DOMAIN 482 581
FT DOMAIN 594 678
FT DISULFID 42 93
FT DISULFID 136 186
FT DISULFID 232 281
FT DISULFID 322 380
FT DISULFID 422 475
FT CARBOHYD 177 177
FT CARBOHYD 219 219
FT CARBOHYD 309 309

FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 694 837 TLNGLGLGAIIGLVAAALLILVVDVSCFFIRQCGLLMC
FT ITRRMCGKSGSGSKELGKAAAYLKDGSKKEPIVEMRTE
FT DERITNHEDGSPVNEPNETTLPTEPEKLPKEENGKEVLNA
FT ETIEIKVSDNIIQSKEDDIKA -> NCCEANKGNGGQSWH
FT LNAVGFITVITMSLSCLF (in isoform Short).
FT /FTId=VSP_002590.
SQ SEQUENCE 837 AA; 93203 MW; 70473B053A2D65A5 CRC64;
Query Match 8.6%; Score 225; DB 1; Length 837;
Best Local Similarity 21.8%; Pred. No. 5.1e-09;
Matches 113; Conservative 78; Mismatches 158; Indels 170; Gaps 26;
QY 2 PIIVPE---HVTAVWGKNVSKLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQ 57
Db 209 PAIMPOKSFNATAERGEEMTLTCKASGSPDPT-ISWFR----- 246
QY 58 GEYQGRVLFKN--YSL--NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP 113
Db 247 ---NGKLEENEKYLKGSNTELTVRNIINKDGGSYVCKA-TNKAGEDQKQAFQVFP 302
QY 114 TVSLIKGDSLIDGNET-----VAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNE 166
Db 303 HILQK-----NETTSENGHVTLVC-EAEGEPVPEITWKRAIDGVFMFSEGDKSPDG 352
QY 167 TATIISQYKLEFTRFARGRRITCVVHKPALEKDIRY-----SFILDIQYAP- 212
Db 353 RIEVKGQH-----GRSSLHIRDVKLSDSGRYDCEAASRIGGHQSRSMHLDIEYAPK 402
QY 213 ----EVSVTGYDGNWFGVGRKGNLKNADANPPPKSV-WSRLDGQWPDGLLASDNTLHF 267
Db 403 FVSNQITMYISWEGN-----PINISCDVTANPP--ASIHWR-----EKLILPAKNTTHL 449
QY 268 -----VHPLTFNYSYVICKVTNSLQGRSDQKVIYISDPPTTTLQPTIQWHP 315
Db 450 KTHSVGRKMLEIAPTSDNDFGRYNCATNTRIGTRFQEIYILELADVSPSPHGVKIIELSQ 509
QY 316 STA-----DIEDLATEPKKLPFPLSTLATIKDDTIAT--IIASV 353
Db 510 TTAKISFNKPESHGGVPIHHYQVDVKEVASETWKI-----VRSHGVQTMVVLSSLE 560
QY 354 GGALFIVLVSVLACIFCYRRRTFRGDYF-----AKNYIPPS-----DMQKESQID 399
Db 561 PNTTYEIRVAVNG-----KGQGDYSKIEIFQTLPREPSPPSIHGQSPSSGKSFKIS 612
QY 400 VLQQDELDSYDPSVKKENKNPNVNLIRKDYLEEPEKTQW 438
Db 613 ITKQD-----DGGAPILEYIVK-YRSKDKEDQW 639
RESULT 10
PGBM_HUMAN
ID PGBM_HUMAN STANDARD; PRT; 4391 AA.
AC P98150; Q16287; Q9H3V5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basement membrane heparan sulfate proteoglycan core protein: a

RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon, and Skin;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple
RT domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
RX MEDLINE=20553141; PubMed=11101850;
RA Nicole S., Davoine C.-S., Topaloglu K., Cattolico L., Barral D.,
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissbach J.,
RA Hentati F., Fontaine B.;
RT "Perlecan, the major proteoglycan of basement membranes, is altered in
RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";
RL Nat. Genet. 26:480-483 (2000).
RN [4]
RP SEQUENCE OF 1016-1470 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [5]
RP SEQUENCE OF 890-1396 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to 1p36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [6]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
RN [7]
RP CARBOHYDRATE-LINKAGE SITE ASN-2121.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel
CC syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder
CC characterized by permanent myotonia (prolonged failure of muscle

CC relaxation) and skeletal dysplasia, resulting in reduced stature,
CC kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.
CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 3 laminin IV domains.
CC -!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
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CC -----
CC EMBL; X62515; CAA44373.1; -;
CC EMBL; M85289; AAA52700.1; -;
CC EMBL; AL445795; CAC18534.1; -;
CC EMBL; M64283; AAA52699.1; -;
CC EMBL; S76436; AAB21121.2; -;
CC EMBL; L22078; -; NOT_ANNOTATED_CDS.
CC PIR; A38096; A38096.
CC HSSP; P00740; LEDM.
CC Siena-2DPAGE; P98160; -;
CC Genew; HGNC:5273; HSPG2.
CC MIM; 142461; -;
CC MIM; 255800; -;
CC InterPro; IPR008985; ConA_like_lect_gl.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003598; Ig_c2.
CC InterPro; IPR003596; Ig_v.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR002172; LDL_receptor_A.
CC InterPro; IPR000082; SEA_domain.
CC Pfam; PF00008; EGF; 4.
CC Pfam; PF00047; Ig; 22.
CC Pfam; PF00052; laminin_B; 3.
CC Pfam; PF00053; laminin_EGF; 7.
CC Pfam; PF00054; laminin_G; 3.
CC Pfam; PF00057; ldl_recept_a; 4.
CC Pfam; PF01390; SEA; 1.
CC PRINTS; PR00261; LDLRECEPTOR.
CC ProDom; PD003031; Laminin_B; 3.
CC SMART; SM00181; EGF; 15.
CC SMART; SM00180; EGF_Lam; 12.
CC SMART; SM00409; IG_22.
CC SMART; SM00408; IGC2; 21.
CC SMART; SM00406; IGV; 7.
CC SMART; SM00281; LamB; 3.
CC SMART; SM00282; LamG; 3.
CC SMART; SM00192; LDLa; 4.
CC SMART; SM00200; SEA; 1.
CC PROSITE; PS00022; EGF_1; 9.
CC PROSITE; PS01186; EGF_2; 6.
CC PROSITE; PS50026; EGF_3; 4.
CC PROSITE; PS50835; IG LIKE; 22.
CC PROSITE; PS50025; LAM G DOMAIN; 3.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
CC PROSITE; PS01209; LDLRA_1; 4.
CC PROSITE; PS50068; LDLRA_2; 4.
CC PROSITE; PS50024; SEA; 1.
CC Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
CC Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
CC Extracellular matrix; EGF-like domain; Disease mutation.
KW
KW

FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	4391	BASEMENT MEMBRANE-SPECIFIC HEPARAN
FT				SULFATE PROTEOGLYCAN CORE PROTEIN.
FT	DOMAIN	80	194	SEA.
FT	DOMAIN	198	235	LDL-RECEPTOR CLASS A 1.
FT	DOMAIN	284	320	LDL-RECEPTOR CLASS A 2.
FT	DOMAIN	324	360	LDL-RECEPTOR CLASS A 3.
FT	DOMAIN	367	404	LDL-RECEPTOR CLASS A 4.
FT	DOMAIN	405	504	IG-LIKE C2-TYPE 1.
FT	DOMAIN	521	530	LAMININ EGF-LIKE 1 (N-TERMINAL).
FT	DOMAIN	531	730	LAMININ DOMAIN IV 1 (DOMAIN III A).
FT	DOMAIN	731	763	LAMININ EGF-LIKE 1 (C-TERMINAL).
FT	DOMAIN	764	813	LAMININ EGF-LIKE 2.
FT	DOMAIN	814	871	LAMININ EGF-LIKE 3.
FT	DOMAIN	879	923	LAMININ EGF-LIKE 4 (INCOMPLETE).
FT	DOMAIN	924	933	LAMININ EGF-LIKE 5 (N-TERMINAL).
FT	DOMAIN	934	1125	LAMININ DOMAIN IV 2 (DOMAIN III B).
FT	DOMAIN	1126	1158	LAMININ EGF-LIKE 5 (C-TERMINAL).
FT	DOMAIN	1159	1208	LAMININ EGF-LIKE 6.
FT	DOMAIN	1209	1265	LAMININ EGF-LIKE 7.
FT	DOMAIN	1275	1324	LAMININ EGF-LIKE 8.
FT	DOMAIN	1325	1334	LAMININ EGF-LIKE 9 (N-TERMINAL).
FT	DOMAIN	1335	1529	LAMININ DOMAIN IV 3 (DOMAIN III C).
FT	DOMAIN	1530	1562	LAMININ EGF-LIKE 9 (C-TERMINAL).
FT	DOMAIN	1563	1612	LAMININ EGF-LIKE 10.
FT	DOMAIN	1613	1670	LAMININ EGF-LIKE 11.
FT	DOMAIN	1677	1771	IG-LIKE C2-TYPE 2.
FT	DOMAIN	1772	1865	IG-LIKE C2-TYPE 3.
FT	DOMAIN	1866	1955	IG-LIKE C2-TYPE 4.
FT	DOMAIN	1956	2051	IG-LIKE C2-TYPE 5.
FT	DOMAIN	2052	2151	IG-LIKE C2-TYPE 6.
FT	DOMAIN	2152	2244	IG-LIKE C2-TYPE 7.
FT	DOMAIN	2245	2340	IG-LIKE C2-TYPE 8.
FT	DOMAIN	2341	2436	IG-LIKE C2-TYPE 9.
FT	DOMAIN	2437	2533	IG-LIKE C2-TYPE 10.
FT	DOMAIN	2534	2629	IG-LIKE C2-TYPE 11.
FT	DOMAIN	2630	2726	IG-LIKE C2-TYPE 12.
Query Match 7.6%; Score 198; DB 1; Length 4391;				
Best Local Similarity 22.8%; Pred. No. 5.5e-06;				
Matches 89; Conservative 55; Mismatches 147; Indels 100; Gaps 18;				
QY		2	PIIVE---	PHVTAVWGNVSLKCLIEVNETITQISWEKIHGSSQTVAVHHPQYGSVQG 58
Db		2926	PIYIEASSSHVTE	-GQTLDLNCVVP-GQAHAVTYWKRGG---SLPARHQTG----- 2973
QY		59	EYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTV	----- 109
Db		2974	-----	SQLRLHLVSPADSGEYVCRASGPGPEQAEASFTVTPPSEGSSYR 3018
QY		110	LVEPTVSLIKGPDLSLDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETAT	169
Db		3019	LRSPVIS-IDPPSSTVQQGD-ASFCKLIHDGAAPISLEWKTRNQELEDNVHISPN--GS	3074
QY		170	IISQYKLFPTRFARGRITCVVKHPALEKDIRYSFI-LDIQYAPEVSVTGYDGNWVVGK	228
Db		3075	IIT---IVGTRPSNHGTYRCVASN---AYGVAQSVVNLVSVHGPTVSVLPPEGVWVKVGK	3128
QY		229	GVNLKCNADANPPPKSVWSRLDG-----QWPDGLASDNTLHFVHPLTFNYSGVYICK	282
Db		3129	AVTLEC-VSAGEPRSSARWTRISSTPAKLEQRTYGLMDSHAVLQ-ISSAKPSDAGTYVCL	3186
QY		283	VTNSLQGRSDQKVIYIS-----DPPTTTTLQ-----PTIQWH	314
Db		3187	AQNALGTAQKQVEVIVDTGAWAPGAPQVQAEAEELTVEAGHTATLRCSATGSPATIHW-	3245
QY		315	PSTADIEDLATEPKLPPFLSTLATIKDDTI	345
Db		3246	-----SKLRSLPWQHRLEGDTL	3263

RESULT 11
NCM2_HUMAN

ID	NCM2_HUMAN	STANDARD;	PRT;	837 AA.
AC	015394;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Neural cell adhesion molecule 2 precursor (N-CAM 2).			
GN	NCAM2 OR NCAM21.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Brain;			
RX	MEDLINE=97369930; PubMed=9226371;			
RA	Paoloni-Giacobino A., Chen H., Antonarakis S.E.;			
RT	"Cloning of a novel human neural cell adhesion molecule gene (NCAM2)			
RT	that maps to chromosome region 21q21 and is potentially involved in			
RT	Down syndrome."			
RL	Genomics 43:43-51(1997).			
RN	[2]			
RP	CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.			
RX	MEDLINE=22660472; PubMed=12754519;			
RA	Zhang H., Li X.-J., Martin D.B., Aebersold R.;			
RT	"Identification and quantification of N-linked glycoproteins using			
RT	hydrazide chemistry, stable isotope labeling and mass spectrometry."			
RT	Nat. Biotechnol. 21:660-666(2003).			
CC	-!- FUNCTION: May play important roles in selective fasciculation and			
CC	zone-to-zone projection of the primary olfactory axons.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal			
CC	brain.			
CC	-!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.			
CC	-!- SIMILARITY: Contains 2 fibronectin type III domains.			
CC	-----			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; U75330; AAB0803.1; --			
DR	Genew; HGNC:7657; NCAM2.			
DR	MM; 602040; --			
DR	GO; GO:0016021; C:integral to membrane; TAS.			
DR	GO; GO:0005886; C:plasma membrane; TAS.			
DR	GO; GO:0007158; P:neuronal cell adhesion; TAS.			
DR	InterPro; IPR008957; FN III-like.			
DR	InterPro; IPR003961; FN_III.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003598; Ig_c2.			
DR	Pfam; PF00041; fn3; 2.			
DR	Pfam; PF00047; ig; 5.			
DR	SMART; SM00060; FN3; 2.			
DR	SMART; SM00408; IGC2; 5.			
DR	PROSITE; PS50835; IG_LIKE; 5.			
KW	Cell adhesion; Transmembrane; Glycoprotein; Repeat;			
KW	Immunoglobulin domain; Signal.			
FT	SIGNAL	1	19	POTENTIAL.
FT	CHAIN	20	837	NEURAL CELL ADHESION MOLECULE 2.
FT	DOMAIN	20	697	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	698	718	POTENTIAL.
FT	DOMAIN	719	837	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	21	108	IG-LIKE C2-TYPE 1.
FT	DOMAIN	113	202	IG-LIKE C2-TYPE 2.
FT	DOMAIN	208	297	IG-LIKE C2-TYPE 3.
FT	DOMAIN	302	396	IG-LIKE C2-TYPE 4.
FT	DOMAIN	401	491	IG-LIKE C2-TYPE 5.
FT	DOMAIN	482	581	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	594	678	FIBRONECTIN TYPE-III 2.
FT	DISULPID	42	93	PROBABLE.

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FT DISULFID 136 186 PROBABLE.
FT DISULFID 232 281 PROBABLE.
FT DISULFID 322 380 PROBABLE.
FT DISULFID 422 475 PROBABLE.
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 309 309 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 474 474 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 837 AA; 92932 MW; C3D034106C5741C1 CRC64;

Query Match 7.3%; Score 189.5; DB 1; Length 837;
Best Local Similarity 20.0%; Pred. No. 2.4e-06;
Matches 104; Conservative 87; Mismatches 163; Indels 165; Gaps 27;

QY 46 AVHHPQYGFVSQGE-----YQGRVLFKN--YSL--NDATITLH 79
Db 210 AISMPQKSFNATAERGEEMTFSCRASGSPPEPAISWFRNGKLIENEXVILKGSNTLTVR 269
QY 80 NIGFSDSGKICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLDGNETVAAICIAA 139
Db 270 NIINSDGGPYVCRA-TNKAGEDEKQAFQVFPVQPHIILQKNETTYENG---QVTLVC-DA 324
QY 140 TGKPVAHIDW-----EGDLGEMESTTTFSPNETATIIISQY-----KLFPTRFARG 184
Db 325 EGEPIPEITWKRAVDGFTFTGED-----KSPDGRIEVKQGHGSSSLHIKDVKLSGS 375
QY 185 RRIITC-----VVKHPALEKDIRYSFILDIQYAP-----EVSVTGYDGNWFVGRKGVNLKC 234
Db 376 GRYDCEAASRIGGH-----QKSMYLDIEYAPKFIISQTIYYSWEGN-----PINISC 422
QY 235 NADANPPFKSVWSRLDQWPDGGLASDNLHF-----VHPLTFNYSGVYICK 282
Db 423 DVKSNPP--ASIHWRDKL---VLPKNTNLTNTYSTGRKMILEIAPTSDNDFGRYNCT 476
QY 283 VTNSLQSRSDQKVIYISDPPTT-----TTLOPT-----IQWHPSTADIED 322
Db 477 ATNHIGTRFQEYILALADVSPSPYGVKIIELSQTAKVSFNKPDSHGGVPIHHYQVDVKE 536
QY 323 LATEPKKLPPPLSTLTIKDDTIATIIA--SVVGGALFIVLVSVLGIFCYRRRTFRGD 380
Db 537 VASEIWKI-----VRSHGVQTMVVVLNNLEPNTTYEIRVAAVNG-----KGQGD 579
QY 381 YF-----AKNYIPPS-----DMQKESQIDVLQDELDSYDPSVKKENKNPNNLIR 426
Db 580 YSKIEIFQTLVPREPPSPSIHGQPSGSKSPKLSITKQD-----DGGAPILEYIV 628
QY 427 KOYLEEPEKTOQNNVENLNRFRPMDYVEDLK--MGMKF 463
Db 629 K-YRSKDKEDQW--LEKKVQGNKDHILLEHLQWTMGMKF 664

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RESULT 12
NCAL_BOVIN
ID NCAL_BOVIN STANDARD; PRT; 853 AA.
AC P31836;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
DE (NCAM-140).
GN NCAM1 OR NCAM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain cortex;

```

```

RX MEDLINE=89378239; PubMed=2776887;
RA Lipkin V.M., Khramtsov N.V., Andreeva S.G., Moshnyakov M.V.,
RA Petukhova G.V., Rakitina T.V., Feshchenko E.A., Ishchenko K.A.,
RA Mirzoeva S.F., Chernova M.N., Dranytsyna S.M.;
RT "Calmodulin-independent bovine brain adenylate cyclase. Amino acid
RT sequence and nucleotide sequence of the corresponding cDNA.";
RL FEBS Lett. 254:69-73(1989).
RN [2]
RP SEQUENCE OF 20-36.
RX MEDLINE=86140120; PubMed=35125556;
RA Rougon G., Marshak D.R.;
RT "Structural and immunological characterization of the amino-terminal
RT domain of mammalian neural cell adhesion molecules.";
RL J. Biol. Chem. 261:3396-3401(1986).
RN [3]
RP IDENTIFICATION AS N-CAM.
RX MEDLINE=92111748; PubMed=1765159;
RA Premont R.T.;
RT "A bovine brain cDNA purported to encode calmodulin-insensitive
RT adenylate cyclase has extensive identity with neural cell adhesion
RT molecules (N-CAMs).";
RL FEBS Lett. 295:230-231(1991).
CC -!- FUNCTION: This protein is a cell adhesion molecule involved in
CC neuron-neuron adhesion, neurite fasciculation, outgrowth of
CC neurites, etc.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=A number of isoforms are produced;
CC Name=1;
CC IsoId=P31836-1; Sequence=Displayed;
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- CAUTION: Was originally (Ref.1) thought to be a calmodulin-
CC independent adenylate cyclase.
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EMBL; X16451; CAA34470.1; -.
PIR; A32976; IJBONC.
HSSP; P40189; 1BQU.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 853 NEURAL CELL ADHESION MOLECULE 1, 140 kDa
FT ISOFORM.
FT DOMAIN 20 719 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 720 737 POTENTIAL.
FT DOMAIN 738 853 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 20 111 IG-LIKE C2-TYPE 1.
FT DOMAIN 115 205 IG-LIKE C2-TYPE 2.
FT DOMAIN 212 300 IG-LIKE C2-TYPE 3.
FT DOMAIN 307 412 IG-LIKE C2-TYPE 4.
FT DOMAIN 415 500 IG-LIKE C2-TYPE 5.
FT DOMAIN 527 604 FIBRONECTIN TYPE-III 1.
FT DOMAIN 633 700 FIBRONECTIN TYPE-III 2.
FT DOMAIN 152 156 HEPARIN-BINDING (POTENTIAL).
FT DOMAIN 161 165 HEPARIN-BINDING (POTENTIAL).

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FT	CARBOHYD	181	181	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	190	190	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPIC	268	278	GELSGVQKMT -> EP (in isoform 2).
FT				/FTID=VSP_002613.
FT	CONFLICT	11	11	S -> C (IN REF. 3).
FT	CONFLICT	46	46	P -> T (IN REF. 1).
SQ	SEQUENCE	278 AA;	31264 MW;	38DF327B382CC970 CRC64;
Query Match 7.2%; Score 187.5; DB 1; Length 278;				
Best Local Similarity 24.8%; Pred. No. 7.3e-07;				
Matches 52; Conservative 36; Mismatches 97; Indels 25; Gaps 4;				
QY	18	SLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGSVQGEYQGRVLFKNYSINDATIT	77	
Db	48	SLKCSLQNAQEAALIVTQKKKAVSPENMVTFSNHHGVVQPAYKDKINITQLGLQNSTIT	107	
QY	78	LHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSL-IGPDSLIDGGNETVAAIC	136	
Db	108	FWNITLEDGECYMCLENTFGFGKISGTACLTIVYQPIVSLHYKFSSEHLN-----IT	159	
QY	137	IAATGKPVAHIDWEGDLGEMESTTT--SFPNETATISQYKLFPTREARGRRITCVVKHP	194	
Db	160	CSATARPAPMVFVKVPRSGIENSTVTLSPNGTTSVLSILHIKPKNQVQKEVICQVLHL	219	
QY	195	ALEKDIRYSFILDIOYAPEVSVTGYDGNWF	224	
Db	220	GTVTDFKQ-----TVNKGYNF	235	
RESULT 14				
ID	SHS1_RAT	STANDARD;	PRT;	509 AA.
AC	P97710;	O08951;	O70426;	Q9QW15;
DT	10-OCT-2003	(Rel. 42,	Created)	
DT	10-OCT-2003	(Rel. 42,	Last sequence update)	
DT	10-OCT-2003	(Rel. 42,	Last annotation update)	
DE	protein-tyrosine phosphatase non-receptor type substrate 1 precursor			
DE	(SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-			
DE	regulatory protein alpha-1) (Slrp-alpha-1) (Brain Ig-like molecule			
DE	with tyrosine-based activation motifs) (Bit) (Macrophage fusion			
DE	receptor) (Macrophage membrane protein MFP150).			
GN	PTPNS1 OR SHPS1 OR SIRP OR BIT OR MFR.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.			
OX	NCBI_TaxID=10116;			
RN	[1]			
RP	SEQUENCE FROM N.A., SEQUENCE OF 42-60; 68-91; 128-137; 150-158;			
RP	174-189; 192-202; 204-212; 218-237; 259-270; 279-282; 405-415 AND			
RP	446-453, N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, AND			
RP	INTERACTIONS WITH PTPN6 AND PTPN11.			
RC	TISSUE=Fetal fibroblast;			
RX	MEDLINE=97098667; PubMed=8943344;			
RA	Fujioka Y., Matozaki T., Noguchi T., Iwamatsu A., Yamao T.,			
RA	Takahashi N., Tsuda M., Takada T., Kasuga M.;			
RT	"A novel membrane glycoprotein, SHPS-1, that binds the SH2-domain-			
RT	containing protein tyrosine phosphatase SHP-2 in response to mitogens			
RT	and cell adhesion.";			
RL	Mol. Cell. Biol. 16:6887-6899(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A., SEQUENCE OF 32-48 AND 446-453, FUNCTION, AND			
RP	PHOSPHORYLATION ON TYROSINE RESIDUES.			
RC	STRAIN=Sprague-Dawley; TISSUE=Brain;			
RX	MEDLINE=97415431; PubMed=9271230;			
RA	Sano S.-I., Ohnishi H., Omori A., Hasegawa J., Kubota M.;			
RT	"BIT, an immune antigen receptor-like molecule in the brain.";			
RL	FEBS Lett. 411:327-334(1997).			
RN	[3]			
RP	SEQUENCE FROM N.A., SEQUENCE OF 99-107; 128-149; 192-217; 405-417;			
RP	419-429; 446-467 AND 496-506, N-GLYCOSYLATION, AND TISSUE SPECIFICITY.			
RC	STRAIN=Fischer 344; TISSUE=Macrophage;			
RX	MEDLINE=98449911; PubMed=9774638;			
RA	Saginario C., Sterling H., Beckers C., Kobayashi R., Solimena M.,			

RA	Ullu E., Vignery A.;
RT	"MFR, a putative receptor mediating the fusion of macrophages.";
RL	Mol. Cell. Biol. 18:6213-6223(1998).
RN	[4]
RP	SEQUENCE OF 1-419 FROM N.A., AND TISSUE SPECIFICITY.
RC	STRAIN=WAG/Rij; TISSUE=Alveolar macrophage;
RX	MEDLINE=98375871; PubMed=9712053;
RA	Adams S., van der Laan L.J.W., Vernon-Wilson E.,
RA	Renardel de Lavalette C., Doepp E.A., Dijkstra C.D., Simmons D.L.,
RA	van den Berg T.K.;
RT	"Signal-regulatory protein is selectively expressed by myeloid and
RT	neuronal cells.";
RL	J. Immunol. 161:1853-1859(1998).
RN	[5]
RP	PHOSPHORYLATION IN RESPONSE TO EGF, AND INTERACTION WITH PTPN11.
RX	MEDLINE=98008865; PubMed=9344856;
RA	Ochi F., Matozaki T., Noguchi T., Fujioka Y., Yamao T., Takada T.,
RA	Tsuda M., Takada H., Fukunaga K., Okabayashi Y., Kasuga M.;
RT	"Epidermal growth factor stimulates the tyrosine phosphorylation of
RT	SHPS-1 and association of SHPS-1 with SHP-2, a SH2 domain-containing
RT	protein tyrosine phosphatase.";
RL	Biochem. Biophys. Res. Commun. 239:483-487(1997).
RN	[6]
RP	PHOSPHORYLATION OF TYR-477 AND TYR-501, AND MUTAGENESIS OF TYR-436;
RP	TYR-460; TYR-477 AND TYR-501.
RX	MEDLINE=98204923; PubMed=9535915;
RA	Takada T., Matozaki T., Takeda H., Fukunaga K., Noguchi T.,
RA	Fujioka Y., Okazaki I., Tsuda M., Yamao T., Ochi F., Kasuga M.;
RT	"Roles of the complex formation of SHPS-1 with SHP-2 in
RT	insulin-stimulated mitogen-activated protein kinase activation.";
RL	J. Biol. Chem. 273:9234-9242(1998).
CC	-!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC	as docking protein and induces translocation of PTPN6,
CC	PTPN11 and other binding partners from the cytosol to the
CC	plasma membrane. Supports adhesion of cerebellar neurons, neurite
CC	outgrowth and glial cell attachment. May play a key role in
CC	intracellular signaling during synaptogenesis and in synaptic
CC	function. Involved in the negative regulation of receptor tyrosine
CC	kinase-coupled cellular responses induced by cell adhesion, growth
CC	factors or insulin. Mediates negative regulation of phagocytosis,
CC	mast cell activation and dendritic cell activation. CD47 binding
CC	prevents maturation of immature dendritic cells and inhibits
CC	cytokine production by mature dendritic cells. May play a role in
CC	the release of nitric oxide by macrophages (By similarity).
CC	-!- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
CC	macrophages, where it primarily binds PTPN6. Binds GRB2 in vitro.
CC	Binds FGR. Binds JAK2 irrespective of its phosphorylation status
CC	and forms a stable complex. Binds SCAP1 and/or SCAP2. The
CC	resulting complex recruits FYB. Binds PRX2B (By similarity).
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-!- TISSUE SPECIFICITY: Highly expressed in brain, spleen, liver
CC	and kidney. Detected at lower levels in heart. Highly expressed in
CC	alveolar and peritoneal macrophages, and at lower levels in
CC	dendritic cells.
CC	-!- PTM: N-glycosylated.
CC	-!- PTM: Phosphorylated on tyrosine residues in response to insulin,
CC	cell adhesion or epidermal growth factors. Dephosphorylated by
CC	PTPN11.
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	the European Bioinformatics Institute. There are no restrictions on its
CC	use by non-profit institutions as long as its content is in no way
CC	modified and this statement is not removed. Usage by and for commercial
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
CC	EMBL; D85183; BAA12734.1; --
DR	EMBL; D38458; BAA20368.1; --
DR	EMBL; U62328; AAC68478.1; --
DR	EMBL; AF055065; AAC18089.1; --

RT "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
RT that supports neurite extension.";
RL Neuron 7:209-220(1991).

RN [3]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.

RC TISSUE=Bursa of fabricius;
RX MEDLINE=92302224; PubMed=1608932;
RA Pourquie O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;
RT "BEN, a surface glycoprotein of the immunoglobulin superfamily, is
RT expressed in a variety of developing systems.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).

RN [4]
RP POSSIBLE FUNCTION.
RX MEDLINE=92211411; PubMed=1313497;

RA Pourquie O., Hallonet M.E.R., le Douarin N.M.;
RT "Association of BEN glycoprotein expression with climbing fiber
RT axonogenesis in the avian cerebellum.";
RL J. Neurosci. 12:1548-1557(1992).

CC -!- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING
CC FIBER AXONOGENESIS. SUPPORTS NEURITE EXTENSION.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
CC WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL

CC FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN
CC EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH

CC DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS
CC OF BEN.

CC -!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
CC DEVELOPMENT.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL; S63276; AAB20170.1; -;
CC EMBL; M76678; AAA48602.1; -;
CC EMBL; X64301; CAA45579.1; -;

CC PIR; A45254; A45254.
CC PIR; JH0464; JH0464.

CC PIR; JH0506; JH0506.
CC HSSP; Q13740; 1KJC.

CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.

CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 5.

CC SMART; SM00409; Ig; 3.
CC PROSITE; PS0835; IG LIKE; 4.

CC PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;

KW Repeat; Signal.
FT SIGNAL 1 33

FT CHAIN 34 588

FT DOMAIN 34 532

FT TRANSMEM 533 553

FT DOMAIN 554 588

FT DOMAIN 42 126

FT DOMAIN 131 240

FT DOMAIN 251 333

FT DOMAIN 338 414

FT DOMAIN 421 501

FT DISULFID 49 119

FT DISULFID 163 226

FT DISULFID 276 319

FT DISULFID 359 397

FT DISULFID 440 490

FT CARBOHYD 101 101

FT CARBOHYD 173 173

FT CARBOHYD 199 199

FT CARBOHYD 271 271

FT CARBOHYD 312 312

FT CARBOHYD 366 366

FT CARBOHYD 462 462

FT CARBOHYD 485 485

FT CARBOHYD 504 504

FT CONFLICT 1 10

FT CONFLICT 25 25

FT CONFLICT 112 113

FT CONFLICT 329 329

FT CONFLICT 401 402

SQ SEQUENCE 588 AA; 65726 MW; 2A28612D0164531E CRC64;

Query Match 7.1%; Score 186; DB 1; Length 588;

Best Local Similarity 20.3%; Pred. No. 2.7e-06;

Matches 107; Conservative 95; Mismatches 220; Indels 104; Gaps 24;

QY 9 VTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQ----GEYQGRV 64

Db 37 VNAVYGDITIMPCRLEVPDGLMFGKWKYEMPNGSPVFIAFRSSTKKNVQYDDVPDYKDRL 96

QY 65 -LFPKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPD 123

Db 97 SLSENY-----TSLKXNARISDEKRFVCMVLTED-DVSEETVVVKVQPSQPEILHQAD 150

QY 124 LIDGNETVAAICIAATGKPVAHIDW--EG-----DLGEMESTTTSFPNETAT 169

Db 151 FLETEKLMGECVVRDSYPEGNVTVYKNGRVLPQVEVVVNLKVENRSTGL----FT 206

QY 170 IISQYKLFPTFRFARRRITCVVKH--PALEKDIRYS-FILDIQYAPE-----VSVTG 218

Db 207 MTSLSQYMPTEKEDANAKFTCIYTHGSPGQKTIQSEPVVVDVHYPTKVTIRVLSQSSTI 266

QY 219 YDGNWVFVGRKGNLKNADANPPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGV 278

Db 267 KEGD-----NVTLCSGNGNPPPEFLF-YIPGE-TEGIRSSDT--YVMTDVRRNATGE 316

QY 279 YICKVTNSLGQRSDQKVIYISDPPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPL---- 334

Db 317 YKC-----SLIDKS-----MMDATTITVHYLDLQLTSPGEVTKQIG---EALPVSC 363

QY 335 ---STLATIKDDT-----IATIIASVVGALFIVLSVLGIFCYRRRRRTFRGDYFAK 384

Db 364 SRNATVFWIKDNTRMKTSPSFSLQYQDAGNYICETTLQVEVEGL---KKRKTLLIVEGK 420

QY 385 NYIPSDMQKESQIDVLQOD---ELDSYPDSV-----KKENKNPVNNLIRKD 428

Db 421 ---PQIKMTKKTNTNKMSTIVCHVEGFPKPAVQWTVTSGSLINKTEETKYVNGKFSSK 477

QY 429 YLEPEKTKQNNVNNLNRFRPMDYIEDLKMGMKFVSDHYDENED 474

Db 478 IIIAPEENVTLTCAENELERTV-----TSLNVSASISIPEDYDEPED 518

Search completed: April 12, 2004, 09:39:47

Job time : 8.86272 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 39.9581 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-6_COPY_58_549
Perfect score: 2611
Sequence: 1 GPIIIEPHVTAVWGKNVSLK.....EDDLVSHVDGVSISRREWYV 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2611	100.0	549	4 Q9NQS3	Q9nqs3 homo sapien
2	2494	95.5	549	11 Q9JLB9	Q9jlb9 mus musculus
3	2450	93.8	549	11 Q9D006	Q9d006 mus musculus
4	2141	82.0	407	4 Q9Y412	Q9y412 homo sapien
5	1629	62.4	304	4 Q9BVA9	Q9bva9 homo sapien
6	1587.5	60.8	510	11 Q9JLB8	Q9jlb8 mus musculus
7	1582.5	60.6	438	11 Q9JLB7	Q9jlb7 mus musculus
8	1218	46.6	267	4 Q8NC05	Q8nc05 homo sapien
9	542	20.8	101	4 Q8WVU4	Q8wvu4 homo sapien
10	534.5	20.5	295	11 Q9ERF5	Q9erf5 mesocricetu
11	528	20.2	298	6 Q9GL74	Q9gl74 cercopithec
12	526.5	20.2	295	6 Q9GL75	Q9gl75 bos taurus
13	524	20.1	510	4 Q96NY8	Q96ny8 homo sapien
14	524	20.1	510	4 Q96K15	Q96k15 homo sapien
15	501.5	19.2	508	11 Q8R007	Q8r007 mus musculus
16	501.5	19.2	508	11 Q8CED8	Q8ced8 mus musculus

17	489	18.7	483	11	Q9DBP8	Q9dbp8 mus musculu
18	475	18.2	467	11	Q8C6P2	Q8c6f2 mus musculu
19	473	18.1	467	11	Q91VT9	Q91vt9 mus musculu
20	453	17.3	530	11	Q80XJ5	Q80xj5 mus musculu
21	432	16.5	449	4	Q9UEI6	Q9uei6 homo sapien
22	405	15.5	400	6	Q8HY16	Q8hy16 cebus apell
23	402	15.4	412	11	Q9R1B1	Q9r1e1 rattus norv
24	397	15.2	412	11	Q63611	Q63611 rattus norv
25	390.5	15.0	401	6	Q08835	Q08835 cercopithec
26	386.5	14.8	417	4	Q96BJ1	Q96bj1 homo sapien
27	382.5	14.6	408	11	Q91WP1	Q91wp1 mus musculu
28	381.5	14.6	403	6	Q8HY15	Q8hy15 lemur catta
29	380.5	14.6	408	11	Q8K094	Q8k094 mus musculu
30	379.5	14.5	408	11	Q8BVF6	Q8bvf6 mus musculu
31	357.5	13.7	412	6	Q8HY14	Q8hy14 oryctolagus
32	338.5	13.0	415	11	Q60977	Q60977 mus musculu
33	316.5	12.1	456	11	Q8R5M8	Q8r5m8 mus musculu
34	314	12.0	445	11	Q8R4L1	Q8r4l1 mus musculu
35	311	11.9	442	4	Q9BY67	Q9by67 homo sapien
36	311	11.9	445	11	Q8K3T6	Q8k3t6 mus musculu
37	305.5	11.7	443	4	Q8N2P4	Q8n2f4 homo sapien
38	273	10.5	417	11	Q7TNL1	Q7tnl1 mus musculu
39	271.5	10.4	394	13	Q7ZXX1	Q7zxx1 xenopus lae
40	263.5	10.1	801	5	Q86LP8	Q86lf8 drosophila
41	257.5	9.9	800	5	Q86LF9	Q86lf9 drosophila
42	256.5	9.8	333	4	Q86WB8	Q86wb8 homo sapien
43	255.5	9.8	435	4	Q8N3J6	Q8n3j6 homo sapien
44	255.5	9.8	437	4	Q8IZP8	Q8izp8 homo sapien
45	253.5	9.7	336	11	Q9D6E7	Q9d6e7 mus musculu

ALIGNMENTS

RESULT 1

Q9NQS3					
ID	Q9NQS3	PRELIMINARY;	PRT;	549	AA.
AC	Q9NQS3;				
DT	01-OCT-2000 (TrEMBLrel. 15, Created)				
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)				
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)				
DE	Nectin 3.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Reymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,				
RA	Dubreuil P., Lopez M.;				
RT	"Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that interacts with afadin.";				
RL	Gene 0:0-0(2000).				
DR	EMBL; AF282874; AAF97597.1; -.				
DR	InterPro; IPR003599; IG.				
DR	InterPro; IPR007110; IG-like.				
DR	Pfam; PF00047; ig; 2.				
DR	SMART; SM00409; IG; 1.				
DR	PROSITE; PS50835; IG LIKE; 3.				
SQ	SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;				

Query Match 100.0%; Score 2611; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 6.3e-204;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	60
Db	58	GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	117
Qy	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIK	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIK	177

QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIISQYKLFPTTR	180
Dd	178	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIISQYKLFPTTR	237
QY	181	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRAKVNLKCNADANP	240
Dd	238	FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRAKVNLKCNADANP	297
QY	241	PPFKSVWSRLDGOWPDGLLASDNTHLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	300
Dd	298	PPFKSVWSRLDGOWPDGLLASDNTHLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	357
QY	301	PPTTTTLQPTIOHWPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGGALFIV	360
Dd	358	PPTTTTLQPTIOHWPSTADIEDLATEPKLPFPPLSTLATIKDDTIATIIASVVGGALFIV	417
QY	361	LVSVLAGIFCYRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYDPSVKKENKNP	420
Dd	418	LVSVLAGIFCYRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYDPSVKKENKNP	477
QY	421	VNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLLVSHV	480
Dd	478	VNNLIRKDYLEEPEKTQWNNVENLNRFERPMDYYEDLKMGMKFVSDEHYDENEDDLLVSHV	537
QY	481	DGSVISRREWYV	492
Dd	538	DGSVISRREWYV	549

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RESULT 2
Q9JLB9
ID Q9JLB9 PRELIMINARY; PRT; 549 AA.
AC Q9JLB9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;

```

Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVLVEPTVSLKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTTR	180
Db	178	PDSLIDGGNETVAAVCVAAATGKPPVAQIDWEGDLGEMESSTSPNETATIVSQYKLFPTTR	237
QY	181	FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLCNADANP	240
Db	238	FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLCNADANP	297
QY	241	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	300
Db	298	PPFKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD	357
QY	301	PPTTTTLQPTIOHWPSTADIEDLATEPKLPFPLSTLATIKDDTIATIIASVVGALFIV	360
Db	358	PPTTTTLQPTVQWHSPPADVQDIATEHKLPFPLSTLATIKDDTIATIIASVVGALFIV	417
QY	361	LVSVLAGIFCYRRRRTRFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPSDVKKENKNP	420
Db	418	LVSILAGVFCYRRRRTRFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSYPSDVKKENKNP	477
QY	421	VNNLIRKDYLEEPEKTQWNNVENLNRFERPMDDYEDLKMGMKFVSDHYDENEDDLVSHV	480
Db	478	VNNLIRKDYLEEPEKTQWNNVENLNRFERPMDDYEDLKMGMKFVSDERYNESEDGLVSHV	537
QY	481	DGSVISRREWYV	492
Db	538	DGSVISRREWYV	549

```

RESULT 3
Q9D006 PRELIMINARY; PRT; 549 AA.
AC Q9D006;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 2610301B19Rik protein.
GN PVRL3 OR 2610301B19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK011949; BAB27933.1; --
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA
```

DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;

Query Match 93.8%; Score 2450; DB 11; Length 549;
Best Local Similarity 92.5%; Pred. No. 8.2e-191;
Matches 455; Conservative 21; Mismatches 16; Indels 0; Gaps 0;

Qy 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GSIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGEY 117
Qy 61 QGRVLPKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLPKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
Qy 121 PDSLIDGGNETVAAICIAATGKPAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPT 180
Db 178 PDSIDGGNETVAAVCVSTGKPAQIDWEGDLGEREFSTISFLNETATIVSQYELEFPT 237
Qy 181 FARGRITCVVKKHPALEKOIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANP 240
Db 238 FARGRITCVVKKHPALEKOIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANP 297
Qy 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 357
Qy 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIV 360
Db 358 PPTTTTLOPTVQWHSPPADVDQIATEHKKLPFPLSTLATIKDDTIATIIASVVGALFLV 417
Qy 361 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKENKPN 420
Db 418 LVSILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSPDSVKKENKPN 477
Qy 421 VNNLIRKDYLEEPEKTQWNNVNNLRFERPMDDYEDLKMGMKFVSDHYDENEDDLVSHV 480
Db 478 VNNLIRKDYLEEPEKTQWNNVNNLRFERPMDDYEDLKMGMKFVSDRYNESEDGLVSHV 537
Qy 481 DGSVISRREWYV 492
Db 538 DGSVISRREWYV 549

RESULT 4
QY412 PRELIMINARY; PRT; 407 AA.
AC QY412;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP566B0846.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ottenwaelder B.; Obermaier B.; Mewes H.W.; Gassenhuber J.; Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 2.
KW Hypothetical protein.

FT NON TER 1 1
SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;

Query Match 82.0%; Score 2141; DB 4; Length 407;
Best Local Similarity 99.3%; Pred. No. 7.8e-166;
Matches 404; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 86 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPSLIDGGNETVAAICIAATGKPA 145
Db 1 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPSLIDGGNETVAAICIAATGKPA 60
Qy 146 HIDWEGDLGEMESTTSPFNETATIIISQYKLFPTFRFARRRITCVVKKHPALEKDIRYSEI 205
Db 61 HIDWEGDLGEMESTTSPFNETATIIISQYKLFPTFRFARRRITCVVKKHPALEKDIRYSEI 120
Qy 206 LDIQYAPEVSVTGYDGNWVGRKGVNLCNADANPPFKSVWSRLDGQWPDGLLASDNTL 265
Db 121 LDIQYAPEVSVTGYDGNWVGRKGVNLCNADANPPFKSVWSRLDGQWPDGLLASDNTL 180
Qy 266 HFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISDPTTTLOPTIQWHPSTADIEDLAT 325
Db 181 HFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISDPTTTTLOPTIQWHPSTADIEDLAT 240
Qy 326 EPKLPFPLSTLATIKDDTIATIIASVVGALFIVLSVLAGIFCYRRRTFRGDYFAKN 385
Db 241 EPKLPFPLSTLATIKDDTIATIIASVVGALFIVLSVLAGIFCYRRRTFRGDYFAKN 300
Qy 386 YIPPSDMQKESQIDVLQDELDSPDSVKKENKPNVNNLIRKDYLEEPEKTQWNNVNNL 445
Db 301 YIPPSDMQKESQIDVLQDELDSPDSVKKENKPNVNNLIRKDYLEEPEKTQWNNVNNL 360
Qy 446 RFRPMDDYEDLKMGMKFVSDHYDENEDDLVSHVDSVSRREWYV 492
Db 361 RFRPMDDYEDLKMGMKFVSDHYDENEDDLVSHVDSVSRREWCV 407

RESULT 5
Q9BVA9 PRELIMINARY; PRT; 304 AA.
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to nectin 3, DKFZP566B0846 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 1
SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 62.4%; Score 1629; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 2.6e-124;
Matches 304; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 189 CVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPFKSVWS 248
Db 1 CVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPFKSVWS 60
Qy 249 RLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISDPTTTTLO 308
Db 61 RLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISDPTTTTLO 120
Qy 309 PTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIVLSVL 368

Db 121 PTIQWHPSTADIEDLATEPKKLPFLSTLATIKDDTIATIIASVVGALFIVLSVLACI 180

Qy 369 FCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELSDYPSVKKENKNPVNNLIRKD 428

Db 181 FCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODELSDYPSVKKENKNPVNNLIRKD 240

Qy 429 YLEEPEKTQWNNVENLNRFERPMDYEDLKMGKMFVSDEHYDENEDDLVSHVDGVSISR 488

Db 241 YLEEPEKTQWNNVENLNRFERPMDYEDLKMGKMFVSDEHYDENEDDLVSHVDGVSISR 300

Qy 489 EYV 492

Db 301 EYV 304

RESULT 6

QJLB8 PRELIMINARY; PRT; 510 AA.

AC QJLB8;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Cell adhesion molecule nectin-3 beta.

GN PVRL3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20209403; PubMed=10744716;

RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,

RA Tachibana K., Mizoguchi A., Takai Y.;

RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules

RT that shows homophilic and heterophilic cell-cell adhesion

RT activities.";

RL J. Biol. Chem. 275:10291-10299 (2000).

DR EMBL; AF195834; AAF63686.1; --

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005193; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

SQ SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;

Query Match 60.8%; Score 1587.5; DB 11; Length 510;

Best Local Similarity 64.6%; Pred. No. 1.3e-120;

Matches 327; Conservative 38; Mismatches 74; Indels 67; Gaps 10;

Qy 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GSIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117

Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 237

Qy 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 297

Qy 241 PPFKSVSRDLGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300

Db 298 PPFKSVSRDLGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357

Qy 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFLSTLATIKDDTIATIIASVVGALFIV 360

Db 358 IPLTQT-----SSIA-----VAGAVIGAVLALF 380

Qy 361 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQK-----ESQIDVLQODEL-----DSYPDS 412

Db 381 IITVFVTLLTPRKK--RPSYLDKVIDLPPTHKPPPVYEERIPSLPQKDLLGQTEHLPLQ 438

Qy 413 VKKENK-----NPVNNLIRKDYLEEPEKT-QWNNVENLNRFERPMDYEDLKMGKMFVSD 466

Db 439 TQFKKGGAGGLQPSNGPISRRFDYDESTMQEDGTQRMCPDLYSQMCHQDRSPR----- 491

Qy 467 EHYDENEDDLVSHVDGVSISRREYV 492

Db 492 QHHPNPERL-----YINPREHYV 510

RESULT 7

QJLB7 PRELIMINARY; PRT; 438 AA.

AC QJLB7;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Cell adhesion molecule nectin-3 gamma.

GN PVRL3.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20209403; PubMed=10744716;

RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,

RA Tachibana K., Mizoguchi A., Takai Y.;

RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules

RT that shows homophilic and heterophilic cell-cell adhesion

RT activities.";

RL J. Biol. Chem. 275:10291-10299 (2000).

DR EMBL; AF195835; AAF63687.1; --

DR MGD; MGI:1930171; Pvrl3.

DR GO; GO:0005193; C:cell-cell adherens junction; IDA.

DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0007155; P:cell adhesion; IDA.

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; Ig-like.

DR Pfam; PF00047; ig; 2.

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG LIKE; 3.

SQ SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;

Query Match 60.6%; Score 1582.5; DB 11; Length 438;

Best Local Similarity 75.4%; Pred. No. 2.7e-120;

Matches 309; Conservative 24; Mismatches 34; Indels 43; Gaps 5;

Qy 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 58 GSIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117

Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTR 237

Qy 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLKCNADANP 297

QY	241	PPFKSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD	300	OS	Homo sapiens (Human).		
Db	298	PPFKSVMSRLDQWPDGGLASDNTLHFVHPLTFNYSGVYCKVNSLQSRSDQKVIYISD	357	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
QY	301	PPTTTTLQPTIQWHPSTADIEDLATEPKLPPPLSTLTIKDDTIATIIASVVGALFIV	360	OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
Db	358	IPLTQT-----SSIA-----VAGAVIGAVLALF	380	OX	NCBI_TaxID=9606;		
QY	361	LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQK---ESQIDVLQDEL	406	RN	[1]		
Db	381	IITVFVTLTPRK--RPSYLDKVIDLPHTKPPPVYEERIPSLPQKDL	428	RP	SEQUENCE FROM N.A.		
RESULT 8							
Q8NC05	Q8NC05	PRELIMINARY;	PRT;	267	AA.		
AC	Q8NC05;						
DT	01-OCT-2002	(TrEMBLrel. 22, Created)					
DT	01-OCT-2002	(TrEMBLrel. 22, Last sequence update)					
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)					
DE	Hypothetical protein FLJ90624.						
OS	Homo sapiens (Human).						
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.						
OX	NCBI_TaxID=9606;						
RN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Placenta;						
RA	Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,						
RA	Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,						
RA	Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,						
RA	Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,						
RA	Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;						
RT	"NEDO human cDNA sequencing project.";						
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.						
DR	EMBL; AK075105; BAC11404.1; -						
DR	InterPro; IPR003599; Ig.						
DR	InterPro; IPR007110; Ig-like.						
DR	Pfam; PF00047; ig; 1.						
DR	SMART; SM00409; IG; 1.						
DR	PROSITE; PS50835; IG_LIKE; 2.						
KW	Hypothetical protein.						
SQ	SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;						
Query Match					46.6%; Score 1218; DB 4; Length 267;		
Best Local Similarity					99.6%; Pred. No. 6.4e-91;		
Matches					232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;		
QY	1	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	60	QY	14	GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS	70
Db	35	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY	94	Db	3	GTDVVLHCSFANPLPSVKITQVTWQKATNGSKQNMAIYNPTMGVSVLPPEYKRVFLRPS	62
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120	QY	71	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG---	127
Db	95	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	154	Db	63	FIDGTIRLSHLEDEGMYICEFATFPTGNRESQLNLTVMKPT-NWIEGTQAVLRARKG	121
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR	180	QY	128	-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKLPFTRFARGR	185
Db	155	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR	214	Db	122	QDDKVVVATCTSANGKPPSVSVSWETRLKGEAEYQEIARNPNGTIVLSRYRLVPSREAHQ	181
QY	181	FARRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFVGKGVNLK	233				
Db	215	FARRRITCVVKHPALEKDIRYSFILDIOVAPEVSVTGYDGNWFVGKGVNLK	267				
RESULT 9							
Q8WVU4	Q8WVU4	PRELIMINARY;	PRT;	101	AA.		
ID	Q8WVU4						
AC	Q8WVU4;						
DT	01-MAR-2002	(TrEMBLrel. 20, Created)					
DT	01-MAR-2002	(TrEMBLrel. 20, Last sequence update)					
DT	01-MAR-2002	(TrEMBLrel. 20, Last annotation update)					
DE	Nectin 3.						

Job time : 40.9581 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 59.4215 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-6_COPY_58_549
Perfect score: 2611
Sequence: 1 GPIIIEPHVTAVGKNVSLK.....EDDLVSHVDGVSISRREWYV 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2611	100.0	542	5	AAE23281 Human del
2	2611	100.0	549	5	AAE23283 Human nec
3	2611	100.0	549	5	AAE23282 Mouse nec
4	2611	100.0	549	6	ABJ20222 Human IG
5	2605	99.8	555	4	AAM39143 Human pol
6	2494	95.5	549	4	AAG63982 Amino aci
7	2494	95.5	549	4	AAG63985 Amino aci
8	2494	95.5	549	5	AAE23291 Mouse nec
9	2317.5	88.8	559	4	AAM40929 Human pol
10	1844	70.6	426	5	AAE23289 Human nec
11	1844	70.6	634	5	AAE23287 Human nec
12	1630.5	62.4	504	5	AAE23284 Human del
13	1630.5	62.4	510	5	AAE23285 Mouse nec
14	1630.5	62.4	510	5	AAE23286 Human nec
15	1613	61.8	595	5	AAE23288 Human nec
16	1612.5	61.8	437	5	AAE23299 Human nec
17	1602	61.4	387	5	AAE23290 Human nec
18	1587.5	60.8	510	4	AAG63983 Amino aci
19	1587.5	60.8	510	5	AAE23292 Mouse nec
20	1582.5	60.6	438	4	AAG63984 Amino aci
21	1582.5	60.6	438	5	AAE23293 Mouse nec
22	1355	51.9	258	5	ABB90250 Human pol
23	1218	46.6	267	4	AAM93536 Human pol
24	649.5	24.9	514	6	ABJ20237 Human IG
25	649.5	24.9	517	3	AAY32390 Herpesvir

26	649.5	24.9	517	5	AAE232294	Aae23294 Human nec
27	627	24.0	518	5	ABG77170	Abg77170 Prostate
28	569	21.8	458	5	AAE232295	Aae23295 Human nec
29	524	20.1	510	4	AAB93365	Aab93365 Human pro
30	524	20.1	510	4	AAU00471	Aau00471 Human TAN
31	524	20.1	510	5	ABJ05562	Abj05562 Breast ca
32	524	20.1	510	6	ABJ20232	Abj20232 Human IG
33	524	20.1	510	6	ABR48229	Abr48229 Human bla
34	524	20.1	510	6	ABU56613	Abu56613 Lung canc
35	524	20.1	510	6	ABP97212	Abp97212 Tumour-as
36	524	20.1	510	7	ADB80512	Adb80512 Ovarian c
37	522	20.0	510	5	AAE23300	Aae23300 Human nec
38	522	20.0	510	6	ABJ20231	Abj20231 Human IG
39	517.5	19.8	511	5	AAE23301	Aae23301 Human nec
40	511.5	19.6	497	5	AAE23303	Aae23303 Human nec
41	505	19.3	498	5	AAE23305	Aae23305 Human nec
42	478.5	18.3	580	5	AAE23302	Aae23302 Human nec
43	432	16.5	479	3	AAY32389	Aay32389 Herpesvir
44	432	16.5	479	5	AAE23296	Aae23296 Human nec
45	432	16.5	479	6	ABJ20239	Abj20239 Human IG

ALIGNMENTS

RESULT 1
AAE23281
ID AAE23281 standard; protein; 542 AA.
XX
AC AAE23281;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3alpha protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; chromosome 3; asthma.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
XX
DR N-PSDB; AAD37440.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 76-78; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

QY 1 GPIIPEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
XX
PI
XX
DR 58 GPIIPEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
DR
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
DB 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIISQYKLFPTTR 180
DB 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
DB 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
DB 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSLTIATIKDDTIATIIASVVGALFIV 360
DB 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSLTIATIKDDTIATIIASVVGALFIV 417
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDDELDSYPSVKENKNP 420
DB 418 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDDELDSYPSVKENKNP 477
QY 421 VNNLIRKDYLEEPEKTOQNNVENLNRRFERPMDYYEDLKMGKMFVSDEHYDENEDDLVSHV 480
DB 478 VNNLIRKDYLEEPEKTOQNNVENLNRRFERPMDYYEDLKMGKMFVSDEHYDENEDDLVSHV 537
QY 481 DGSVISRREWYV 492
DB 538 DGSVISRREWYV 549

RESULT 3
AAE23282
ID AAE23282 standard; protein; 549 AA.
XX AAE23282;
XX
XX 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin 3alpha fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
KW chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..7
FT /note= "Mouse nectin-3 protein"
FT Region 8..549
FT /note= "Human nectin-3alpha protein"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
PF
XX 05-OCT-2000; 2000US-0238557P.
XX
XX

(IMMV) IMMUNEX CORP.
Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
WPI; 2002-426103/45.
N-PSDB; AAD37441.
Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
sepsis, stroke.
Claim 1; Page 80-82; 141pp; English.
The invention relates to a substantially purified nectin3alpha, beta,
gamma and nectin-4 polypeptides and their corresponding polynucleotides.
Nectin DNA and protein are useful for treating a disease associated with
cell adhesion activity, adherens junction formation activity, epithelial
or endothelial barrier function activity, endothelial proliferation or
migration activity, viral polypeptide binding activity. The epithelial or
endothelial barrier function disorder which is treated by the above
mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
asthma, allergy, allograft rejection, metastasis of cancer cells,
paracellular transport disorders such as magnesium transport defects in
the kidney or inflammatory bowel disease. Nectin DNA is also useful for
inhibiting angiogenesis in a mammal and treating endothelial migration,
proliferation or angiogenic condition of a tissue or a subject, such as
ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
stroke, restenosis, tumour growth and treating herpesvirus infection.
Nectin is also useful for modulating proliferation or migration of an
endothelial cell, an epithelial cell or a smooth muscle cell (vascular
smooth muscle cell). The present sequence is a fusion protein containing
mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
standardise OS field)
Sequence 549 AA;

Query Match 100.0%; Score 2611; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 3.1e-213;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
DB 58 GPIIPEPHVTAVWGKNSVLSKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
DB 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIISQYKLFPTTR 180
DB 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSPFNETATIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
DB 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300
DB 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSLTIATIKDDTIATIIASVVGALFIV 360
DB 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSLTIATIKDDTIATIIASVVGALFIV 417
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDDELDSYPSVKENKNP 420
DB 418 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDDELDSYPSVKENKNP 477
QY 421 VNNLIRKDYLEEPEKTOQNNVENLNRRFERPMDYYEDLKMGKMFVSDEHYDENEDDLVSHV 480
DB 478 VNNLIRKDYLEEPEKTOQNNVENLNRRFERPMDYYEDLKMGKMFVSDEHYDENEDDLVSHV 537

QY 481 DGSVISRREWYV 492
Db 538 DGSVISRREWYV 549

RESULT 4
ABJ20222
ID ABJ20222 standard; protein; 549 AA.
XX
AC ABJ20222;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human IG gene related protein SEQ ID No 45.

XX
KW Breast cancer; p53 pathway modulating agent; IG; colon cancer;
KW kidney cancer; lung cancer; ovary cancer; human.

XX Homo sapiens.

XX WO200299040-A2.

XX 12-DEC-2002.

XX 03-JUN-2002; 2002WO-US017313.

XX 05-JUN-2001; 2001US-0296076P.

XX 10-OCT-2001; 2001US-0328605P.

XX 22-OCT-2001; 2001US-0338733P.

XX 15-FEB-2002; 2002US-0357253P.

XX 15-FEB-2002; 2002US-0357600P.

XX (EXEL-) EXELIXIS INC.

XX Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;

XX Lioubin MN;

XX WPI; 2003-148660/14.

XX Claim 13; Page 206-209; 248pp; English.

XX The invention relates to a novel method for identifying a candidate p53 pathway modulating agent. The method comprises providing an assay system having a purified IG polypeptide or nucleic acid, or their functionally active fragment or derivative. The method is useful for identifying modulators of the p53 pathway, particularly for identifying agents for treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung cancer or cancer of the ovary) associated with defective p53 function. The identified modulators are useful as targets for novel therapeutics. The method is also useful for diagnosing disorders associated with defective p53 function. The IG proteins or nucleic acids are useful as modifiers of the p53 pathway, and as therapeutic targets for disorders associated with defective p53 function. This sequence represents a human protein relating to the human IG genes used in the assay for identifying modulators of the p53 pathway of the invention

XX Sequence 549 AA;

Query Match 100.0%; Score 2611; DB 6; Length 549;
Best Local Similarity 100.0%; Pred. No. 3.1e-213;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGXSQTAVHHPOYGFVSQGEY 60

Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGXSQTAVHHPOYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTPR 180
Db 178 PDSLIDGGNETVAAICIAATKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTPR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGNLKNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGNLKNADANP 297
QY 241 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQWPDPGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFIV 360
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFIV 417
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPDSVKKENKNP 420
Db 418 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPDSVKKENKNP 477
QY 421 VNNLIRKDYLEEPEKTQWNNVNNRFRPMDYYEDLKMGMKFVSDHYDENEDDLVSHV 480
Db 478 VNNLIRKDYLEEPEKTQWNNVNNRFRPMDYYEDLKMGMKFVSDHYDENEDDLVSHV 537
QY 481 DGSVISRREWYV 492
Db 538 DGSVISRREWYV 549

RESULT 5

AAM39143
ID AAM39143 standard; protein; 555 AA.

XX AAM39143;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 2288.

DE Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;

DR WPI; 2001-442253/47.
DR N-PSDB; AAI58299.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
XX
PS Example 4; SEQ ID NO 2288; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 555 AA;

Query Match 99.8%; Score 2605; DB 4; Length 555;
Best Local Similarity 99.8%; Pred. No. 1e-212;
Matches 491; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
DB 64 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 123
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
DB 124 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 183
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTTR 180
DB 184 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTTR 243
QY 181 FARGRRITCVWKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 240
DB 244 FARGRRITCVWKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 303
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
DB 304 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 363
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIATIIASVVGALFIV 360
DB 364 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIATIIASVVGALFIV 423
QY 361 LVSVLAGIFCYRRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPSVKKENKNP 420
DB 424 LVSVLAGIFCYRRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPSVKKENKNP 483
QY 421 VNNLIRKDYLEPEKTKQNNVNNLNRFRPMDYEDLLKMGKMFVSDHYDENEDDLVSHV 480
DB 484 VNNLIRKDYLEPEKTKQNNVNNLNRFRPMDYEDLLKMGKMFVSDHYDENEDDLVSHV 543
QY 481 DGSVISRREWYV 492
DB 544 DGSVISRREWYV 555

RESULT 6
AAG63982
ID AAG63982 standard; protein; 549 AA.
XX
AC AAG63982;
XX

DT 26-NOV-2001 (first entry)
XX
DE Amino acid sequence of murine nectin-3.
XX
KW Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
XX
OS Mus sf.
XX
PN WO200166736-A1.
XX
PD 13-SEP-2001.
XX
PF 09-MAR-2001; 2001WO-JP001871.
XX
PR 09-MAR-2000; 2000JP-00065595.
XX
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.
XX
XX Takahashi K, Takai Y, Nakanishi H, Sato K;
PI WPI; 2001-570771/64.
XX N-PSDB; AAH78179.
DR
DR
XX
PT New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and
PT corresponding antibodies.
XX
PS Claim 1; Page 37-40; 64pp; Japanese.
XX

The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer

Sequence 549 AA;

Query Match 95.5%; Score 2494; DB 4; Length 549;
Best Local Similarity 94.1%; Pred. No. 2.8e-203;
Matches 463; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
DB 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTAVVHHPQYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
DB 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTTR 180
DB 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVWKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 240
DB 238 FARGRRITCVWKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 300
DB 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIATIIASVVGALFIV 360
DB 358 PPTTTTLOPTIQWHSPADVDQDIATEHKKLPFPLSTLTIKDDTIATIIASVVGALFIV 417
QY 361 LVSVLAGIFCYRRRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPSVKKENKNP 420
DB 418 LVSILAGVFCYRRRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQQDELDSYPSVKKENKNP 477
QY 421 VNNLIRKDYLEPEKTKQNNVNNLNRFRPMDYEDLLKMGKMFVSDHYDENEDDLVSHV 480

Db478VNNLRKDYLEEPEKTQWNNVNLTRFRPMDYYEDLKMGMKFVSDERYNESEDGLVSHV537

QY481DGSVISRREWYV492

Db538DGSVISRREWYV549

RESULT 7

AAG63985

IDAAG63985standard; protein; 549 AA.

XX

ACAAG63985;

XX

DT26-NOV-2001(first entry)

XX

DEAmino acid sequence of murine nectin-3.

XX

KWNectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.

XX

OSMus sp.

XX

PNWO200166736-A1.

XX

PD13-SEP-2001.

XX

PF09-MAR-2001; 2001WO-JP001871.

XX

PR09-MAR-2000; 2000JP-00065595.

XX

PA(NISC-) JAPAN SCI & TECHNOLOGY CORP.

PA(TAKA/) TAKAHASHI K.

XX

PITakahashi K, Takai Y, Nakanishi H, Sato K;

XX

DRWPI; 2001-570771/64.

DRN-PSDB; AAH78182.

XX

PTNew protein family for diagnosing and treating tumor infiltration and

PTmetastasis comprises the mouse nectin-3 protein families and

PTcorresponding antibodies.

XX

PSDisclosure; Page 56-61; 64pp; Japanese.

XX

CCThe present sequence represents a murine nectin-3 polypeptide. Nectin-3

CCis an immunoglobulin-like cell adhesion molecule that shows homophilic

CCand heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and

CCpolynucleotides are useful for investigating the mechanisms of cell

CCadhesion, infiltration and metastasis of cancer cells, the diagnosis of

CCmalignancies of various cancers, and the development of methods for the

CCtreatment and prevention of cancer

XX

SQSequence 549 AA;

Query Match95.5%; Score 2494; DB 4; Length 549;

Best Local Similarity94.1%; Pred. No. 2.8e-203;

Matches 463; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY1GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY60

Db58GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY117

QY61QGRVLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG120

Db118QGRVLFKNYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG177

QY121PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR180

Db178PDSLIDGGNETVAAICVAAATGKPVQAIDWEGDLGEMESSTTSFPNETATISQYKLFPTTR237

QY181FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP240

Db238FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP297

QY241PPFKSVWSRLDQWPDGILLASDNTLHVFHPLTFNYSYVYICKVTNSLGORSQDKVIYISD300

Db298PPFKSVWSRLDQWPDGILLASDNTLHVFHPLTFNYSYVYICKVTNSLGORSQDKVIYISD357

QY301PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLTIKDDTIATIIASVVGALFIV360

Db358PPTTTTLOPTVQWHSPPADVQDIATEHKLPFPLSTLTIKDDTIATIIASVVGALFIV417

QY361LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPDSVKKENKNP420

Db418LVSILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQQDELDSYPDSVKKENKNP477

QY421VNNLRKDYLEEPEKTQWNNVNLNRFRPMDYYEDLKMGMKFVSDHYDENEDDLVSHV480

Db478VNNLRKDYLEEPEKTQWNNVNLTRFRPMDYYEDLKMGMKFVSDERYNESEDGLVSHV537

QY481DGSVISRREWYV492

Db538DGSVISRREWYV549

RESULT 8

AAE23291

IDAAE23291standard; protein; 549 AA.

XX

ACAAE23291;

XX

DT27-AUG-2002(first entry)

XX

DEMouse nectin-3alpha protein.

XX

KWMouse; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;

KWparacellular transport disorder; kidney; diabetic retinopathy; allergy;

KWallograft rejection; metastasis; restenosis; inflammatory bowel disease;

KWcedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

KWstroke; tumour; cancer; herpesvirus infection; asthma.

XX

OSMus musculus.

XX

PNWO200228902-A2.

XX

PD11-APR-2002.

XX

PF05-OCT-2001; 2001WO-US031392.

XX

PR05-OCT-2000; 2000US-0238557P.

XX

PA(IMMV) IMMUNEX CORP.

XX

PIBaum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX

DRWPI; 2002-426103/45.

XX

PTNovel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,

PTuseful for treating or preventing heart failure, malaria,

PTglomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,

PTsepsis, stroke.

XX

PSDisclosure; Page 107-109; 141pp; English.

XX

CCThe invention relates to a substantially purified nectin3alpha, beta,

CCgamma and nectin-4 polypeptides and their corresponding polynucleotides.

CCNectin DNA and protein are useful for treating a disease associated with

CCcell adhesion activity, adherens junction formation activity, epithelial

CCor endothelial barrier function activity, endothelial proliferation or

CCmigration activity, viral polypeptide binding activity. The epithelial or

CCendothelial barrier function disorder which is treated by the above

CCmentioned method is inflammation, sepsis, oedema, diabetic retinopathy,

CCasthma, allergy, allograft rejection, metastasis of cancer cells,

CCparacellular transport disorders such as magnesium transport defects in

CCthe kidney or inflammatory bowel disease. Nectin DNA is also useful for

CCinhibiting angiogenesis in a mammal and treating endothelial migration,

```
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is mouse nectin-3alpha protein
XX
SQ Sequence 549 AA;

Query Match          95.5%; Score 2494; DB 5; Length 549;
Best Local Similarity 94.1%; Pred. No. 2.8e-203;
Matches 463; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GSIVPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAVCVAATGKPVQAIDWEGDLGEMESTTSPFNETATIVSQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
Db 298 PPFSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATIIASVVGALFIV 360
Db 358 PPTTTTLQPTVQWHSSPADVQDIATEHKLPFPLSTLATIKDDTIATIIASVVGALFLV 417
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKENKNP 420
Db 418 LVSILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSPDSVKKENKNP 477
QY 421 VNNLIRKDYLEPEKTOQNNVNNLRFERPMDYEDLKMGMKFVSDRYNESEDGLVSHV 480
Db 478 VNNLIRKDYLEPEKTOQNNVNNLRFERPMDYEDLKMGMKFVSDRYNESEDGLVSHV 537
QY 481 DGSVISRREWYV 492
Db 538 DGSVISRREWYV 549

RESULT 9
AAM40929
ID AAM40929 standard; protein; 559 AA.
XX
AC AAM40929;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5860.
XX
KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
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PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI60085.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 5860; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 559 AA;

Query Match          88.8%; Score 2317.5; DB 4; Length 559;
Best Local Similarity 90.5%; Pred. No. 3.1e-188;
Matches 455; Conservative 4; Mismatches 33; Indels 11; Gaps 8;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 57 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 116
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 117 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 176
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTR 180
Db 177 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTR 236
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 237 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 296
QY 241 PPFSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORS-DQKVIYIS 299
Db 297 PPFSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSPFSKEVTQKVHPTF 356
QY 300 DPPTTTTLQP-----TIQW-HPSTADI-BDLATEPKKL-PFPLSTLATIKDDT-IATIIAS 351
Db 357 QDPSLPTYPPLPALQFQWASPSTAXTSRDLATEPKXIAPSPSLSTLATIKGWTQLPTIIAX 416
QY 352 VVG-GALFIVLSVLA-GIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSDY 409
```


Db 417 CSGVGALFIVLVKCFGLGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDPY 476
QY 410 PDSVKKENKPNVNNLRKDYLEPEKTKQNNVNNLRNFRPMDYYEDLKMGMKFVSDHY 469
Db 477 PDSVKKENKPNVNNLRKDYLEPEKTKQNNVNNLRNFRPMDYYEDLKMGMKFVSDHY 536
QY 470 DENEDDLVSHVDGSGVISRREWYV 492
Db 537 DENEDDLVSHVDGSGVISRREWYV 559

RESULT 10
AAE23289
ID AAE23289 standard; protein; 426 AA.
XX
AC AAE23289;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-FLAGpolyHis fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
FH Key
FT Region 1. .404
FT /note= "Human nectin-3alpha protein"
FT Region 405. .420
FT /note= "FLAG peptide"
FT Region 421. .426
FT /note= "PolyHis tag"

XX
PN WO200228902-A2.
XX
XX 11-APR-2002.
PD
XX
XX 05-OCT-2001; 2001WO-US031392.
PF
XX 05-OCT-2000; 2000US-0238557P.
PR
XX (IMMV) IMMUNEX CORP.
PA
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX

PS Claim 9; Page 104-105; 141pp; English.
XX
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,

CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha-
CC FLAGpolyHis fusion protein

XX
SQ Sequence 426 AA;
Query Match 70.6%; Score 1844; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 4.3e-148;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGSVQGEY 60
Db 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTYDGNWFGVGRKGNLKNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTYDGNWFGVGRKGNLKNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFENYGVYICKVTNSLGORSQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFENYGVYICKVTNSLGORSQKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 404

RESULT 11
AAE23287
ID AAE23287 standard; protein; 634 AA.
XX
AC AAE23287;
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-IgG1Fc region fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
PA
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX WPI; 2002-426103/45.
DR

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 100-102; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 634 AA;

Query Match 70.6%; Score 1844; DB 5; Length 634;
Best Local Similarity 100.0%; Pred. No. 7.7e-148;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
Db 298 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIAT 347
Db 358 PPTTTTLQPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIAT 404

RESULT 12
AAE23284
ID AAE23284 standard; protein; 504 AA.
XX
AC AAE23284;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3beta protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;

KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX Homo sapiens.
XX WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37443.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 89-91; 141pp; English.

CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX
SQ Sequence 504 AA;

Query Match 62.4%; Score 1630.5; DB 5; Length 504;
Best Local Similarity 64.4%; Pred. No. 8.3e-130;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
QY 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 52 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 111
QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 112 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 231
QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 240
Db 232 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP 291
QY 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
Db 292 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 351

QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKLPPLPLTLATIKDDTIATIIASVVGALFIV 360
Db 352 VP-----
QY 361 LVSVLGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQDDELDSYPSVKKENKN 419
Db 375 IIAIFVTVLLTPRKX--RPSYLDKVIDLPPTHK-----PPPLYEERSP 415
QY 420 PV--NNLIRKDYLEEPEKTQW-----NNVENLNR-ERPMDYYEDLKMGMKFVSD----- 466
Db 416 PLPQKDLFQPEHL--PLQTQFKEREVGNLQHSNGLNSRFDYEDENPVGEDGIQOMYPLY 473
QY 467 -----EHYDENEDDLVSHVDGSGVISRREWYV 492
Db 474 NQMCYQDRSPGKHQNDPKRV-----YIDPREHYV 504

RESULT 13
AAE23285
ID AAE23285 standard; protein; 510 AA.
AC AAE23285;
DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX Mouse nectin-3-human nectin-3beta fusion protein.
DE Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..6
FT /note= "Mouse nectin-3 pprotein"
FT Region 7..510
FT /note= "Human nectin-3beta protein"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37444.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 94-95; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above

CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 510 AA;

Query Match 62.4%; Score 1630.5; DB 5; Length 510;
Best Local Similarity 64.4%; Pred. No. 8.4e-130;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLKNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLKNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPT 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPT 237
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQSDQKVIYISD 357
QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKLPPLPLTLATIKDDTIATIIASVVGALFIV 360
Db 358 VP-----FKQTSSIAVAGAVIGAVLALF 380
QY 361 LVSVLGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQDDELDSYPSVKKENKN 419
Db 381 IIAIFVTVLLTPRKX--RPSYLDKVIDLPPTHK-----PPPLYEERSP 421
QY 420 PV--NNLIRKDYLEEPEKTQW-----NNVENLNR-ERPMDYYEDLKMGMKFVSD----- 466
Db 422 PLPQKDLFQPEHL--PLQTQFKEREVGNLQHSNGLNSRFDYEDENPVGEDGIQOMYPLY 479
QY 467 -----EHYDENEDDLVSHVDGSGVISRREWYV 492
Db 480 NQMCYQDRSPGKHQNDPKRV-----YIDPREHYV 510

RESULT 14
AAE23286
ID AAE23286 standard; protein; 510 AA.
XX
AC AAE23286;
XX
DT 27-AUG-2002 (first entry)
XX Human nectin-3beta protein.
DE Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 102-104; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 595 AA;

Query Match		61.8%;	Score 1613;	DB 5;	Length 595;
Best Local Similarity		73.4%;	Pred. No. 3.3e-128;		
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QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120		
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	177		
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTTR	180		
Db	178	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTTR	237		
QY	181	FARGRRITCVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGKGVNLKCNADANP	240		
Db	238	FARGRRITCVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVFGKGVNLKCNADANP	297		
QY	241	PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTENYSVYICKVTNSLGQRSDQKVIYISD	300		
Db	298	PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTENYSVYICKVTNSLGQRSDQKVIYISD	357		
QY	301	PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIA	346		
Db	358	VFPKQTSRRSCDKTHTCPPCPAPEAEGAPSV-----FLFPPK----PKDTLMISRTPEVT	408		
QY	347	TIASVVGALFIVLVSVLAGIFCYRRRRRTFRGDYFAKNYIPPSDMQKESQIDVLOQDEL	406		
Db	409	CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYNSTY-----RVVSVLTVLHQDWL	462		
QY	407	DSYPDSVKKENK---NPVNNLIRK	427		
Db	463	NGKEYCKKVSNNKALPAPIEKTISK	486		

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 41.1182 Seconds
(without alignments)
3146.189 Million cell updates/sec

Title: US-09-972-268-6_COPY_58_549
Perfect score: 2611
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
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8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2611	100.0	542	10	US-09-972-268-2
2	2611	100.0	549	10	US-09-972-268-4
3	2611	100.0	549	10	US-09-972-268-6
4	2611	100.0	549	14	US-10-161-572-45
5	2494	95.5	549	10	US-09-959-845-2
6	2494	95.5	549	10	US-09-972-268-17
7	1844	70.6	426	10	US-09-972-268-15
8	1844	70.6	634	10	US-09-972-268-13
9	1630.5	62.4	504	10	US-09-972-268-8
10	1630.5	62.4	510	10	US-09-972-268-10
11	1630.5	62.4	510	10	US-09-972-268-12
12	1613	61.8	595	10	US-09-972-268-14
13	1612.5	61.8	437	10	US-09-972-268-31
14	1602	61.4	387	10	US-09-972-268-16
15	1587.5	60.8	510	10	US-09-959-845-4

16	1587.5	60.8	510	10	US-09-972-268-18	Sequence 18, Appl
17	1582.5	60.6	438	10	US-09-959-845-6	Sequence 6, Appl
18	1582.5	60.6	438	10	US-09-972-268-19	Sequence 19, Appl
19	1355	51.9	258	15	US-10-264-237-2626	Sequence 2626, Ap
20	649.5	24.9	514	14	US-10-161-572-60	Sequence 60, Appl
21	649.5	24.9	517	10	US-09-972-268-20	Sequence 20, Appl
22	627	24.0	518	9	US-09-919-172-20	Sequence 20, Appl
23	569	21.8	458	10	US-09-972-268-21	Sequence 21, Appl
24	524	20.1	479	10	US-09-766-511B-35	Sequence 35, Appl
25	524	20.1	510	10	US-09-766-511B-33	Sequence 33, Appl
26	524	20.1	510	12	US-10-058-270A-54	Sequence 54, Appl
27	524	20.1	510	14	US-10-161-572-55	Sequence 55, Appl
28	524	20.1	510	14	US-10-241-220-94	Sequence 94, Appl
29	524	20.1	510	15	US-10-295-027-66	Sequence 66, Appl
30	524	20.1	510	15	US-10-173-999-76	Sequence 76, Appl
31	522	20.0	510	10	US-09-972-268-24	Sequence 24, Appl
32	522	20.0	510	14	US-10-161-572-54	Sequence 54, Appl
33	517.5	19.8	511	10	US-09-972-268-34	Sequence 34, Appl
34	511.5	19.6	497	10	US-09-972-268-37	Sequence 37, Appl
35	505	19.3	498	10	US-09-972-268-39	Sequence 39, Appl
36	478.5	18.3	580	10	US-09-972-268-36	Sequence 36, Appl
37	476.5	18.2	314	10	US-09-766-511B-36	Sequence 36, Appl
38	432	16.5	479	10	US-09-972-268-22	Sequence 22, Appl
39	432	16.5	479	14	US-10-161-572-62	Sequence 62, Appl
40	430	16.5	522	15	US-10-264-049-2969	Sequence 2969, Ap
41	418.5	16.0	538	10	US-09-972-268-23	Sequence 23, Appl
42	418.5	16.0	538	10	US-09-984-130-138	Sequence 138, App
43	418.5	16.0	538	10	US-09-836-353A-138	Sequence 138, App
44	418.5	16.0	538	14	US-10-161-572-61	Sequence 61, Appl
45	418.5	16.0	538	15	US-10-411-010-17	Sequence 17, Appl

ALIGNMENTS

RESULT 1
US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match	100.0%	Score 2611;	DB 10;	Length 542;
Best Local Similarity	100.0%	Pred. No. 7.8e-221;		
Matches 492;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVHHPOYGFVSVOGEY	60	
Db	51	GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVHHPOYGFVSVOGEY	110	
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTTTLVEPTVSLIKG	120	
Db	111	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFFPLGNAQSSTTTTLVEPTVSLIKG	170	
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATILISQYKLPFTR	180	


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QY 421 VNNLIRKDYLEEPEKTQWNNVNNLNRFRPMDYEDLKMGMKFVSDHYDENEDDLVSHV 480
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QY 481 DGSVISRREWYV 492
Db 531 DGSVISRREWYV 542

RESULT 2
US-09-972-268-4
; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from
; OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match 100.0%; Score 2611; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 7.9e-221;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPTR 180
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QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 297
QY 297 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANP 350
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Db 418 LVSVLAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQQDELDSYPDSVKKENKNP 477
QY 421 VNNLIRKDYLEEPEKTQWNNVNNLNRFRPMDYEDLKMGMKFVSDHYDENEDDLVSHV 480
Db 478 VNNLIRKDYLEEPEKTQWNNVNNLNRFRPMDYEDLKMGMKFVSDHYDENEDDLVSHV 537
QY 481 DGSVISRREWYV 492
Db 538 DGSVISRREWYV 549

RESULT 3
US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-6

Query Match 100.0%; Score 2611; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 7.9e-221;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 58 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
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RESULT 4
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 100.0%; Score 2611; DB 14; Length 549;
Best Local Similarity 100.0%; Pred. No. 7.9e-221;
Matches 492; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFFVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFFVGRKGVNLCNADANP 297
QY 241 PPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 300
Db 298 PPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 357
QY 301 PPTTTTLOPTIOQHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFIV 360
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QY 361 LVSVLGAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPDSVKKENKNP 420
Db 418 LVSVLGAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPDSVKKENKNP 477

QY 421 VNNLIRKDYLEEPEKTQNNVNNLNRFRPMDYYEDLKMGMKFVSDEHYDENEDDLVSHV 480
Db 478 VNNLIRKDYLEEPEKTQNNVNNLNRFRPMDYYEDLKMGMKFVSDEHYDENEDDLVSHV 537
QY 481 DGSVISRREWYV 492
Db 538 DGSVISRREWYV 549

RESULT 5
US-09-959-845-2
; Sequence 2, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: YOSHIMI TAKAI
; APPLICANT: HIROYUKI NAKANISHI
; APPLICANT: KEIKO SATO
; APPLICANT: KENICHI TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-2

Query Match 95.5%; Score 2494; DB 10; Length 549;
Best Local Similarity 94.1%; Pred. No. 1.6e-210;
Matches 463; Conservative 18; Mismatches 11; Indels 0; Gaps 0;
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Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVLEPTVSLIKG 120
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Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPT 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFFVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFFVGRKGVNLCNADANP 297
QY 241 PPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 300
Db 298 PPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQQRSDQKVIYISD 357
QY 301 PPTTTTLOPTIOQHPSTADIEDLATEPKLPPLSTLATIKDDTIATIIASVVGALFIV 360
Db 358 PPTTTTLOPTIOQHPSSPADVQDIATEHKLPPLSTLATIKDDTIATIIASVVGALFLV 417
QY 361 LVSVLGAGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDELDSYPDSVKKENKNP 420
Db 418 LVSILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLHQDELDSYPDSVKKENKNP 477
QY 421 VNNLIRKDYLEEPEKTQNNVNNLNRFRPMDYYEDLKMGMKFVSDEHYDENEDDLVSHV 480
Db 478 VNNLIRKDYLEEPEKTQNNVNNLNRFRPMDYYEDLKMGMKFVSDEHYDENEDDLVSHV 537
QY 481 DGSVISRREWYV 492

Db 538 DGSVISRREWYV 549

RESULT 6

US-09-972-268-17

; Sequence 17, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 549

; TYPE: PRT

; ORGANISM: mus musculus

US-09-972-268-17

Query Match 95.5%; Score 2494; DB 10; Length 549;

Best Local Similarity 94.1%; Pred. No. 1.6e-210;

Matches 463; Conservative 18; Mismatches 11; Indels 0; Gaps 0;

Qy 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60

Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGDY 117

Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 237

Qy 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANP 240

Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANP 297

Qy 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357

Qy 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIATIIASVVGALFIV 360

Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIATIIASVVGALFLV 417

Qy 361 LVSILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKENKNP 420

Db 418 LVSILAGVFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQDELDSPDSVKKENKNP 477

Qy 421 VNNLRKDYLEPEKTKQNNVNNLNRFRPMDYEDLKMGMKFVSDRYNEDEDGLVSHV 480

Db 478 VNNLRKDYLEPEKTKQNNVNNLNRFRPMDYEDLKMGMKFVSDRYNEDEDGLVSHV 537

Qy 481 DGSVISRREWYV 492

Db 538 DGSVISRREWYV 549

RESULT 7

US-09-972-268-15

; Sequence 15, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 15

; LENGTH: 426

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis

US-09-972-268-15

Query Match 70.6%; Score 1844; DB 10; Length 426;

Best Local Similarity 100.0%; Pred. No. 1.8e-153;

Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60

Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117

Qy 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

Qy 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 237

Qy 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANP 240

Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGNLKNADANP 297

Qy 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357

Qy 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIAT 347

Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPPLSTLTIKDDTIAT 404

RESULT 8

US-09-972-268-13

; Sequence 13, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 13

; LENGTH: 634

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13
Query Match 70.6%; Score 1844; DB 10; Length 634;
Best Local Similarity 100.0%; Pred. No. 3.2e-153;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLFPT 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLFPT 237
QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVIICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVIICKVTNSLGQRSDQKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 404
RESULT 9
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8
Query Match 62.4%; Score 1630.5; DB 10; Length 504;
Best Local Similarity 64.4%; Pred. No. 1.4e-134;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 52 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 111
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLFPT 180
Db 172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLFPT 231
QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240

Db 232 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 291
QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVIICKVTNSLGQRSDQKVIYISD 300
Db 292 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVIICKVTNSLGQRSDQKVIYISD 351
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIATIIASVVGALFIV 360
Db 352 VP-----FKQTSSIAVAGAVIGAVLALF 374
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQQDELDSYDPSVKKENKN 419
Db 375 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP 415
QY 420 PV--NNLIRKDYLEPEKIQW-----NNVENLRF-ERPMDYYEDLKMGKMFVSD----- 466
Db 416 PLPQKDLFQPEHL--PLQTQPKEREVGNLQHSNGLNSRSPDYEDENPVGEDGIQQMYPLY 473
QY 467 -----EYDENEEDLVSHVDGSGVISRREWYV 492
Db 474 NQMCYQDRSPGKHQNNDPKRV-----YIDPREHYV 504
RESULT 10
US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest ar
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10
Query Match 62.4%; Score 1630.5; DB 10; Length 510;
Best Local Similarity 64.4%; Pred. No. 1.4e-134;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLFPT 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFPNETATIIISQYKLFPT 237
QY 181 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSVGVIICKVTNSLGQRSDQKVIYISD 300

Db 298 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRDQKVIYISD 357
QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFFPLSTLATIKDDTIATIIASVVGALFIV 360
Db 358 VP-----FKQTSIAVAGAVIGAVLALF 380
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQOQDELDSYDPSVKKENKN 419
Db 381 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP 421
QY 420 PV--NNLIRKOYLEEPEKTQW-----NNVENLNRF-ERPMDYYEDLKMGMKFVSD-----466
Db 422 PLPQKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVGEDGIGQMPLY 479
QY 467 -----EYDENEDDLVSVDGSGVISRREWYV 492
Db 480 NQMCYQDRSPGKHQNNDPKRV-----YIDPREHYV 510

RESULT 11
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match 62.4%; Score 1630.5; DB 10; Length 510;
Best Local Similarity 64.4%; Pred. No. 1.4e-134;
Matches 333; Conservative 33; Mismatches 62; Indels 89; Gaps 10;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSFVQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSFVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLEPPTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLEPPTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRDQKVIYISD 300
Db 298 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRDQKVIYISD 357
QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFFPLSTLATIKDDTIATIIASVVGALFIV 360
Db 358 VP-----FKQTSIAVAGAVIGAVLALF 380
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQKESQIDVLQOQDELDSYDPSVKKENKN 419

Db 381 IIAIFVTVLLTPRKK--RPSYLDKVIDLPPTHK-----PPPLYEERSP 421
QY 420 PV--NNLIRKOYLEEPEKTQW-----NNVENLNRF-ERPMDYYEDLKMGMKFVSD-----466
Db 422 PLPQKDLFQPEHL--PLQTFKEREVGNLQHSNLSRSDYEDENPVGEDGIGQMPLY 479
QY 467 -----EYDENEDDLVSVDGSGVISRREWYV 492
Db 480 NQMCYQDRSPGKHQNNDPKRV-----YIDPREHYV 510
RESULT 12
US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match 61.8%; Score 1613; DB 10; Length 595;
Best Local Similarity 73.4%; Pred. No. 6.2e-133;
Matches 326; Conservative 16; Mismatches 70; Indels 32; Gaps 5;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSFVQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSFVQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLEPPTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLEPPTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRDQKVIYISD 300
Db 298 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRDQKVIYISD 357
QY 301 PPTTTTLQ-----PTIQWHPSTADIEDLATEPKKLPFFPLSTLATIKDDTIA 346
Db 358 VPFKQTSRSCDKTHTCPPCPAPEAGAPSV-----FLFPPK-----PKDTLMTSRTPEVT 408
QY 347 TTIASVVGALFIVLVSVLGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQOQDEL 406
Db 409 CVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQNSTY-----RVVSVLTVLHQDWL 462
QY 407 DSYDPSVKKENK---NPVNNLIRK 427
Db 463 NGKEYCKKSVSNKALPAPIEKTISK 486

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RESULT 13
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
; US-09-972-268-31

Query Match      61.8%; Score 1612.5; DB 10; Length 437;
Best Local Similarity 76.5%; Pred. No. 4.3e-133;
Matches 315; Conservative 16; Mismatches 32; Indels 49; Gaps 4;

QY      1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
      |||||||
Db      58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
      |||||||

QY      61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
      |||||||
Db      118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
      |||||||

QY      121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
      |||||||
Db      178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
      |||||||

QY      181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 240
      |||||||
Db      238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 297
      |||||||

QY      241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSDQKVIYISD 300
      |||||||
Db      298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSDQKVIYISD 357
      |||||||

QY      301 PPTTTTQTIQWHPSTADIEDLATEPKLFPPLSTLTIKDDTIATIKDIDPPLQ 402
      |||
Db      358 VP-----FKQTSSIAVACAVIGAVLALF 380

QY      361 LVSVLAGIFCYRRRTFRGDYFAK-----NYIPPSDMQKES-----QIDVLQ 402
      :::::
Db      381 IIAIFVTVLLTPRKX--RPSYLDKVIDLPPTHKPPPLYEERSPPPLPQKDLFQ 430

RESULT 14
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
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; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
; US-09-972-268-16

Query Match      61.4%; Score 1602; DB 10; Length 387;
Best Local Similarity 98.7%; Pred. No. 3e-132;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
      |||||||
Db      58 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
      |||||||

QY      61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
      |||||||
Db      118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
      |||||||

QY      121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
      |||||||
Db      178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237
      |||||||

QY      181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 240
      |||||||
Db      238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 297
      |||||||

QY      241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSDQKVIYISD 300
      |||||||
Db      298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSDQKVIYISD 357
      |||||||

QY      301 PPTTTT 306
      |||
Db      358 VPFKQT 363

RESULT 15
US-09-959-845-4
; Sequence 4, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Mouse
; US-09-959-845-4

Query Match      60.8%; Score 1587.5; DB 10; Length 510;
Best Local Similarity 64.6%; Pred. No. 8.7e-131;
Matches 327; Conservative 38; Mismatches 74; Indels 67; Gaps 10;

QY      1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
      |||||||
Db      58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDY 117
      |||||||
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QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISOYKLFPTTR 180
Db 178 PDSLIDGGNETVAAAVCAATGKPVAQIDWEGDLGEMESSTTSFPNETATIVSOYKLFPTTR 237
QY 181 FARRRITCVVKHPALEKDIRYSFILDIQVAPESVGTGYDGNWFVGRKGVNLKCNADANP 240
Db 238 FARRRITCVVKHPALEKDIRYSFILDIQVAPESVGTGYDGNWFVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFENYSGVYICKVTNSLQORSDDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFVNYSGVYCKVNSLSLQORSDDQKVIYISD 357
QY 301 PPTTTTLQPTTIQWHPSTADIEDLATEPKLPPPLSTLATIKDDTIATIIASVVGALFIV 360
Db 358 IPLTQT-----SSIA-----VAGAVIGAVLALF 380
QY 361 LVSVLAGIFCYRRRTFRGDYFAKNY-IPPSDMQK---ESQIDVLQQDEL---DSYPDS 412
Db 381 IITVFVTVLLTPRKK--RPSYLDKVIDLPPTHKPPPPVVEERIPSLPQKDLLGQTEHPLQ 438
QY 413 VKKENK-----NPVNNLIRKDYLEEPEKT-QWNNVENLNRFERPMDYIEDLKMGMKFVSD 466
Db 439 TQFKEKGAGGLQPSNGPISRRFDYEDESTMQEDGTQRMCPLYSQMCHQDRSPR----- 491
QY 467 EHYDENEDDLVSHVDGVSISRREWYV 492
Db 492 QHHPRNPERL-----YINPREHYV 510

Search completed: April 12, 2004, 10:25:25
Job time : 42.1182 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 16.241 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-6_COPY_58_549
Perfect score: 2611
Sequence: 1 GPIIPEPHVTAVGKNVSLK.....EDDLVSHVDGVSISRREWYV 492

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649.5	24.9	517	4	US-09-723-368-4
2	627	24.0	518	4	US-09-919-172-20
3	566	21.7	458	4	US-09-435-956A-1
4	432	16.5	479	4	US-09-723-368-2
5	380.5	14.6	408	4	US-09-724-864-62
6	314	12.0	423	4	US-09-778-510-22
7	312	11.9	440	4	US-09-866-028-61
8	312	11.9	442	4	US-09-778-510-20
9	312	11.9	442	4	US-09-930-803-1
10	255.5	9.8	421	2	US-08-659-984A-1
11	255.5	9.8	421	3	US-08-660-531-1
12	255.5	9.8	444	2	US-08-659-984A-5
13	255.5	9.8	444	3	US-08-660-531-5
14	242	9.3	398	4	US-09-778-510-4
15	233	8.9	398	4	US-09-778-510-6
16	233	8.9	398	4	US-09-907-794A-84
17	233	8.9	398	4	US-09-905-125A-84
18	233	8.9	398	4	US-09-902-775A-84
19	233	8.9	432	4	US-09-778-510-2
20	190.5	7.3	227	4	US-09-205-258-947
21	187.5	7.2	274	4	US-09-570-367C-19
22	187.5	7.2	274	4	US-09-915-524-19
23	164	6.3	477	2	US-08-432-016-3
24	164	6.3	477	2	US-08-684-594-3
25	162.5	6.2	278	4	US-09-570-367C-2
26	162.5	6.2	278	4	US-09-915-524-2
27	162	6.2	1059	4	US-09-907-794A-290

28	162	6.2	1059	4	US-09-905-125A-290	Sequence 290, App
29	162	6.2	1059	4	US-09-902-775A-290	Sequence 290, App
30	162	6.2	1119	4	US-09-907-794A-294	Sequence 294, App
31	162	6.2	1119	4	US-09-905-125A-294	Sequence 294, App
32	162	6.2	1119	4	US-09-902-775A-294	Sequence 294, App
33	159.5	6.1	278	4	US-09-570-367C-21	Sequence 21, Appl
34	159.5	6.1	278	4	US-09-915-524-21	Sequence 21, Appl
35	159.5	6.1	1101	3	US-08-986-485-2	Sequence 2, Appli
36	158	6.1	642	1	US-08-217-299-1	Sequence 1, Appli
37	158	6.1	698	2	US-08-602-725-36	Sequence 36, Appl
38	158	6.1	734	2	US-08-389-459A-17	Sequence 17, Appl
39	158	6.1	734	3	US-08-987-867A-17	Sequence 17, Appl
40	154.5	5.9	1018	1	US-08-408-093-6	Sequence 6, Appli
41	154.5	5.9	1018	1	US-08-408-420A-6	Sequence 6, Appli
42	154.5	5.9	1018	1	US-08-714-901-6	Sequence 6, Appli
43	154.5	5.9	1018	3	US-08-040-741-6	Sequence 6, Appli
44	154	5.9	1268	4	US-08-506-296B-28	Sequence 28, Appl
45	151	5.8	467	3	US-09-046-736-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match	24.9%;	Score	649.5;	DB 4;	Length	517;
Best Local Similarity	31.9%;	Pred. No.	2.6e-52;			
Matches	167;	Conservative	80;	Mismatches	182;	Indels 95; Gaps 17;
QY	14	GKNVSLKCLIE---	VNETITQISWEKIHGKSSQTAVVHHPOYGFVSQGEYQGRVLFKNYS	70		
Db	44	GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS	103			
QY	71	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLDG---	127			
Db	104	FTDGTIRLSRLELEDEGVYICEFATFPTTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG	162			
QY	128	-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTTFFNETATIIISQYKLFPTREARGR	185			
Db	163	QDDKVLVATCTSANGKPPSVVSWETRLKGEAEYQEIENPNTGTVTVISRYRLVPSREAHQQ	222			
QY	186	RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPFKS	245			

Db 223 SLACIVNYHM--DRFKESLTNLVQYEPVETIEGDFGNWYLQRMVVKLTCKADANPPATEY 280
QY 246 VWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTT 305
Db 281 HWTTLNGLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYT- 339
QY 306 TLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTTIATIIASVVGALFIVLVSVL 365
Db 340 ---PSPPEHGRRAG-----PVP-----TAIIGGVAGSILLVLI-VV 371
QY 366 AGIF--CYRRRTFRGDYFAKNYI-----PPSDMQKESQIDVLQOQDELDSY 409
Db 372 GGIIVVALRRRHTFKGDYSTKKHVGNGYSKAGIPQHHP--MAQNLQ-----Y 418
QY 410 PDSVKKENK-NPVNNLIRKDYLEEPEKTQWNN-----VENLNRFE 448
Db 419 PDDSDDEKAGPLGG---SSYEEEEEEEGGGERKVGPHPKYDEDAKRPYFTVDEAE 475
QY 449 RPYMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVISRREWYV 492
Db 476 ARQDGYGDRTLGYQY--DPEQLDLAENMVSNQDGSFISKKEWYV 517

RESULT 2

US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20

Query Match 24.0%; Score 627; DB 4; Length 518;
Best Local Similarity 30.8%; Pred. No. 3.4e-50;
Matches 164; Conservative 80; Mismatches 177; Indels 112; Gaps 18;
QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTAVVHHPQYGFSGVQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLELEDEGVYICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWE-----GDLCGEMESTTTSPNETATIISQYKL 176
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGARVPGDSGT-----PMAPTVVISRYRL 214
QY 177 FPRFARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGKGVNLCNA 236
Db 215 VPSREAHQOSLACIVNYHM--DRFKESLTNLVQYEPVETIEGDFGNWYLQRMVVKLTCKA 272
QY 237 DANPPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVI 296
Db 273 DANPPATEYHWTTLNGLSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332
QY 297 YTSDBPTTTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTTIATIIASVVGGA 356

Db 333 NITEFPYT---PSPPEHGRRAG-----PVP-----TAIIGGVAGS 364
QY 357 LFIVLVSVLAGIF--CYRRRTFRGDYFAKNYI-----PPSDMQKESQIDV 400
Db 365 ILLVLI-VVGGIVVALRRRHTFKGDYSTKKHVGNGYSKAGIPQHHP--MAQNLQ--- 418
QY 401 LQOQDELDSYPDSVKKENK-NPVNNLIRKDYLEEPEKTQWNN----- 440
Db 419 -----YPDDSDDEKAGPLGG---SSYEEEEEEEGGGERKVGPHPKYDEDAKR 467
QY 441 -VENLNRFERPMDYYEDLKMGMKFVSDHYDENEDDLVSHVDGSGVISRREWYV 492
Db 468 PYFTVDEAEARQDGYGDRTLGYQY--DPEQLDLAENMVSNQDGSFISKKEWYV 518
RESULT 3
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: HIGR and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 21.7%; Score 566; DB 4; Length 458;
Best Local Similarity 31.3%; Pred. No. 1.5e-44;
Matches 141; Conservative 75; Mismatches 169; Indels 66; Gaps 12;
QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTAVVHHPQYGFSGVQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDG--- 127
Db 104 FTDGTIRLSRLELEDEGVYICGFAFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSPNETATIISQYKLPTRFARGR 185
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGAEYQEIARNPNTVTVISRYRLVPSREAHQO 222
QY 186 RITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGKGVNLCNADANPPPFKS 245
Db 223 SLACIVNYHM--DRFKESLTNLVQYEPVETIEGDFGNWYLQRMVVKLTCKADANPPATEY 280
QY 246 VWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTT 305
Db 281 HWTTLNGLSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEKPR-- 338
QY 306 TLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTTIATIIASVVGALFIVLVSVL 365
Db 339 -----PQRLG-----SAARLLAGTV--AVFLILVAVL 364
QY 366 AGIFCYRRRTFRGDYFAKNYIPPSDMQKESQIDVLQODE-LDSYDPSVKKENKPNPVNNL 424

Db 365 TVFFLYNRQK-----SPP-----ETDGAGTDQPLSQKPEPSRQSSLVPED 407

QY 425 IRKDYLEEPEKTQWNVNENLNRFRPMDYYE 455

Db 408 IQVVHL-DPGRQQQBEEDLQKLSLQPPYYD 437

RESULT 4

US-09-723-368-2

; Sequence 2, Application US/09723368

; Patent No. 6641818

; GENERAL INFORMATION:

; APPLICANT: NORTHWESTERN UNIVERSITY

; APPLICANT: SPEAR, Patricia G.

; APPLICANT: WARNER, Morgyn S.

; APPLICANT: GERAGHTY, Robert G.

; APPLICANT: MARTINEZ, Wanda M.

; APPLICANT: MONTGOMERY, Rebecca I.

; APPLICANT: COHEN, Gary H.

; APPLICANT: EISENBERG, Roselyn J.

; APPLICANT: WHITBECK, Charles J.

; APPLICANT: KRUMENACHER, Claude

; APPLICANT: UNIVERSITY OF PENNSYLVANIA

; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY

; FILE REFERENCE: 200290.0050/2U1

; CURRENT APPLICATION NUMBER: US/09/723,368

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. 60/087,862

; PRIOR FILING DATE: 1998-06-03

; PRIOR APPLICATION NUMBER: PCT/US99/12235

; PRIOR FILING DATE: 1999-06-02

; NUMBER OF SEQ ID NOS: 26

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 479

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-723-368-2

Query Match 16.5%; Score 432; DB 4; Length 479;

Best Local Similarity 24.7%; Pred. No. 6.7e-32;

Matches 135; Conservative 74; Mismatches 175; Indels 162; Gaps 18;

QY 5 VEPHVTAVWGNVSKLCI---EVNETITQISWEKIHGKSS-QTVAVHHPOYGFVSQGEY 60

Db 38 VLPEVRGQLGGTVLPCLLPVPGLYISLVTWQRDPANHQNVAAFHFKMGPSFSPK 97

QY 61 QG--RVLF-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVVAHI-----DWEGDLGE 155

Db 98 PGSERLSFVSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFATFPKGSVRGWTWLR 157

QY 109 VLVEP-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVVAHI-----DWEGDLGE 155

Db 158 VIAKPKNAEAKVTFSQDP-----TTVALCISKEGRPPARISWLSLSDWEAKETQ 208

QY 156 MESTTTSFPNETATIIISQKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPEVS 215

Db 209 VSGTLAG----TVTVTSRFTLVPSGRADGVTVTCCKVEHESFEFPALIPVTLSVRYPPEVS 264

QY 216 VTGYDGNWFVGRKGNLKNADANPPPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNY 275

Db 265 ISGYDDNWYLGRTDATALSCDVRNPEPTGYDWMSTTSGTFTPSAQAQGSQ-L-VIHAVDSLF 323

QY 276 SGVYICKVTNSLQGRSDQKVIYISDPPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLS 335

Db 324 NTTFCVCTVNAVGMGRAEQVIFVRETPR-----

QY 336 TLATIKDDTTIATIIASVVGGLFVILVSVLAG-----IFCYHRRRTF----- 377

Db 352 --ASPRD--VGPLVWGAVGGLLVLL--LLAGGSLAFILLRVRRRRKSPGGAGGASGDG 405

QY 378 -----RGDYFAKNIYIPPSDMQKESQIDVLQDELDSYPPSVKKNKPNVNNLIR 426

Db 406 GFYDPKAQVLGNQDPPVFWTPVPVPGPME-----PDG----- 435

QY 427 KDYLEEPEKTQWNVNENLNRFRPMDYYEDLKMGKMKFVSDHYDENEDDLVSHVDGVSIS 486

Db 436 KDEEEEE-----EKAKKGLMLPPPPAL---EDDMESQLDGSLSIS 473

QY 487 RREWYV 492

Db 474 RRAVYV 479

RESULT 5

US-09-724-864-62

; Sequence 62, Application US/09724864

; Patent No. 6380362

; GENERAL INFORMATION:

; APPLICANT: Watson, James D

; APPLICANT: Murison, James G.

; TITLE OF INVENTION: Polynucleotides, polypeptides expressed

; TITLE OF INVENTION: by the polynucleotides and methods for their use.

; FILE REFERENCE: 11000.1050U1

; CURRENT APPLICATION NUMBER: US/09/724,864

; CURRENT FILING DATE: 2000-11-28

; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678

; PRIOR FILING DATE: 1999-12-23

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 62

; LENGTH: 408

; TYPE: PRT

; ORGANISM: Mouse

US-09-724-864-62

Query Match 14.6%; Score 380.5; DB 4; Length 408;

Best Local Similarity 27.6%; Pred. No. 3.6e-27;

Matches 119; Conservative 68; Mismatches 171; Indels 73; Gaps 15;

QY 3 IIVEPHVTAVWGNVSKLCIEVNE--TITQISW-EKIHGKSSQTVAVHHPOYGFVSQGE 59

Db 32 VLVPYNSTGVLGSGTTLHCSLTSNENVTITQITWMKKDSGGSHALVAVFHPKKGPNIKEP 91

QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVLEP--TVSL 117

Db 92 ERVKFLAAQQDLRNASLAISNLSVEDEGIYECQIATPPGRSRTNWLKVQARPKNTABE 151

QY 118 IKGPDSLI--DGCNETVAAICIAATGKPVVAHIDW----EGDLGEMESTTTSFPNETATII 171

Db 152 LEPSPTLILQD-----VAKCISANGHPPPGRISWPSNVNGSHREMKE-PGSQPG-TTIVT 203

QY 172 SQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWFVGRKGV 230

Db 204 SYLSMVPSRQADGKNITCTVEHESLQELDQLLVTLTSQYPPENVISIGYDGNWYVGLTNL 263

QY 231 NLKCNADANPPPKS--VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 288

Db 264 TLTCEAHSKPAPDMAGYNWSTNTGDFPNSVKROQNMMLLISTVEDGLNNTVIVCEVTNALG 323

QY 289 QRSQDKVIYISDPPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIATI 348

Db 324 SGQGVHIIIVKEP--ENMQQTRLHL----- 348

QY 349 IASVVGGLFIV-----LVSVLAGIFCYRRRRRTFRGDYFAKNIYIPPSDMQKESQIDVLQ 403

Db 349 -----GYIFLIVFLAVVIIIAALYTIRRCR--HGRALQSN---PSERENVOYSSVNGD 397

QY 404 DELDSYPPDSVK 414

Db 398 CRLNMEPNSTR 408

RESULT 6

US-09-778-510-22

; Sequence 22, Application US/09778510

Db 52 VTVEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YFRDPRPLKDSRFQLLN 101

QY 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIK-GPDSLIDG 127

Db 102 FSSSELKVSLSNVSISDEGRYFCQLYTDP--POESYTTITVLVPPRNLMDIQDITAVEG 159

QY 128 GNETVAAICIAATGKPVAHIDW-EGDL-----GEMESTTTSFPNETATIISQYKLFPTRF 181

Db 160 --EEIEVNCTAMASKPATIRFWKGNTELKKGSEVEEWSDMY-----TVTSQMLMKVHKE 212

QY 182 ARGRRITCVVKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWFWVGRKG--VNLKCNADAN 239

Db 213 DDGVPVICQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTREGDALELTCEAIGK 272

QY 240 PPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVVICKVTNSLQGRSDQKVYIS 299

Db 273 PQPVMVTWVRVDDMPQHAVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLVY 331

QY 300 DPPTTTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATI-----KDDTIATIASV 352

Db 332 DPP--TTIPP-----PTTTTTTTTTT-----TTILTITDSRAGEEGSIRAVDHA 376

QY 353 VGGALFIVLVSLAGIFCYRRRRRTFRGDYFAKN 385

Db 377 IGGVVAVVVFAMLCCLI-----ILGRYFARH 402

RESULT 9

US-09-930-803-1

; Sequence 1, Application US/09930803

; Patent No. 6596493

; GENERAL INFORMATION:

; APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

; APPLICANT: REEVES, Roger

; APPLICANT: YOSHINORI, Muramaki

; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF TUMOR-SUPPRESSOR ASSOCIATED DISORDERS

; FILE REFERENCE: JHUI770-1

; CURRENT APPLICATION NUMBER: US/09/930,803

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 1

; LENGTH: 442

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-930-803-1

Query Match 11.9%; Score 312; DB 4; Length 442;

Best Local Similarity 25.4%; Pred. No. 1.2e-20;

Matches 100; Conservative 79; Mismatches 156; Indels 58; Gaps 16;

QY 9 VTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKN 68

Db 52 VTVEGEVATISC--QVNKSDSVI--QLLNPNRQTI-----YFRDPRPLKDSRFQLLN 101

QY 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIK-GPDSLIDG 127

Db 102 FSSSELKVSLSNVSISDEGRYFCQLYTDP--POESYTTITVLVPPRNLMDIQDITAVEG 159

QY 128 GNETVAAICIAATGKPVAHIDW-EGDL-----GEMESTTTSFPNETATIISQYKLFPTRF 181

Db 160 --EEIEVNCTAMASKPATIRFWKGNTELKKGSEVEEWSDMY-----TVTSQMLMKVHKE 212

QY 182 ARGRRITCVVKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWFWVGRKG--VNLKCNADAN 239

Db 213 DDGVPVICQVEHPAVTGNLQRYLEVQYKQVHIQMTYPLQGLTREGDALELTCEAIGK 272

QY 240 PPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSVVICKVTNSLQGRSDQKVYIS 299

Db 273 PQPVMVTWVRVDDMPQHAVLSGPNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLVY 331

QY 300 DPPTTTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATI-----KDDTIATIASV 352

Db 332 DPP--TTIPP-----PTTTTTTTTTT-----TTILTITDSRAGEEGSIRAVDHA 376

QY 353 VGGALFIVLVSLAGIFCYRRRRRTFRGDYFAKN 385

Db 377 IGGVVAVVVFAMLCCLI-----ILGRYFARH 402

RESULT 10

US-08-659-984A-1

; Sequence 1, Application US/08659984A

; Patent No. 5942400

; GENERAL INFORMATION:

; APPLICANT: Anderson, John P.

; APPLICANT: Sinha, Sukanto

; APPLICANT: Jacobson-Croak, Kirsten L.

; TITLE OF INVENTION: Assays for Detecting Beta-Secretase

; TITLE OF INVENTION: Inhibition

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Townsend and Townsend and Crew LLP

; STREET: Two Embarcadero Ctr., 8th Floor

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111-3834

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/659,984A

; FILING DATE: 07-JUN-1996

; CLASSIFICATION: 436

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/485,152

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Heslin, James M.

; REGISTRATION NUMBER: 29,541

; REFERENCE/DOCKET NUMBER: 15270-002810US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-326-2400

; TELEFAX: 415-326-2422

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 421 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-659-984A-1

Query Match 9.8%; Score 255.5; DB 2; Length 421;

Best Local Similarity 23.4%; Pred. No. 2.2e-15;

Matches 94; Conservative 82; Mismatches 175; Indels 51; Gaps 19;

QY 1 GPIIIEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60

Db 10 GQFPLTQNTVTVVEGGTAILTCRVQNDN-TSLQWS---NPAQQTL-----YFDDKKALR 59

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVE-PTVSLIK 119

Db 60 DNRIELVRASWHELISISVDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFS 119

QY 120 GPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATIISQYK 175

Db 120 SP--VMEG--DLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSSTD 175

QY 176 LFPTRFARGRRITCVVKHPALEKDIRYSP-ILDIQYAPEVSVT-----GYDGNWFWVGRKG 229

Db 176 FRVDRSDDGVAVICRVDSHESLNATPQVAMQVLEIHYPSTPSVKIIPSTPFPQEQPLI----- 231

QY 230 VNLKCNADANPPPKSVWSRLDGW--PDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSL 287
Db 232 --LTCESKGPPLPEPVLWTKDGGELPDPRMVSRELNLIF-LNKTDNGTYRCEATNTI 288
QY 288 GQRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKD-D 343
Db 289 GQSSAEYVLIVHDPNTLLPTTIIPSLTATVTTVA-ITTSPT-----TSATTSSIRDPN 343
QY 344 TIA-----TIIASVVGALFIVLVSV-LAGIFCYRRRRTF 377
Db 344 ALAGONGPDHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTY 385

RESULT 11
US-08-660-531-1
; Sequence 1, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-660-531-1

Query Match 9.8%; Score 255.5; DB 3; Length 421;
Best Local Similarity 23.4%; Pred. No. 2.2e-15;
Matches 94; Conservative 82; Mismatches 175; Indels 51; Gaps 19;
QY 1 GPIIIVPHVTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEY 60
Db 10 GQFPLTQNVTVVEGGTALTTCRVQDNDN-TSLQWS---NPAQQTLL-----YFDDKKALR 59
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVE-PTVSLIK 119
Db 60 DNRIELVRASWHELISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFS 119
QY 120 GPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTSPFN-ETATIIISQYK 175

Db 120 SP--VMEG--DLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLD 175
QY 176 LFFTRFARGRRITCVVXHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWFVGRKG 229
Db 176 FRVDRSDDGVAVICRVDSHESLNATPQVAMQVLEIHVTPSVKIIIPSTFPFQEGQPLI----- 231
QY 230 VNLKCNADANPPPKSVWSRLDGW--PDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSL 287
Db 232 --LTCESKGPPLPEPVLWTKDGGELPDPRMVSRELNLIF-LNKTDNGTYRCEATNTI 288
QY 288 GQRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKD-D 343
Db 289 GQSSAEYVLIVHDPNTLLPTTIIPSLTATVTTVA-ITTSPT-----TSATTSSIRDPN 343
QY 344 TIA-----TIIASVVGALFIVLVSV-LAGIFCYRRRRTF 377
Db 344 ALAGONGPDHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTY 385

RESULT 12
US-08-659-984A-5
; Sequence 5, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 9.8%; Score 255.5; DB 2; Length 444;
Best Local Similarity 23.4%; Pred. No. 2.4e-15;
Matches 94; Conservative 82; Mismatches 175; Indels 51; Gaps 19;
QY 1 GPIIIVPHVTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEY 60
Db 33 GQFPLTQNVTVVEGGTALTTCRVQDNDN-TSLQWS---NPAQQTLL-----YFDDKKALR 82

QY 61 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVE-PTVSLIK 119
Db 83 DNRIELVRASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFS 142
QY 120 GPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATIIISQYK 175
Db 143 SP--VMEG--DLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLD 198
QY 176 LFPTRFARRRITCVVVKHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWVFGVRKG 229
Db 199 FRVDRSDDGVAVICRVDSHESLNATPQVAMQVLEIHYTPSVKIIIPSTPPQEGQPLI---- 254
QY 230 VNLKCNADANPPPKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFENYSGVYICKVTNSL 287
Db 255 --LTCESKGKPLPEPVLWTKDGGELPDPPDRMVVSGRELNILF-LNKTDNGTYRCEATNTI 311
QY 288 QGRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKLPPFLSTLTIKD-D 343
Db 312 QSSAEYVLIHVDVNTLLPTTIIPSLTTATVTTVA-ITTSPT----TSATTSSIRDPN 366
QY 344 TIA-----TIIASVVGALFIVLSV-LAGIFCYRRRRTF 377
Db 367 ALAQONGPDHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTY 408

RESULT 13
US-08-660-531-5
; Sequence 5, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chryslar, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-660-531-5

Query Match 9.8%; Score 255.5; DB 3; Length 444;

Best Local Similarity 23.4%; Pred. No. 2.4e-15;
Matches 94; Conservative 82; Mismatches 175; Indels 51; Gaps 19;
QY 1 GPIIIEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 33 GQFPLTQNVTVVEGGTALLTCRVQNDN-TSLQWS---NPAQQL-----YFDDKKALR 82
QY 61 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVE-PTVSLIK 119
Db 83 DNRIELVRASWHELISISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFS 142
QY 120 GPDSLIDGGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATIIISQYK 175
Db 143 SP--VMEG--DLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLD 198
QY 176 LFPTRFARRRITCVVVKHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWVFGVRKG 229
Db 199 FRVDRSDDGVAVICRVDSHESLNATPQVAMQVLEIHYTPSVKIIIPSTPPQEGQPLI---- 254
QY 230 VNLKCNADANPPPKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFENYSGVYICKVTNSL 287
Db 255 --LTCESKGKPLPEPVLWTKDGGELPDPPDRMVVSGRELNILF-LNKTDNGTYRCEATNTI 311
QY 288 QGRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKLPPFLSTLTIKD-D 343
Db 312 QSSAEYVLIHVDVNTLLPTTIIPSLTTATVTTVA-ITTSPT----TSATTSSIRDPN 366
QY 344 TIA-----TIIASVVGALFIVLSV-LAGIFCYRRRRTF 377
Db 367 ALAQONGPDHALIGGIVAVVVFVTLCSIFLLGRYLARHKGTY 408

RESULT 14
US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-4

Query Match 9.3%; Score 242; DB 4; Length 398;
Best Local Similarity 24.3%; Pred. No. 3.7e-14;
Matches 91; Conservative 62; Mismatches 165; Indels 56; Gaps 14;
QY 10 TAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNY 69
Db 39 TVVAGGTVVLKQVKDHD-SLQWS---NPAQQL-----YFGEKRALRDNRIQLVSS 88
QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDGN 129
Db 89 TPHELISISINVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145
QY 130 ETVAACIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTFRAGR 185
Db 146 ETATLNCQSSGSKPAAQLTWKGDQELHGDQTRIQEDENCKTFTVSSVSFQVTTREDDGA 205
QY 186 RITCVVVKHPALE-KOIRYSFILDIIQYAPEVSVTGYDGNWVFGVRKGVLKCNADANPPPK 244
Db 206 NIVCSVNHESLKGADRSTQRIEVLTYPTAMIRPEPAHPREGQK-LLLHCEGRGNFVPOQ 264

Query Match

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 7.72649 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-10_COPY_74_365
Perfect score: 1546
Sequence: 1 VSLKCLIEVNETITQISWEK.....QRSQKVIYISDVPFKQTSS 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: Pirl1:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1149	74.3	407	2 T08732	hypothetical prote
2	517.5	33.5	518	2 JC4024	poliovirus recepto
3	409	26.5	467	1 HLMSP3	poliovirus recepto
4	403	26.1	530	2 A53437	poliovirus recepto
5	392	25.4	478	2 I53960	PRR2 alpha - human
6	392	25.4	538	2 I68093	PRR2 delta - human
7	383.5	24.8	392	2 B44194	poliovirus recepto
8	383.5	24.8	417	2 A44194	poliovirus recepto
9	371.5	24.0	392	1 RWHUPD	poliovirus recepto
10	371.5	24.0	417	1 RWHUPA	poliovirus recepto
11	309.5	20.0	416	2 A54017	colon carcinoma-as
12	206.5	13.4	764	2 A49448	irregular chiasm C
13	187.5	12.1	274	2 A47639	OX-2 membrane glyc
14	184.5	11.9	5175	2 T20992	hypothetical prote
15	184.5	11.9	5198	2 T43290	hemacentin precurs
16	169.5	11.0	4391	2 A38096	perlecan precursor
17	167	10.8	637	2 B33785	myelin-associated
18	166	10.7	626	1 A61084	myelin-associated
19	165	10.7	582	1 BNRT3S	myelin-associated
20	165	10.7	626	1 BNRT3	myelin-associated
21	164.5	10.6	853	1 IJBONC	neural cell adhesi
22	161	10.4	765	2 C42632	cell adhesion mole
23	161	10.4	812	2 B42632	cell adhesion mole
24	161	10.4	932	2 A42632	cell adhesion mole
25	160	10.3	858	1 IJRTNC	neural cell adhesi
26	158.5	10.3	278	1 TDRTOX	OX-2 membrane glyc
27	157	10.2	1091	1 IJCHNL	neural cell adhesi
28	153.5	9.9	702	2 A36319	carcinoembryonic a
29	153.5	9.9	7962	2 I38346	elastic titin - hu

30	152	9.8	739	2 JN0581	vascular cell adhe
31	152	9.8	761	1 ICHUNG	neural cell adhesi
32	149.5	9.7	725	1 IJMSNG	neural cell adhesi
33	149.5	9.7	1115	1 IJMSNL	neural cell adhesi
34	148	9.6	1896	2 T08851	Down syndrome cell
35	147.5	9.5	725	2 JE0099	neural cell adhesi
36	147.5	9.5	1088	1 IJXLNL	neural cell adhesi
37	147	9.5	588	2 JH0506	adhesion molecule
38	147	9.5	588	2 A45254	surface glycoprote
39	146	9.4	847	2 JH0371	B-cell adhesion pr
40	145.5	9.4	725	2 JE0100	neural cell adhesi
41	143.5	9.3	1092	1 JN0635	neural cell adhesi
42	143	9.2	1651	2 T14160	transmembrane rece
43	142	9.2	1612	2 T30805	dutt1 protein - mo
44	141	9.1	646	2 I38049	cell surface glyco
45	140	9.1	647	2 B41288	vascular cell adhe

ALIGNMENTS

RESULT 1
T08732
hypothetical protein DKFZp566B0846.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999
C;Accession: T08732
R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A;Reference number: Z16474
A;Accession: T08732
A;Molecule type: mRNA
A;Residues: 1-407 <OTT>
A;Cross-references: EMBL:AL050071
A;Experimental source: fetal kidney; clone DKFZp566B0846
C;Genetics:
A;Note: DKFZp566B0846.1

Query Match 74.3%; Score 1149; DB 2; Length 407;
Best Local Similarity 98.2%; Pred. No. 1.9e-81;
Matches 217; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	70	SGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKGPDSLIDGNETVAAICIAATGKQVA	129
Db	1	SGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKGPDSLIDGNETVAAICIAATGKQVA	60
Qy	130	HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARRRITCVVKHPALEKDIRYSFI	189
Db	61	HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARRRITCVVKHPALEKDIRYSFI	120
Qy	190	LDIQAPEVSVTGYDGNWVGRKGNLKNADANPPPFKSVWSRLDGQWPDGLLASDNTL	249
Db	121	LDIQAPEVSVTGYDGNWVGRKGNLKNADANPPPFKSVWSRLDGQWPDGLLASDNTL	180
Qy	250	HFVHPLTFNYSGVYICKVTNSLGORSDDQKVIYISDVPFKQT	290
Db	181	HFVHPLTFNYSGVYICKVTNSLGORSDDQKVIYISDPPTTTT	221

RESULT 2
JC4024
poliovirus receptor-related protein precursor - human
C;Species: Homo sapiens (man)
C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999
C;Accession: JC4024
R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Maroc, C.; Dubi
Gene 155, 261-265, 1995
A;Title: Complementary DNA characterization and chromosomal localization of a human gene
A;Reference number: JC4024; MUID:95237621; PMID:7721102
A;Accession: JC4024
A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796

C:Genetics:
A:Gene: GDB:PVRR1
A:Cross-references: GDB:583951
A:Map position: 11q23-11q24
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: glycoprotein; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F:356-379/Domain: transmembrane #status predicted <TM>
F:36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.5%; Score 517.5; DB 2; Length 518;
Best Local Similarity 36.3%; Pred. No. 2e-32;
Matches 105; Conservative 55; Mismatches 104; Indels 25; Gaps 5;

QY 13 ITQISWEKIHGKSSQTVAVHHPQYGFSGVQGRVLFKNYSLNDATITLHNIGFSDSGK 72
Db 62 ITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPSFTDGTIRLSRLEDEGV 121

QY 73 YICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDG---GNETVAAICIAATGKPV 128
Db 122 YICEFATPTGNRESQNLTVMAKPT-NWIEGTQAVLRAKKGQDDKVLVATCTSANGKPP 180

QY 129 AHIDWE-----GDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRITCVWKHP 178
Db 181 SVVSWETRLKGEARVPGDSGT-----PMAPVTVISRYRLVPSREAHQQLACIVNYH 232

QY 179 ALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLCNADANPPPKSVWSRLDGQW 238
Db 233 M--DRFKESLTNLNQVEPEVTIEGFGNWLQRMVVKLTCKADANPPATEYHWTTLNGSL 290

QY 239 PDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVIYISDVFP 287
Db 291 PKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPY 339

RESULT 3
HLMSP3
poliovirus receptor homolog precursor - mouse
C:Species: Mus musculus domesticus (western European house mouse)
C:Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C:Accession: A38211
R:Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A:Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
A:Reference number: A38211; MUID:92219365; PMID:1560525
A:Accession: A38211
A:Molecule type: DNA
A:Residues: 1-467 <MOR>
A:Cross-references: GB:M80206; NID:g199785; PIDN:AAA39734.1; PID:g199786
C:Superfamily: poliovirus receptor; immunoglobulin homology
C:Keywords: duplication; glycoprotein; transmembrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F:26-354/Domain: extracellular #status predicted <EXT>
F:47-133/Domain: immunoglobulin homology <IMM1>
F:167-231/Domain: immunoglobulin homology <IMM2>
F:267-322/Domain: immunoglobulin homology <IMM3>
F:355-374/Domain: transmembrane #status predicted <TMN>
F:375-467/Domain: intracellular #status predicted <INT>
F:54-131,174-229,274-320/Disulfide bonds: #status predicted
F:128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 26.5%; Score 409; DB 1; Length 467;
Best Local Similarity 31.9%; Pred. No. 4.3e-24;
Matches 97; Conservative 48; Mismatches 129; Indels 30; Gaps 9;

QY 1 VSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEY--QGRVLF----- 50
Db 50 VELPCHLLPPTTTERVSVQVWQRLDG---TVVAAFHPSPGVDFPNNSQFSKDRLSFVRARPE 106

QY 51 KNYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSITVTVLVEP-----TVSLIKGP 105

Db 107 TNADLRDATLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAEQVITGP 166

QY 106 DSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTFPN---ETATIIISQYKLPF 162
Db 167 QSV-----AVARCVSTGGRPPARITWISSLGG-EAKDTQEPGIGAGTVTIISRYSLVP 218

QY 163 TRFARGRRITCVVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLCNADA 222
Db 219 VGRADGVKVTCTRVEHESFEFILLPVTLVSRYPPEVSIISGVDNWNWYLGSRSEAILTCDVRS 278

QY 223 NPPPKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVIYI 282
Db 279 NPEPTDYDWSITTSQVFPASAVAQGSQQL-LVHSVDRMVNTTICTATNAVGTGRAEQVILV 337

QY 283 SDVP 286
Db 338 RDTTP 341

RESULT 4
A53437
poliovirus receptor mpVR - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C:Accession: A53437
R:Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A:Title: Amino acid residues on human poliovirus receptor involved in interaction with
A:Reference number: A53437; MUID:94179228; PMID:8132569
A:Accession: A53437
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-530 <AOK>
A:Cross-references: GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g8255507
A:Experimental source: C57/BL6, brain
A:Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIIP:146667)
C:Superfamily: poliovirus receptor; immunoglobulin homology
F:47-133/Domain: immunoglobulin homology <IMM>

Query Match 26.1%; Score 403; DB 2; Length 530;
Best Local Similarity 31.6%; Pred. No. 1.5e-23;
Matches 96; Conservative 49; Mismatches 129; Indels 30; Gaps 9;

QY 1 VSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEY--QGRVLF----- 50
Db 50 VELPCHLLPPTTTERVSVQVWQRLDG---TVVAAFHPSPGVDFPNNSQFSKDRLSFVRARPE 106

QY 51 KNYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSITVTVLVEP-----TVSLIKGP 105
Db 107 TNADLRDATLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQPENHAEAEQVITGP 166

QY 106 DSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTFPN---ETATIIISQYKLPF 162
Db 167 QSV-----AVARCVSTGGRPPARITWISSLGG-EAKDTQEPGIGAGTVTIISRYSLVP 218

QY 163 TRFARGRRITCVVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFGVGRKGVNLCNADA 222
Db 219 VGRADGVKVTCTRVEHESFEFILLPVTLVSRYPPEVSIISGVDNWNWYLGSRSEAILTCDVRS 278

QY 223 NPPPKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQGRSDQKVIYI 282
Db 279 NPEPTDYDWSITTSQVFPASAVAQGSQQL-LVHSVDRMVNTTICTATNAVGTGRAEQVILV 337

QY 283 SDVP 286
Db 338 RESP 341

RESULT 5
I53960
PRR2 alpha - human
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000

F;105,120,188,218,237,278,307,313/Binding site: carbohydrate (Asn) (covalent) #status pr

Query Match 24.0%; Score 371.5; DB 1; Length 417;
Best Local Similarity 30.6%; Pred. No. 3e-21;
Matches 91; Conservative 52; Mismatches 135; Indels 19; Gaps 8;

Qy 1 VSLKCLIEVNET---ITQISWEKIHGKSSQTVAVHH---PQYGFVSQGEYQGRVLFKNY 53
Db 45 VTLPYQVQVMEVTHVSQTLTWR-HGESGSMVAFHQTPQSPSYSESKRLEFVAARL--GA 101

Qy 54 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEP--TVSLIKGPDSDLIDG 111
Db 102 ELRNASLRMFLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVLAQKQNTAEVQKVQLT--- 157

Qy 112 GNETVAAICIAATGKPVAHIDWEGDLGEMESTT--TSFPNETATIIISQYKLFPTFRFARGR 169
Db 158 GEPVPMARCVSTGGRPPAQITWHSDLGGMPNTSQVPGFSLGTVTTSWLWILVPSSQVDGK 217

Qy 170 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVLNLCNADANPPPFKS 229
Db 218 NVTKVEHESFEKPPQLLTVNLTVYYPPEVSIISGYNWYLGQNEATLTCDARSNPEPTGY 277

Qy 230 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVP 286
Db 278 NWSTTMGPLPPFAVQAQAL-LIRPVDKPIINTTLCNVTNALGARQAEALTQVKEGP 333

RESULT 11
A54017
colon carcinoma-associated antigen pE4 precursor - rat
N;Alternate names: pE4 protein
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 01-Dec-1995
C;Accession: A54017; A61206
R;Chadaneau, C.; LeMoullac, B.; Denis, M.G.
J. Biol. Chem. 269, 15601-15605, 1994
A;Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinoma
A;Reference number: A54017; MUID:94253144; PMID:8195207
A;Accession: A54017
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-416 <CHA>
A;Cross-references: GB:L12025
R;Chadaneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K.
Int. J. Cancer 47, 903-908, 1991
A;Title: Characterization, isolation and amino terminal sequencing of a rat colon carcinoma
A;Reference number: A61206; MUID:91184910; PMID:2010233
A;Accession: A61206
A;Molecule type: protein
A;Residues: 34-41, 'X', 43-53 <CH2>
A;Note: the residue at position 9 is suggested to be glycosylated asparagine
C;Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma cell
C;Keywords: glycoprotein; membrane protein

Query Match 20.0%; Score 309.5; DB 2; Length 416;
Best Local Similarity 29.6%; Pred. No. 1.9e-16;
Matches 84; Conservative 44; Mismatches 141; Indels 15; Gaps 7;

Qy 10 NETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLF-KNY-SLNDATITLHNIGF 67
Db 62 NVTITQLTWMKRPDGDGSPFRACLPPQEGPSISDPERVFLVAKVYEDLNASLAISNLRV 121

Qy 68 SDGKYICKAVTFPLGNAQSSITVTVLVEP--TVSLIKGPDSDLIDGNETVAAICIAATG 125
Db 122 EDEGIYECQIATFPFGSKSANVWLKVFAKPKNTAEALEPSPTLMPQD---VAKCISADG 177

Qy 126 KPVAHIDW---EGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRITCVVKHPALE 181
Db 178 HPPGRITWSSNVNGSVREMKETGSSRAPPLQSATSFPWCLLARQMAKTSAPQWNMK--ASR 235

Qy 182 KDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVLNLCNADANPPPFKSVMVSRDLGQWPDG 241
Db 236 SRTSRPLILSLPYPPPEVSIISGYEGNWIYGLTNVNLTCARSKPPPTNYSWSTATGPLPNS 295

Qy 242 LLASDNTLHFVHPLTFNYSQ-VYICKVTNSLQGRSDQKVIYISD 284
Db 296 THFQENGSHLLISTVDDLNNITIFVCKAINALGSGQGQVTLVKE 339

RESULT 12
A49448
irregular chiasm C-roughest precursor - fruit fly (Drosophila melanogaster)
N;Alternate names: irreC-roughest protein
C;Species: Drosophila melanogaster
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 07-May-1999
C;Accession: A49448; S34129
R;Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brands
Genes Dev. 7, 2533-2547, 1993
A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal proj
A;Reference number: A49448; MUID:94102535; PMID:7503814
A;Accession: A49448
A;Status: preliminary
A;Molecule type: DNA; mRNA
A;Residues: 1-764 <RAM>
A;Cross-references: GB:L11040; NID:g304790; PID:g304791; EMBL:Z21641; NID:g312985; PID:
C;Genetics:
A;Gene: FlyBase:rst
A;Cross-references: FlyBase:FBgn0003285
C;Keywords: transmembrane protein

Query Match 13.4%; Score 206.5; DB 2; Length 764;
Best Local Similarity 23.9%; Pred. No. 3.8e-08;
Matches 79; Conservative 55; Mismatches 130; Indels 67; Gaps 16;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSL----- 55
Db 45 VTLPYQVQVMEVTHVSQTLTWR-HGESGSMVAFHQTPQSPSYSESKRLEFVAARL--GA 101

Qy 56 -NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSIT---VTVLVEPTVSLIKGPDSDLIDG 111
Db 87 EGDYSLDIYPVMLDDDDARYQCQVSPGEGQPAIRSTFAGTLVLPPEAPKITQGDVIYAT 146

Qy 112 GNETVAAICIAATGKPVAHIDWEGDLG-----EMESTTTSFPNETA-TIISQYKLFPTFRF 165
Db 147 ADRKVEIECVSVGGKPAAEITWIDGLGNVLTDNIEYTVIPLDQRRFTAKSVLRLTPKKE 206

Qy 166 ARGRRITCVVKHPALEKDIRYSFI-LDIYAPEVSVT-----GYDGNWFVGRKG----- 213
Db 207 HHNTNPFSCQAQNTA-DRTYRSKIRVEVKYAPKVKVNVMSGVLPFGAGGS--VGGAGGGSV 263

Qy 214 -----VNLKCNADANPPPFKSVMVSRDLGQWPDGLLASDNTLHFVHPLTFNYS 260
Db 264 HMSTGSRIVEHSQVRLECRADANPSDVRYRWFIN-----EPIGGQKTEMVIRNVTTRKFH 319

Qy 261 GVYI-CKVTNSLQGRSDQKVIYISDVP-FKQ 289
Db 320 DAIVKCEVQNSVGKSEDSSETLDSIYAPSRQ 350

RESULT 13
A47639
OX-2 membrane glycoprotein precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000
C;Accession: A47639
R;McCaughan, G.W.; Clark, M.J.; Barclay, A.N.
Immunogenetics 25, 329-335, 1987
A;Title: Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein
A;Reference number: A47639; MUID:87192943; PMID:3032785
A;Accession: A47639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-274 <MCC>
A;Cross-references: GB:X05323; NID:g34742; PIDN:CAA28943.1; PID:g1335216; GB:M17226; GB:
C;Superfamily: MRC OX-2 antigen; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein

F:40-119/Domain: immunoglobulin homology <IMM>

Query Match	12.1%;	Score 187.5;	DB 2;	Length 274;
Best Local Similarity	24.8%;	Pred. No. 3.1e-07;		
Matches 52;	Conservative 36;	Mismatches 97;	Indels 25;	Gaps 4;

[illegible]

RESULT 14

T20992

hypothetical protein F15G9.4a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C;Accession: T20992; T24733

R;Sulston, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19355

A;Accession: T20992

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5175 <W12>

A;Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone F15G9

R;Kershaw, J.

submitted to the EMBL Data Library, December 1994

A;Reference number: Z19929

A;Accession: T24733

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5175 <W12>

A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a

A;Experimental source: clone T09B9

C;Genetics:

A;Gene: CESP:F15G9.4a

A;Map position: X

	Query Match	11.9%;	Score 184.5;	DB 2;	Length 5175;
	Best Local Similarity	25.9%;	Pred. No. 2e-05;		
	Matches 82; Conservative	40;	Mismatches 131;	Indels 63;	Gaps 17
QY	1	VSLKCLIEVNETITQISWEKIHKSSQTVAVHHPPQYGFSVOGEYQGRVLFKNYSLNDATI	60		
Db	810	VTLQCL-AVGIPPEIEWQK---GNVLLATLNPNRYTQLADG-----NLLITDAQI	856		
QY	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSLLIKPDSLIDGGNETVAA	118		
Db	857	-----EDQGQFTCIARN-TYGOQSQSSTLMVTGLVSPVLGHVPPEQLLEGQDLTLS-	907		
QY	119	ICIAATGKPVAHIDWEGDLGEMESTTSFPNETATIIISOYKLFFPTRFARGR---RITCVV	175		
Db	908	-CWWVLGTPKPSIVWIKKDKKPVEE-----GPTIKIEGGSSLRLRGGNPKDEGKYTCIA	960		
QY	176	KHPALEKDIRYSFIL---DIQYAPE-----VSVTYGDGNW-----FVGRKGVN	216		
Db	961	VSPAGNSTLHINVOLIKKPEFYVKPEGGIVEKPTISGMDEKKHAVNVNSHDVLDGEGFAI	102		

QY	217	KCNADANPPPFKSVWSRLDGQWP-----DGLLASDNTHLFVHPPLTFENYSGVYICKVTNS	270
		: :	
Dδ	1021	PCVWVGTPPPI-ITW-YLDGR-PITPNSRDFTVTADNTL-IVRKADKSYSGVYTCQATNS	1076
		: :	
QY	271	LQRSDQKVVIYISDVP	286
		:	
Dδ	1077	AGDNEQKTTIRIMNTP	1092

RESULT 15

T43290
hemicentin precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43290; T20993; T24734
R;Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemicentin is required for hemidesmosome mediated cell adhesion and germ
A;Reference number: Z22396
A;Accession: T43290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
A;Cross-references: EMBL:AF074901; PIDN:AAC26792.1
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20993
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87336.1; GSPDB:GN000028; CESP:F15G9.4b
A;Experimental source: clone F15G9
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24734
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5198 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN000028; CESP:F15G9.4b
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: him-4; F15G9.4b
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
1; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/
1; 5100/1; 5100/1; 5100/1; 5100/1; 5100/1; 5100/1; 5100/1; 5100/1; 5100/1; 5100/1;

Query Match	11.9%;	Score 184.5;	DB 2;	Length 5198;
Best Local Similarity	25.9%;	Pred. No. 2e-05;		
Matches 82;	Conservative 40;	Mismatches 131;	Indels 63;	Gaps 17;

QY	1	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATI	60
Db	810	VTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG-----NLLITDAQI	856
QY	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSLIKGPDSLDGNETVAA	118
Db	857	-----EDQGQFTCIARN-TYQQQSQSTTLMVTGLVSPVLGHVPPEEQLEIGQDLTLS-	907
QY	119	ICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGR---RITCVV	175
Db	908	-CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGSLLRLRGGNPKDEGKYTCIA	960
QY	176	KHPALEKDIRYSFIL----DIQYAPE-----VSVTGYDGNW-----FVGRKGVNL	216
Db	961	VSPAGNSTLHINVQLIKPPEFVYKPEGGIVFKPTISGMDEKHHVAVVNSTHVDLDGEGFAI	1020
QY	217	KCNADANPPPFKSVWSRLDGQWP-----DGLLASDNTLHFVHPLTFNYSGVYICKVTNS	270
Db	1021	PCVVSGETPPII-ITW-YLDGR-PITPNSRDEFTVTADNLI-IVRKADKSYSGVYTCOATNS	1076

Qy 271 LQQRSDQKVIYISDVP 286
| : | : |
Db 1077 AGDNEQKTTIRIMNTP 1092

Search completed: April 12, 2004, 09:47:04
Job time : 8.72649 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 4.66649 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-10_COPY_74_365
Perfect score: 1546
Sequence: 1 VSLKCLIEVNETITQISWEK.....QRSDQKVIYISDVFPFKQTSS 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	551	35.6	515	1	PVR1_MOUSE
2	540	34.9	517	1	PVR1_HUMAN
3	537	34.7	515	1	PVR1_PIG
4	403	26.1	530	1	PVR2_MOUSE
5	392	25.4	538	1	PVR2_HUMAN
6	383.5	24.8	417	1	PVR_CERAE
7	371.5	24.0	417	1	PVR_HUMAN
8	206.5	13.4	764	1	ICCR_DROME
9	199	12.9	837	1	NCM2_MOUSE
10	187.5	12.1	278	1	OX2G_HUMAN
11	175	11.3	837	1	NCM2_HUMAN
12	169.5	11.0	4391	1	PGBM_HUMAN
13	167	10.8	626	1	MAG_MOUSE
14	166	10.7	626	1	MAG_HUMAN
15	165	10.7	626	1	MAG_RAT
16	164.5	10.6	853	1	NCA1_BOVIN
17	160	10.3	858	1	NCA1_RAT
18	158.5	10.3	278	1	OX2G_MOUSE
19	158.5	10.3	278	1	OX2G_RAT
20	157	10.2	1091	1	NCA1_CHICK
21	153.5	9.9	702	1	CEA5_HUMAN
22	152	9.8	739	1	VCA1_MOUSE
23	152	9.8	761	1	NCA2_HUMAN
24	152	9.8	848	1	NCA1_HUMAN
25	151.5	9.8	509	1	SHS1_RAT
26	149.5	9.7	725	1	NCA2_MOUSE
27	149.5	9.7	1115	1	NCA1_MOUSE
28	149	9.6	353	1	CEPU_CHICK
29	148	9.6	2012	1	DSCA_HUMAN
30	147.5	9.5	1088	1	NCA1_XENLA
31	147	9.5	588	1	C166_CHICK
32	147	9.5	1709	1	SN_HUMAN
33	146	9.4	847	1	CD22_HUMAN
					Q9jfk6 mus musculu
					Q15223 homo sapien
					Q9gl76 sus scrofa
					P32507 mus musculu
					Q92692 homo sapien
					P32506 cercopithec
					P15151 homo sapien
					Q08180 drosophila
					O35136 mus musculu
					P41217 homo sapien
					O15394 homo sapien
					P98160 homo sapien
					P20917 mus musculu
					P20916 homo sapien
					P07722 rattus norv
					P31836 bos taurus
					P13596 rattus norv
					O54901 mus musculu
					P04218 rattus norv
					P13590 gallus gall
					P06731 homo sapien
					P29533 mus musculu
					P13592 homo sapien
					P13591 homo sapien
					P97710 r protein-t
					P13594 mus musculu
					P13595 mus musculu
					Q90773 gallus gall
					O60469 homo sapien
					P16170 xenopus lae
					P42292 gallus gall
					Q9b222 homo sapien
					P20273 homo sapien

34	145	9.4	330	1	CD22_PONPY	Q9nle3 pongo pygma
35	144	9.3	359	1	LACH_XENLA	Q24372 drosophila
36	143.5	9.3	1092	1	NCA2_XENLA	P36335 xenopus lae
37	142.5	9.2	332	1	CD22_PANPA	Q9nle5 pan paniscu
38	142.5	9.2	332	1	CD22_PANTR	Q9nle6 pan troglod
39	142	9.2	569	1	SILF_MOUSE	Q92093 mus musculu
40	141	9.1	646	1	MU18_HUMAN	P43121 homo sapien
41	139.5	9.0	467	1	SIL7_HUMAN	Q9Y286 homo sapien
42	139.5	9.0	3707	1	PGBM_MOUSE	Q05793 mus musculu
43	139	9.0	337	1	OPCM_CHICK	Q98892 gallus gall
44	138.5	9.0	271	1	OX2V_KSHV	P88963 kaposi's sa
45	138.5	9.0	519	1	ECTO_RAT	P16573 rattus norv

ALIGNMENTS

RESULT 1
PVR1_MOUSE STANDARD; PRT; 515 AA.
ID Q9JKF6; Q9ERL5; Q9JIL7;
AC 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HveC) (Nectin 1).
GN PVR1 OR PRR1 OR HVEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubreuil P., Campadelli-Fiume G.;
RT "The murine homolog of human nectin1 delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-lalpha to human nectin-lalpha (HveC) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -|- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -|- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -|- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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CC -----
CC EMBL: AF239762; AAF60333.1; -

DR	EMBL; AF270977; AAF76195.1; -.	DE	(CD111 antigen).
DR	EMBL; AF297665; AAG22808.1; -.	GN	PVRL1 OR PRR1 OR HVEC.
DR	MGD; MGI:1926483; Pvr11.	OS	Homo sapiens (Human).
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
DR	GO; GO:0005515; F:protein binding; IPI.	OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
DR	GO; GO:0004872; F:receptor activity; IDA.	OX	NCBI_TaxID=9606;
DR	InterPro; IPR007110; Ig-like.	RN	[1]
DR	InterPro; IPR003599; Ig.	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
DR	Pfam; PF00047; Ig; 2.	RX	MEDLINE=95237621; PubMed=7721102;
DR	SMART; SM00409; IG; 2.	RA	Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
DR	PROSITE; PS50835; IG LIKE; 2.	RA	Dubreuil P.;
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;	RT	"cDNA characterization and chromosomal localization of a gene related
KW	Repeat; Glycoprotein; Signal.	RT	to the poliovirus receptor gene.";
FT	SIGNAL 1 30	RL	Gene 155:261-265(1995).
FT	CHAIN 31 515	RN	[2]
FT	DOMAIN 31 354	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
FT	TRANSMEM 355 375	RX	MEDLINE=98279152; PubMed=9616127;
FT	DOMAIN 376 515	RA	Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
FT	DOMAIN 31 141	RA	Spear P.G.;
FT	DOMAIN 145 243	RT	"Entry of alphaherpesviruses mediated by poliovirus receptor-related
FT	DOMAIN 247 334	RT	protein 1 and poliovirus receptor.";
FT	DOMAIN 436 442	RL	Science 280:1618-1620(1998).
FT	DOMAIN 443 447	RN	[3]
FT	DISULFID 51 124	RP	SEQUENCE FROM N.A. (ISOFORM GAMMA).
FT	DISULFID 172 226	RX	MEDLINE=21256041; PubMed=11356977;
FT	DISULFID 269 316	RA	Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
FT	CARBOHYD 36 36	RA	Campadelli-Fjume G., Dubreuil P.;
FT	CARBOHYD 72 72	RT	"Novel, soluble isoform of the herpes simplex virus (HSV) receptor
FT	CARBOHYD 139 139	RT	nectin1 (or prrl-HIGR-Hvec) modulates positively and negatively
FT	CARBOHYD 202 202	RT	susceptibility to hsv infection.";
FT	CARBOHYD 286 286	RL	J. Virol. 75:5684-5691(2001).
FT	CARBOHYD 297 297	RN	[4]
FT	CARBOHYD 332 332	RP	SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
FT	CONFLICT 138 138	RX	MEDLINE=20392396; PubMed=10932188;
FT	CONFLICT 165 165	RA	Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
FT	CONFLICT 342 342	RA	Helms J.A., Spritz R.A.;
FT	CONFLICT 428 428	RT	"Mutations of PVRL1, encoding a cell-cell adhesion
FT	SEQUENCE 515 AA; 57064 MW; FFF608EB5FFB7A0F CRC64;	RT	molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
SQ		RT	dysplasia.";
		RL	Nat. Genet. 25:427-430(2000).
	Query Match 35.6%; Score 551; DB 1; Length 515;	CC	-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
	Best Local Similarity 39.6%; Pred. No. 6e-38;	CC	ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
	Matches 112; Conservative 56; Mismatches 107; Indels 8; Gaps 5;	CC	CELLS.
QY	13 ITQISWEKIHGSSQTAVVHPQYGFSGVEYQGRVLFKNYSINDATITLHNIGFSDSGK 72	CC	-!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
Db	62 ITQVTWQKASNGSKQNMAIYNPTMGVSVLPPEYKRVFLRPSFDITRLSGLELEDEGM 121	CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
QY	73 YICKAVTFPLGNAQSSTTVTLVPEVTVSLIKGPDSLIDG----GNETVAAICIAATGKPV 128	CC	delta). Secreted (isoform gamma).
Db	122 YICEFATFPNGRESQNLNLTVMKPT-NWIEGTRAVLRARKGQDNKVLVATCTSANGKPP 180	CC	-!- ALTERNATIVE PRODUCTS:
QY	129 AHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPALEKDIRYS 187	CC	Event=Alternative splicing; Named isoforms=3;
Db	181 SAVSWETRLKGEAEYQEIIRPNPGTIVTSRYRLVPSREAHRSQSLACIVNY-HLDR-FRES 238	CC	Name=Delta;
QY	188 FILDIQAPEVSVTGVDGNWVGRKGVNLCNADANPPPFKSVMSRLDGQWPDGLLASDN 247	CC	ISOId=Q15223-1; Sequence=Displayed;
Db	239 LTLNVQYEPEVTIEGFDGNWYLQRTDVKLTCKADANPPATEYHWTTLNGSLPKGVEAQR 298	CC	Name=Alpha;
QY	248 TLHFVHPLTFNYSVGVIKVTNSLQSRSDQKVIYISDVPFKQT 290	CC	ISOId=Q15223-2; Sequence=VSP_002626, VSP_002627;
Db	299 TLFFRGPIYSLAGTYICEATNPIGTRSGQVEVNIETFPYTPT 341	CC	Name=Gamma;
		CC	ISOId=Q15223-3; Sequence=VSP_002624, VSP_002625;
RESULT 2		CC	DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
PVRL1_HUMAN		CC	ectodermal dysplasia syndrome (CLPED1) [MIM:225000]. CLPED1 is
ID	PVRL1_HUMAN STANDARD; PRT; 517 AA.	CC	responsible for allelic forms known as Margarita island ectodermal
AC	Q15223; O75465; Q9HBE6; Q9HBE2;	CC	dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
DT	16-OCT-2001 (Rel. 40, Created)	CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
DT	16-OCT-2001 (Rel. 40, Last sequence update)	CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
DT	10-OCT-2003 (Rel. 42, Last annotation update)	CC	-!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
DE	Poliovirus receptor related protein 1 precursor (Herpes virus entry	CC	WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
DE	mediator C) (Hvec) (Nectin 1) (Herpesvirus Ig-like receptor) (HIGR)	CC	-----
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		CC	the European Bioinformatics Institute. There are no restrictions on its
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		CC	modified and this statement is not removed. Usage by and for commercial
		CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
		CC	or send an email to license@isb-sib.ch).
		CC	-----
		CC	EMBL; X76400; CAA53980.2; ALT INIT.
		CC	EMBL; AF060231; AAC23798.1; --.


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FT DOMAIN 437 443 POLY-GLU.
FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;

Query Match 34.7%; Score 537; DB 1; Length 515;
Best Local Similarity 38.6%; Pred. No. 8.5e-37;
Matches 108; Conservative 54; Mismatches 110; Indels 8; Gaps 4;

QY 13 ITQISWEKHGKSSQTAVVHHPOYGFVSQGEYQGRVLFKNYSLNDAITLHNIGFSDSGK 72
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Dd 62 ITQVTWQKATNGSKQNVAIYNPAMGVSVLAPYRERVEFLRPSFTDGTIRLSRLEDEGV 121
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
QY 73 YICKAVTFPLGNAQSSSTTVTLVVEPTVSLIKGPDSLIDG----GNETVAAICIAATGKPV 128
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Dd 122 YICFATFPAGNRESQNLNLTVMAKPT-NWIEGTQAVLRRAKKGDDKVLVATCTSANGKPP 180
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
QY 129 AHIDWEGDL-GEMESTTTSPNETATIIISQYKLFPTFRFAGRRITCVKHPALEKDIRYS 187
: : : : : |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Dd 181 SVVSWETHLKGEAEYQEIRNPNGTIVISRYRLVPSREDHRQSLACIVNYHM--DRFRES 238
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
QY 188 FILDIOYAPEVSVTGYDGNWVFGKGVNLCNADANPPPKVSVWSRLDQWPDGLASDN 247
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Dd 239 LTLNVQYEPEVTIEGFDGNWYLRQMDVVKLTCKADANPPATPEYHWTTLNGLSLPKGVQEAQNR 298
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
QY 248 TLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPF 287
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
Dd 299 TLFFRGFINYSMAGTYICEATNPICTRSGQVEVNITEFPY 338
|||::||| |||::||| |||::||| |||::||| |||::||| |||::||| |||::|||
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RESULT 4
PVR2_MOUSE STANDARD; PRT; 530 AA.
ID PVR2_MOUSE
AC P32507; Q62096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
entry protein B) (mHvB) (Nectin 2) (Poliovirus receptor homolog).
GN PVR2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
poliovirus receptor gene.";
RL J. Virol. 66:2807-2813(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
interaction with poliovirus.";
RL J. Biol. Chem. 269:8431-8438(1994).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[4]
CHARACTERIZATION.
MEDLINE=99214397; PubMed=10196354;
Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
"The murine homolog (Mph) of human herpesvirus entry protein B (HvB)
mediates entry of pseudorabies virus but not herpes simplex virus
types 1 and 2.";
J. Virol. 73:4493-4497(1999).
-!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY
INTO CELLS.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=Beta;
IsoId=P32507-1; Sequence=Displayed;
Name=Alpha;
IsoId=P32507-2; Sequence=VSP_002630, VSP_002631;
-!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
liver.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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EMBL; M80206; AAA39734.1; -
EMBL; D26107; BAA05103.1; -
EMBL; BC059941; AAH59941.1; -
PIR; A38211; HLMSP3.
PIR; A53437; A53437.
MGD; MGI:97822; Pvr12.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 3.
Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
Repeat; Alternative splicing.
SIGNAL 1 31 POTENTIAL.
CHAIN 32 530 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.
DOMAIN 32 351 EXTRACELLULAR (POTENTIAL).
TRANSMEM 352 372 POTENTIAL.
DOMAIN 373 530 CYTOPLASMIC (POTENTIAL).
DOMAIN 32 147 IG-LIKE V-TYPE.
DOMAIN 153 247 IG-LIKE C2-TYPE 1.
DOMAIN 252 337 IG-LIKE C2-TYPE 2.
DISULFID 54 131 BY SIMILARITY.
DISULFID 174 229 BY SIMILARITY.
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FT DISULFID 274 320 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 339 467 ESPSTAGAGATGGIIGIIAIIATAVAGTGILICRQORKE
FT QRLQAADDEEELEGPPSYKPTPKAKLEPEMPSQLFTLGA
FT SEHSPVKTPYFDAGVSCADQEMPRYHELPTLEBSGPLLIG
FT ATGLGP -> DTPOARDVGPLVWGAAGTLLVLLLAGGFL
FT ALILGRRRRKSPGGGNDGDRGSDYDKTQVFGNGPVFW
FT RSASPEPMRPDGREDEDEEEEMKAEGLMLPHSPKDDM
FT ESHLDGSLISRRAYV (in isoform Alpha).
FT /FTid=VSP 002630.
FT Missing (in isoform Alpha).
FT /FTid=VSP 002631.
FT VARSPLIC 468 530
FT SEQUENCE 530 AA; 57317 MW; 0ED71BF2B231BBE CRC64;
SQ
Query Match 26.1%; Score 403; DB 1; Length 530;
Best Local Similarity 31.6%; Pred. No. 9.8e-26;
Matches 96; Conservative 49; Mismatches 129; Indels 30; Gaps 9;
QY 1 VSLKLC--LIEVNETITQISWEKIHGKSSQTVAVHPQYGFVSQGEY--QGRVLF----- 50
Db 50 VELPCHLLPPTTERVSVQVWQLDG---TVVAAFHPSPFGVDFPNSQFSKDRLSFVRARPE 106
QY 51 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNQAQSSITVTVLVEP-----TVSLIKGP 105
Db 107 TNADLRDATLAFRLGRVEDEGNYTCEFAFPNGTRRGVTWLRVIAQPENHAAEQEVTIGP 166
QY 106 DSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPN---ETATIIISQYKLEP 162
Db 167 QSV-----AVARCVSTGGRPPARITWISSLGG-EAKDTPGCIQAGTVTIIISRYSLVP 218
QY 163 TRFARGRRITCWKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWFVGRKGNLKNADA 222
Db 219 VGRADGVKVTCTVEHESFEPIPLPVTLVSRYPPEVSISGYDDNWYLGSRSEAILTCDVRS 278
QY 223 NPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYI 282
Db 279 NPEPTDYDWSITSGVFAPASAVAQGSQSL-LVHSVDRMVTNTTICTATNAVGTGRAEQVILV 337
QY 283 SDVP 286
Db 338 RESP 341
RESULT 5
PVR2 HUMAN STANDARD; PRT; 538 AA.
AC Q92692; O75455; Q96J29;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Herpes virus entry mediator B) (Hvrb) (Nectin 2) (CD112 antigen).
GN PVR2 OR PRR2 OR HVB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM DELTA).
RX MEDLINE=95347610; PubMed=7622062;
RA Eberle F., Dubreuil P., Mattei M.-G., Devillard E., Lopez M.;
RT "The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the true homolog of the murine MPH gene.";
RL Gene 159:267-272(1995).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=98321161; PubMed=9657005;
RA Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
RA Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
RA "A cell surface protein with herpesvirus entry activity (Hvrb) confers susceptibility to infection by mutants of herpes simplex virus type
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RT 1, herpes simplex virus type 2, and pseudorabies virus.";
RL Virology 246:179-189(1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP SEQUENCE OF 31-538 FROM N.A.
RA Yoshiura K., Murray J.C.;
RT "A transcriptional map in the region of 19q13 derived using direct sequencing and exon trapping.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 449-538 FROM N.A.
RX MEDLINE=99449047; PubMed=10520737;
RA Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
RA Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;
RT "Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene: PEREC1.";
RL DNA Seq. 9:89-101(1998).
CC -!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Delta;
CC IsoId=Q92692-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=Q92692-2; Sequence=VSP_002628, VSP_002629;
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROW; NOTE=PROW 1:74-77(2000);
CC WWW="http://www.ncbi.nlm.nih.gov/prow/guide/204270028_g.htm".
CC -----
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CC -----
CC EMBL; X80038; CAA56342.1; --
CC EMBL; AF058448; AAC23797.1; --
CC EMBL; BC003091; AAH03091.1; --
CC EMBL; AF044968; AAC82348.1; --
CC EMBL; AF044962; AAC82348.1; JOINED.
CC EMBL; AF044963; AAC82348.1; JOINED.
CC EMBL; AF044964; AAC82348.1; JOINED.
CC EMBL; AF044966; AAC82348.1; JOINED.
CC EMBL; AF044967; AAC82348.1; JOINED.
CC EMBL; AF050154; AAD02503.1; --
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DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS50835; IG LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Antigen; Alternative splicing; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 417
FT DOMAIN 21 343
FT TRANSMEM 344 367
FT DOMAIN 368 417
FT DOMAIN 24 139
FT DOMAIN 145 237
FT DOMAIN 244 328
FT DISULFID 49 123
FT DISULFID 166 221
FT DISULFID 266 312
FT CARBOHYD 105 105
FT CARBOHYD 120 120
FT CARBOHYD 188 188
FT CARBOHYD 218 218
FT CARBOHYD 237 237
FT CARBOHYD 278 278
FT CARBOHYD 307 307
FT CARBOHYD 313 313
FT VARSPLIC 340 384
FT VARSPLIC 331 331
FT VARSPLIC 332 384
FT VARSPLIC 385 392
FT VARSPLIC 393 417
FT VARIANT 67 67
FT VARIANT 340 340
FT SEQUENCE 417 AA; 45302 MW; D15C012CE853169B CRC64;
Query Match 24.0%; Score 371.5; DB 1; Length 417;
Best Local Similarity 30.6%; Pred. No. 2.9e-23;
Matches 91; Conservative 52; Mismatches 135; Indels 19; Gaps 8;
QY 1 VSLKCLIEVNET---ITQISWEKIHGKSSQTVAVHH---PQYGFVSQGEYQGRVLFKNY 53
Db 45 VTLPCLYQVPPNMEVTHVSQLTWAR-HGESGSMVAFHQYQGPSYSESKRLEFVAARL--GA 101
QY 54 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVPE--TVSLIKGPDSDLIDG 111
Db 102 ELRNASLRMFGRLVEDEGNTCLFVTFPQGSRSVDIWLRLAKPQNTAEVQKVLQTLT--- 157
QY 112 GNETVAAICIAATKPVVAHIDWEGDLGEMEST--TSFPNETATIIISQYKLPPTFRFARGR 169
Db 158 GEPVPMARCVSTGGRPPAQITWHSIDLGMPTNSQVPGFLSGTIVTSLWILVPSQVDGK 217
QY 170 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGKGNLKNADANPPPFKS 229
Db 218 NVTCCKVEHESFEKPOLLVNLTIVYYPPEVVISGYDNNWYLGONEATLTCDARSNPEPTGY 277
QY 230 VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKQVIYISDVP 286
Db 278 NWSTMGRLPPFAVAQQAQL-LIRPVDKPINTTLCNVNLTALGARQAELTVQKEGP 333

RESULT 8
ICCR_DROME STANDARD; PRT; 764 AA.
AC Q08180;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Irregular chiasm C-roughest protein precursor (IRREC protein).
GN RST.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94102535; PubMed=7503814;
RA Ramos R.G., Igloi G.L., Lichte B., Baumann U., Maier D.,
RA Schneider T., Brandstaetter J.H., Froehlich A., Fischbach K.-F.;
RT "The irregular chiasm C-roughest locus of Drosophila, which affects
RT axonal projections and programmed cell death, encodes a novel
RT immunoglobulin-like protein.";
RL Genes Dev. 7:2533-2547(1993).
CC -!- FUNCTION: REQUIRED FOR CORRECT AXONAL PATHWAY FORMATION IN
CC THE OPTIC LOBE AND FOR PROGRAMMED CELL DEATH IN THE DEVELOPING
CC RETINA.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: POSTEMBRYONIC EXPRESSION IS STRONG IN THE
CC DEVELOPING OPTIC LOBE AND IN THE EYE IMAGINAL DISC.
CC -!- DEVELOPMENTAL STAGE: STRONGLY EXPRESSED IN EMBRYOS. ALSO FOUND
CC IN LATE LARVAL AND PUPAL STAGES.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -----
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CC -----
CC EMBL; Z21641; CAA79756.1; -.
CC EMBL; L11040; AAA16632.1; -.
CC PIR; A49448; A49448.
CC FlyBase; FBgn0003285; rst.
CC GO; GO:0016202; P:regulation of myogenesis; IMP.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003598; IG_c2.
CC Pfam; PF00047; ig; 4.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS50835; IG LIKE; 5.
KW Transmembrane; Immunoglobulin domain; Glycoprotein; Signal; Repeat;
KW Cell adhesion.
FT SIGNAL 1 19
FT CHAIN 20 764
FT DOMAIN 20 533
FT TRANSMEM 534 556
FT DOMAIN 557 764
FT DOMAIN 21 123
FT DOMAIN 117 230
FT DOMAIN 245 261
FT DOMAIN 237 343
FT DOMAIN 346 419
FT DOMAIN 430 530
FT DOMAIN 637 660
FT CARBOHYD 211 211
FT CARBOHYD 313 313
FT CARBOHYD 393 393
FT CARBOHYD 400 400
FT CARBOHYD 507 507
SQ SEQUENCE 764 AA; 82947 MW; 262225D2B2A1C181 CRC64;
Query Match 13.4%; Score 206.5; DB 1; Length 764;
Best Local Similarity 23.9%; Pred. No. 2.4e-09;
Matches 79; Conservative 55; Mismatches 130; Indels 67; Gaps 16;
QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSL----- 55
Db 45 VTLPCLRV-INKQGT-LQWTK-----DDFGLGTSRDLG---PERYAMVGSDE 86

Db	423	DVTANPP--ASIHWR--	-----EKLLPAKNTTHLKTHSVGRKMILEIAPTSDNDFGRNC	475
QY	266	KVTNSLQSRSDQKVIYISDVP	286	
Db	476	TATNRIGTRFQEYILELADVP	496	
RESULT 10				
OX2G_HUMAN				
ID	OX2G_HUMAN	STANDARD;	PRT;	278 AA.
AC	P41217; Q8TB85; Q9H3J3;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	OX-2 membrane glycoprotein precursor (CD200 antigen) (My033 protein).			
GN	MOX2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE OF 5-278 FROM N.A. (ISOFORM 1).			
RC	TISSUE=Blood;			
RX	MEDLINE=87192943; PubMed=3032785;			
RA	McCaughan G.W., Clark M.J., Barclay A.N.;			
RT	"Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein.";			
RL	Immunogenetics 25:329-335 (1987).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Fetal brain;			
RA	Mao Y.M., Xie Y., Zheng Z.H.;			
RL	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	TISSUE=Brain;			
RX	MEDLINE=22388257; PubMed=12477932;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Mullahy S.J., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalrus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
CC	-!- FUNCTION: Costimulate T cell proliferation. May regulate myeloid cell activity in a variety of tissues.			
CC	-!- SUBUNIT: Interacts with OX2R.			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=1;			
CC	Isoid=P41217-1; Sequence=Displayed;			
CC	Name=2;			
CC	Isoid=P41217-2; Sequence=VSP_002613;			
CC	Note=No experimental confirmation available;			
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.			
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.			
CC	-----			
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CC	-----			
CC	EMBL; X05323; CAA28943.1; -.			
DR	EMBL; X05324; CAA28943.1; JOINED.			
DR	EMBL; X05325; CAA28943.1; JOINED.			
DR	EMBL; X05326; CAA28943.1; JOINED.			
DR	EMBL; AF063591; AAG43150.1; -.			
DR	EMBL; BC022522; AAH22522.1; -.			
DR	PIR; A47639; A47639.			
DR	Genew; HGNC:7203; MOX2.			
DR	MIM; 155970; -.			
DR	GO; GO:0005887; C:integral to plasma membrane; TAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig; 2.			
DR	SMART; SM00409; IG; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 1.			
KW	Antigen; Neurone; T-cell; Signal; Transmembrane;			
KW	Immunoglobulin domain; Glycoprotein; Alternative splicing.			
FT	SIGNAL 1 30			
FT	CHAIN 31 278			
FT	DOMAIN 31 232			
FT	TRANSMEM 233 259			
FT	DOMAIN 260 278			
FT	DOMAIN 31 141			
FT	DOMAIN 142 232			
FT	DISULFID 51 121			
FT	DISULFID 160 214			
FT	CARBOHYD 95 95			
FT	CARBOHYD 103 103			
FT	CARBOHYD 110 110			
FT	CARBOHYD 157 157			
FT	CARBOHYD 181 181			
FT	CARBOHYD 190 190			
FT	VARSPPLIC 268 278			
FT	CONFLICT 11 11			
FT	CONFLICT 46 46			
FT	SEQUENCE 278 AA; 31264 MW; 38DF327B382CC970 CRC64;			
SQ	SEQUENCE 278 AA; 31264 MW; 38DF327B382CC970 CRC64;			
Query Match	12.1%; Score 187.5; DB 1; Length 278;			
Best Local Similarity	24.8%; Pred. No. 2.5e-08;			
Matches	52; Conservative 36; Mismatches 97; Indels 25; Gaps 4;			
QY	2 SLKCLIEVNETITQISWEKIHGKSSQTAVVHPQYGFVQGVQGRVLFKNYSLNDATIT 61			
Db	48 SLKCSLQNAQEALIVTWQKKAVSPENMVTFSNHGVVIOQPAYKDKINITQLGLQNSTIT 107			
QY	62 LHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSL-IKGPDSLIDGGNETVAAIC 120			
Db	108 FWNITLEDGECYMCLENTFGFGKISGTACTLVVYVQPIVSLHYKFSSEHNLN-----IT 159			
QY	121 IAATGKPVAHIDWEGDLGEMESTT--SFPNETATIIISQYKLFPTFRFARRGRITCVVKHP 178			
Db	160 CSAIARPPAPMVFWKVPFRSGIENSTVLSHPNGTTSVLSILHKDPKNQGVKEVICQVLHL 219			
QY	179 ALEKDIRYSPILDIQYAPEVSVTGYDGNWF 208			
Db	220 GTVTDPKQ-----TVNKGWYF 235			
RESULT 11				
NCM2_HUMAN				
ID	NCM2_HUMAN	STANDARD;	PRT;	837 AA.
AC	O15394;			
DT	15-JUL-1998 (Rel. 36, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			

DT	10-OCT-2003 (Rel. 42, Last annotation update)	FT	CARBOHYD	177	177	N-LINKED (GLCNAC. . .)	(POTENTIAL).
DE	Neural cell adhesion molecule 2 precursor (NCAM 2).	FT	CARBOHYD	219	219	N-LINKED (GLCNAC. . .)	(POTENTIAL).
GN	NCAM2 OR NCAM21.	FT	CARBOHYD	309	309	N-LINKED (GLCNAC. . .)	(POTENTIAL).
OS	Homo sapiens (Human).	FT	CARBOHYD	406	406	N-LINKED (GLCNAC. . .)	(POTENTIAL).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT	CARBOHYD	419	419	N-LINKED (GLCNAC. . .)	(POTENTIAL).
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	FT	CARBOHYD	445	445	N-LINKED (GLCNAC. . .)	(POTENTIAL).
OX	NCBI_TaxID=9606;	FT	CARBOHYD	474	474	N-LINKED (GLCNAC. . .)	(POTENTIAL).
RN	[1]	FT	CARBOHYD	562	562	N-LINKED (GLCNAC. . .)	(POTENTIAL).
RP	SEQUENCE FROM N.A.	SQ	SEQUENCE	837	92932	MW; C3D034106C5741C1	CRC64;
RC	TISSUE=Brain;						
RX	MEDLINE=97369930; PubMed=9226371;						
RA	Paoloni-Giacobino A., Chen H., Antonarakis S.E.;						
RT	"Cloning of a novel human neural cell adhesion molecule gene (NCAM2)						
RT	that maps to chromosome region 21q21 and is potentially involved in						
RT	Down syndrome.";						
RL	Genomics 43:43-51 (1997).						
RN	[2]						
RP	CARBOHYDRATE-LINKAGE SITES ASN-445 AND ASN-562.						
RX	MEDLINE=22660472; PubMed=12754519;						
RA	Zhang H., Li X.-J., Martin D.B., Aebersold R.;						
RT	"Identification and quantification of N-linked glycoproteins using						
RT	hydrazide chemistry, stable isotope labeling and mass spectrometry.";						
RL	Nat. Biotechnol. 21:660-666 (2003).						
CC	-!- FUNCTION: May play important roles in selective fasciculation and						
CC	zone-to-zone projection of the primary olfactory axons.						
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.						
CC	-!- TISSUE SPECIFICITY: Expressed most strongly in adult and fetal						
CC	brain.						
CC	-!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.						
CC	-!- SIMILARITY: Contains 2 fibronectin type III domains.						
CC	-----						
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CC	-----						
DR	EMBL; U75330; AAB80803.1; -.						
DR	Genew; HGNC:7657; NCAM2.						
DR	MIM; 602040; -.						
DR	GO; GO:0016021; C:integral to membrane; TAS.						
DR	GO; GO:0005886; C:plasma membrane; TAS.						
DR	GO; GO:0007158; P:neuronal cell adhesion; TAS.						
DR	InterPro; IPR008957; FN_III-like.						
DR	InterPro; IPR003961; FN_III.						
DR	InterPro; IPR007110; Ig-like.						
DR	InterPro; IPR003598; Ig_c2.						
DR	Pfam; PF00041; fn3; 2.						
DR	Pfam; PF00047; ig; 5.						
DR	SMART; SM00060; FN3; 2.						
DR	SMART; SM00408; IGC2; 5.						
DR	PROSITE; PS50835; IG_LIKE; 5.						
KW	Cell adhesion; Transmembrane; Glycoprotein; Repeat;						
KW	Immunoglobulin domain; Signal.						
FT	SIGNAL	1	19	POTENTIAL.			
FT	CHAIN	20	837	NEURAL CELL ADHESION MOLECULE 2.			
FT	DOMAIN	20	697	EXTRACELLULAR (POTENTIAL).			
FT	TRANSMEM	698	718	POTENTIAL.			
FT	DOMAIN	719	837	CYTOPLASMIC (POTENTIAL).			
FT	DOMAIN	21	108	IG-LIKE C2-TYPE 1.			
FT	DOMAIN	113	202	IG-LIKE C2-TYPE 2.			
FT	DOMAIN	208	297	IG-LIKE C2-TYPE 3.			
FT	DOMAIN	302	396	IG-LIKE C2-TYPE 4.			
FT	DOMAIN	401	491	IG-LIKE C2-TYPE 5.			
FT	DOMAIN	482	581	FIBRONECTIN TYPE-III 1.			
FT	DOMAIN	594	678	FIBRONECTIN TYPE-III 2.			
FT	DISULFID	42	93	PROBABLE.			
FT	DISULFID	136	186	PROBABLE.			
FT	DISULFID	232	281	PROBABLE.			
FT	DISULFID	322	380	PROBABLE.			
FT	DISULFID	422	475	PROBABLE.			

RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
RX MEDLINE=20553141; PubMed=11101850;
RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
RA Hentati F., Fontaine B.;
RT "Perlecan, the major proteoglycan of basement membranes, is altered in
RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";
RL Nat. Genet. 26:480-483(2000).
RN [4]
RP SEQUENCE OF 1016-1470 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [5]
RP SEQUENCE OF 890-1396 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to lp36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [6]
RP SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
RN [7]
RP CARBOHYDRATE-LINKAGE SITE ASN-2121.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes.
CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel
CC syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder
CC characterized by permanent myotonia (prolonged failure of muscle
CC relaxation) and skeletal dysplasia, resulting in reduced stature,
CC kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.
CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 3 laminin IV domains.
CC -!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62515; CAA44373.1; -
DR EMBL; M85289; AAA52700.1; -
DR EMBL; AL445795; CAC18534.1; -
DR EMBL; M64283; AAA52699.1; -
DR EMBL; S76436; AAB21121.2; -
DR EMBL; L22078; -; NOT_ANNOTATED_CDS.
DR PIR; A38096; A38096.
DR HSSP; P00740; 1EDM.
DR Siena-2DPAGE; P98160; -
DR Genew; HGNC:5273; HSPG2.
DR MIM; 142461; -
DR MIM; 255800; -
DR InterPro; IPR008985; ConA_like_lect_gl.
DR InterPro; IPR000742; EGF_2.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003596; Ig_v.
DR InterPro; IPR000034; Laminin_B.
DR InterPro; IPR001791; Laminin_EGF.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000082; SEA_domain.
DR Pfam; PF00008; EGF; 4.
DR Pfam; PF00047; ig; 22.
DR Pfam; PF00052; laminin_B; 3.
DR Pfam; PF00053; laminin_EGF; 7.
DR Pfam; PF00054; laminin_G; 3.
DR Pfam; PF00057; ldl_recept_a; 4.
DR Pfam; PF01390; SEA; 1.
DR PRINTS; PR00261; LDLRECEPTOR.
DR ProDom; PD003031; Laminin_B; 3.
DR SMART; SM00181; EGF; 15.
DR SMART; SM00180; EGF_Lam; 12.
DR SMART; SM00409; IG; 22.
DR SMART; SM00408; IGC2; 21.
DR SMART; SM00406; IGV; 7.
DR SMART; SM00281; LamB; 3.
DR SMART; SM00282; LamG; 3.
DR SMART; SM00192; LDLa; 4.
DR SMART; SM00200; SEA; 1.
DR PROSITE; PS00022; EGF_1; 9.
DR PROSITE; PS01186; EGF_2; 6.
DR PROSITE; PS50026; EGF_3; 4.
DR PROSITE; PS50835; IG_LIKE; 22.
DR PROSITE; PS50025; LAM_G_DOMAIN; 3.
DR PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
DR PROSITE; PS01209; LDLRA_1; 4.
DR PROSITE; PS50068; LDLRA_2; 4.
DR PROSITE; PS50024; SEA; 1.
KW Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; EGF-like domain; Disease mutation.
FT SIGNAL 1 21
FT CHAIN 22 4391
FT
FT DOMAIN 80 194
FT DOMAIN 198 235
FT DOMAIN 284 320
FT DOMAIN 324 360
FT DOMAIN 367 404
FT DOMAIN 405 504
FT DOMAIN 521 530
FT DOMAIN 531 730
FT DOMAIN 731 763
FT DOMAIN 764 813
FT DOMAIN 814 871
FT DOMAIN 879 923
SEA.
LDL-RECEPTOR CLASS A 1.
LDL-RECEPTOR CLASS A 2.
LDL-RECEPTOR CLASS A 3.
LDL-RECEPTOR CLASS A 4.
IG-LIKE C2-TYPE 1.
LAMININ EGF-LIKE 1 (N-TERMINAL).
LAMININ DOMAIN IV 1 (DOMAIN III A).
LAMININ EGF-LIKE 1 (C-TERMINAL).
LAMININ EGF-LIKE 2.
LAMININ EGF-LIKE 3.
LAMININ EGF-LIKE 4 (INCOMPLETE).


```
FT DOMAIN 924 933 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 934 1125 LAMININ DOMAIN IV 2 (DOMAIN III B).
FT DOMAIN 1126 1158 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 1159 1208 LAMININ EGF-LIKE 6.
FT DOMAIN 1209 1265 LAMININ EGF-LIKE 7.
FT DOMAIN 1275 1324 LAMININ EGF-LIKE 8.
FT DOMAIN 1325 1334 LAMININ EGF-LIKE 9 (N-TERMINAL).
FT DOMAIN 1335 1529 LAMININ DOMAIN IV 3 (DOMAIN III C).
FT DOMAIN 1530 1562 LAMININ EGF-LIKE 9 (C-TERMINAL).
FT DOMAIN 1563 1612 LAMININ EGF-LIKE 10.
FT DOMAIN 1613 1670 LAMININ EGF-LIKE 11.
FT DOMAIN 1677 1771 IG-LIKE C2-TYPE 2.
FT DOMAIN 1772 1865 IG-LIKE C2-TYPE 3.
FT DOMAIN 1866 1955 IG-LIKE C2-TYPE 4.
FT DOMAIN 1956 2051 IG-LIKE C2-TYPE 5.
FT DOMAIN 2052 2151 IG-LIKE C2-TYPE 6.
FT DOMAIN 2152 2244 IG-LIKE C2-TYPE 7.
FT DOMAIN 2245 2340 IG-LIKE C2-TYPE 8.
FT DOMAIN 2341 2436 IG-LIKE C2-TYPE 9.
FT DOMAIN 2437 2533 IG-LIKE C2-TYPE 10.
FT DOMAIN 2534 2629 IG-LIKE C2-TYPE 11.
FT DOMAIN 2630 2726 IG-LIKE C2-TYPE 12.

Query Match 11.0%; Score 169.5; DB 1; Length 4391;
Best Local Similarity 23.2%; Pred. No. 2.4e-05;
Matches 69; Conservative 48; Mismatches 128; Indels 53; Gaps 13;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFKNYSLNDATI 60
Db 2942 LDLCNCVVP-GQAHQVTVYKRGG-----SLPARHQTHG-----SQL 2976

QY 61 TLHNIGFSDSGKVICAKVTFPLGNAQSSITVTV-----LVEPTVSLIKGPDSDLIDG 111
Db 2977 RLHLVSPADSGEYVCRAASGPGPEQEAFTVTPPSEGSSYRLRSPVIS-IDPPSSTVQQ 3035

QY 112 GNETVAACIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLPPTFRFARGRI 171
Db 3036 GQD-ASFCKLIHDGAAPISLEWKTRNQELEDNVHISP-NSIIT---IVGTRPSNHGTY 3089

QY 172 TCWKHPALEKDIRYSFI-LDIQYAPEVSVTGYDGNWVFGRKGVLNKNADANPPFKSV 230
Db 3090 RCVASN---AYGVAQSVNLSVHGPTVSVLPBGPVWVKGVKAVTLEC-VSAGEPRSSAR 3145

QY 231 WSRLDG-----QWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGSQSDQKVIYI 282
Db 3146 WTRISSTPAKLEQRYGLMDSHAVLQ-ISSAKPSDAGTYVCLAQNALGTACKQVEVIV 3202
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RESULT 13
MAG_MOUSE
ID MAG_MOUSE STANDARD; PRT; 626 AA.
AC P20317; P16880;
DT 01-AUG-1990 (Rel. 15, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-associated glycoprotein precursor (Siglec-4a).
GN MAG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS L-MAG AND S-MAG).
RX MEDLINE=90121220; PubMed=2482022;
RA Fujita N., Sato S., Kurihara T., Kuwano R., Sakimura K., Inuzuka T.,
RA Takahashi Y., Miyatake T.;
RT "CDNA cloning of mouse myelin-associated glycoprotein: a novel
RT alternative splicing pattern.";
RL Biochem. Biophys. Res. Commun. 165:1162-1169(1989).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM S-MAG).
RC TISSUE=Brain;
RX MEDLINE=91298961; PubMed=1712586;
```

Nakano R., Fujita N., Sato S., Inuzuka T., Sakimura K.,
Ishiguro H., Mishina M., Miyatake T.;
"Structure of mouse myelin-associated glycoprotein gene.";
Biochem. Biophys. Res. Commun. 178:282-290(1991).
[3]
TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX MEDLINE=91366725; PubMed=1716323;
RA Pedraza L., Frey A.B., Hempstead B.L., Colman D.R., Salzer J.L.;
RT "Differential expression of MAG isoforms during development.";
J. Neurosci. Res. 29:141-148(1991).
RN [4]
SIALIC ACID BINDING.
RX MEDLINE=95179521; PubMed=7533044;
RA Kelm S., Pelz A., Schauer R., Filbin M.T., Tang S., de Bellard M.E.,
RA Schnaar R.L., Mahoney J.A., Hartnell A., Bradfield P., Crocker P.R.;
RT "Sialoadhesin, myelin-associated glycoprotein and CD22 define a new
family of sialic acid-dependent adhesion molecules of the
immunoglobulin superfamily.";
Curr. Biol. 4:965-972(1994).
RN [5]
FUNCTION, AND TISSUE SPECIFICITY.
RX MEDLINE=20090811; PubMed=10625334;
RA Schachner M., Bartsch U.;
RT "Multiple functions of the myelin-associated glycoprotein MAG
(siglec-4a) in formation and maintenance of myelin.";
Glia 29:154-165(2000).
RN [6]
INTERACTION WITH RTN4R.
RX MEDLINE=22171378; PubMed=12089450;
RA Liu B.P., Fournier A., GrandPre T., Strittmatter S.M.;
RT "Myelin-associated glycoprotein as a functional ligand for the Nogo-66
receptor.";
Science 297:1190-1193(2002).
CC -!- FUNCTION: Adhesion molecule in postnatal neural development that
mediates sialic acid dependent cell-cell interactions between
neuronal and myelinating cells. Preferentially binds to alpha2,3-
linked sialic acid. Isoform L-MAG is critical for the formation of
myelin in the CNS, whereas isoform S-MAG is sufficient to maintain
the integrity of myelin in PNS.
CC -!- SUBUNIT: Binds to RTN4R.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=2;
Name=L-MAG;
IsoId=P20917-1; Sequence=Displayed;
Name=S-MAG;
IsoId=P20917-2; Sequence=VSP_002527, VSP_002528;
CC -!- TISSUE SPECIFICITY: Expressed by myelinating glial cells in the
central and peripheral nervous system. Detected in oligodendrocyte
processes before formation of compact myelin. Restricted to the
periaxonal space after myelination. Isoform S-MAG is the
predominant isoform in CNS and PNS of the adult.
CC -!- DEVELOPMENTAL STAGE: In CNS isoform L-MAG is the major form
synthesized early in development, and it persists as a significant
proportion of the MAG present in the adult. In the PNS isoform L-
MAG is expressed at modest levels during development; it is absent
in the adult.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
(sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

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EMBL; M31811; AAA39487.1; -;
EMBL; M74793; AAA91743.1; -;
EMBL; M74783; AAA91743.1; JOINED.

DR EMBL; M29273; AAA59545.1; -.
DR EMBL; AC002132; AAB58805.1; -.
DR EMBL; BC053347; AAB53347.1; -.
DR PIR; A61084; A61084.
DR HSP; Q62230; 1QFP.
DR Genew; HGNC:6783; MAG.
DR MIM; 159460; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00408; IGC2; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Palmitate; Lipoprotein.
FT SIGNAL 1 19
FT CHAIN 20 626 MYELIN-ASSOCIATED GLYCOPROTEIN.
FT DOMAIN 20 516 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 517 536 POTENTIAL.
FT DOMAIN 537 626 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 120 IG-LIKE V-TYPE.
FT DOMAIN 139 237 IG-LIKE C2-TYPE 1.
FT DOMAIN 241 325 IG-LIKE C2-TYPE 2.
FT DOMAIN 327 412 IG-LIKE C2-TYPE 3.
FT DOMAIN 413 508 IG-LIKE C2-TYPE 4.
FT DISULFID 37 165 BY SIMILARITY.
FT DISULFID 42 100 BY SIMILARITY.
FT DISULFID 159 217 BY SIMILARITY.
FT DISULFID 261 305 BY SIMILARITY.
FT DISULFID 347 392 BY SIMILARITY.
FT DISULFID 421 430 BY SIMILARITY.
FT DISULFID 432 488 BY SIMILARITY.
FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 223 223 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 406 406 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. .) (POTENTIAL).
FT LIPID 531 531 S-palmitoyl cysteine (By similarity).
SQ SEQUENCE 626 AA; 69068 MW; ED2D36B24F21CAAA CRC64;

Query Match 10.7%; Score 166; DB 1; Length 626;
Best Local Similarity 25.8%; Pred. No. 4.1e-06;
Matches 73; Conservative 40; Mismatches 124; Indels 46; Gaps 14;
Qy 26 SQTAVVHPQYGFVSQGEYQGRV-LFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLG- 83
Db 76 SRTQVVHE-----SFQGRSRLLDGLRNLCTLLSNVSPELGGKYFRG---DLGG 123
Qy 84 -NAQSSTVTVL-VEPTVSLIKGPDLSLDGNETVAAICIAATGKPV--AHIDWEGDLGE 139
Db 124 YNQYTFSEHSVLDIVNTPNIVPPE--VVAGTE-VEVSCMVPDNCPELRPELSWLGHEGL 180
Qy 140 MESTTTSFPNE--TATIIISQYKLPPTFRFARRRITCVVKHPALEKDIRYSFILDIIQYAP 196
Db 181 GEPAVLGRLEDEGTWQVSLHLHFVPTREANGHRLGCGASFNTTLQFEGYASMDVKYPP 240
Qy 197 EV-----SVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLL----ASDN 247
Db 241 VIVEMNSSVEAIEGS-----HVSLLCGADSNPPPLLT-WMR-----DGTVLREAVAES 287
Qy 248 TLHFVHPLTFNYSGVYICKVTNSLQPSDQKVIYISDVPFKQT 290
Db 288 LLELEEVTPAEDGVYACLAENAYGQDNRTVGLSVMYAPWKPT 330

RESULT 15
MAG RAT STANDARD; PRT; 626 AA.
ID MAG RAT
AC P07722; P02685; P07723;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-associated glycoprotein precursor (Siglec-4a) (Brain neuron
DE cytoplasmic protein 3).
GN MAG.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS L-MAG AND S-MAG).
RX MEDLINE=87232001; PubMed=2438699;
RA Lai C., Brow M.A., Nave K.-A., Noronha A.B., Quarles R.H., Bloom F.E.,
RA Milner R.J., Sutcliffe J.G.;
RT "Two forms of 1B236/myelin-associated glycoprotein, a cell adhesion
RT molecule for postnatal neural development, are produced by
RT alternative splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:4337-4341(1987).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM L-MAG).
RX MEDLINE=87092455; PubMed=2432614;
RA Arqunt M., Roder J., Chia L.S., Down J., Wilkinson D., Bayley H.,
RA Braun P., Dunn R.;
RT "Molecular cloning and primary structure of myelin-associated
RT glycoprotein.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:600-604(1987).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM L-MAG).
RX MEDLINE=87166195; PubMed=2435742;
RA Salzer J.L., Holmes W.P., Colman D.R.;
RT "The amino acid sequences of the myelin-associated glycoproteins:
RT homology to the immunoglobulin gene superfamily.";
RL J. Cell Biol. 104:957-965(1987).
RN [4]
RP SEQUENCE OF 309-626 FROM N.A.
RX MEDLINE=84206577; PubMed=6586369;
RA Sutcliffe J.G., Milner R.J., Bloom F.E.;
RT "Cellular localization and function of the proteins encoded by brain-
RT specific mRNAs.";
RL Cold Spring Harb. Symp. Quant. Biol. 48:477-484(1983).
RN [5]
RP SEQUENCE OF 309-626 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=85263773; PubMed=4020419;
RA Bloom F.E., Battenberg E.L.F., Milner R.J., Sutcliffe J.G.;
RT "Immunocytochemical mapping of 1B236, a brain-specific neuronal
RT polypeptide deduced from the sequence of a cloned mRNA.";
RL J. Neurosci. 5:1781-1802(1985).
RN [6]
RP SEQUENCE OF 309-626 FROM N.A.
RX MEDLINE=83259254; PubMed=6347394;
RA Sutcliffe J.G., Milner R.J., Shinnick T.M., Bloom F.E.;
RT "Identifying the protein products of brain-specific genes with
RT antibodies to chemically synthesized peptides.";
RL Cell 33:671-682(1983).
RN [7]
RP DISULFIDE BONDS, PALMITOYLATION, AND PARTIAL SEQUENCE.
RX MEDLINE=91115956; PubMed=1703542;
RA Pedraza L., Owens G.C., Green L.A.D., Salzer J.L.;
RT "The myelin-associated glycoproteins: membrane disposition, evidence
RT of a novel disulfide linkage between immunoglobulin-like domains, and
RT posttranslational palmitylation.";
RL J. Cell Biol. 111:2651-2661(1990).
CC -|- FUNCTION: Adhesion molecule in postnatal neural development that
CC mediates sialic-acid dependent cell-cell interactions between
CC neuronal and myelinating cells. Preferentially binds to alpha2,3-
CC linked sialic acid (By similarity).
CC -|- SUBUNIT: Binds to RTN4R (By similarity).
CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
CC -|- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=L-MAG;
CC IsoId=P07722-1; Sequence=Displayed;
CC Name=S-MAG;

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 23.715 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-10_COPY_74_365
Perfect score: 1546
Sequence: 1 VSLKCLIEVNETITQISWEK.....QRSDQKVIYISDVPFKQTSS 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1512	97.8	549	4	Q9NQS3	Q9nqs3 homo sapien
2	1500	97.0	438	11	Q9JLB7	Q9jlb7 mus musculu
3	1500	97.0	510	11	Q9JLB8	Q9jlb8 mus musculu
4	1479	95.7	549	11	Q9JLB9	Q9jlb9 mus musculu
5	1435	92.8	549	11	Q9D006	Q9d006 mus musculu
6	1149	74.3	407	4	Q9Y412	Q9y412 homo sapien
7	1128	73.0	267	4	Q8NC05	Q8nc05 homo sapien
8	620	40.1	304	4	Q9BVA9	Q9bva9 homo sapien
9	533	34.5	295	11	Q9ERF5	Q9erf5 mesocrictetu
10	526.5	34.1	298	6	Q9GL74	Q9gl74 cercopithec
11	526	34.0	295	6	Q9GL75	Q9gl75 bos taurus
12	450.5	29.1	510	4	Q96NY8	Q96ny8 homo sapien
13	450.5	29.1	510	4	Q96K15	Q96k15 homo sapien
14	432.5	28.0	483	11	Q9DBP8	Q9dbp8 mus musculu
15	432.5	28.0	508	11	Q8R007	Q8r007 mus musculu
16	432.5	28.0	508	11	Q8CED8	Q8ced8 mus musculu

17	409	26.5	467	11	Q91VT9	Q91vt9 mus musculu
18	409	26.5	467	11	Q8C6F2	Q8c6f2 mus musculu
19	403	26.1	530	11	Q80XJ5	Q80xj5 mus musculu
20	392	25.4	449	4	Q9UEI6	Q9uei6 homo sapien
21	383	24.8	412	11	Q9RIE1	Q9riel rattus norv
22	378	24.5	412	11	Q63611	Q63611 rattus norv
23	376.5	24.4	400	6	Q8HY16	Q8hy16 cebus apell
24	371.5	24.0	417	4	Q96BJ1	Q96bj1 homo sapien
25	369.5	23.9	403	6	Q8HY15	Q8hy15 lemur catta
26	361	23.4	408	11	Q91WP1	Q91wp1 mus musculu
27	359.5	23.3	401	6	Q08835	Q08835 cercopithec
28	359	23.2	408	11	Q8K094	Q8k094 mus musculu
29	358	23.2	408	11	Q8BVF6	Q8bvf6 mus musculu
30	334.5	21.6	412	6	Q8HY14	Q8hy14 oryctolagus
31	328	21.2	415	11	Q60977	Q60977 mus musculu
32	257.5	16.7	442	4	Q9BY67	Q9by67 homo sapien
33	255.5	16.5	445	11	Q8K3T6	Q8k3t6 mus musculu
34	255.5	16.5	445	11	Q8R4L1	Q8r4l1 mus musculu
35	255.5	16.5	456	11	Q8R5M8	Q8r5m8 mus musculu
36	254.5	16.5	394	13	Q7ZXX1	Q7zxx1 xenopus lae
37	253.5	16.4	443	4	Q8N2F4	Q8n2f4 homo sapien
38	250.5	16.2	417	11	Q7TNL1	Q7tnl1 mus musculu
39	249.5	16.1	333	4	Q86WB8	Q86wb8 homo sapien
40	246.5	15.9	336	11	Q9D6E7	Q9d6e7 mus musculu
41	246.5	15.9	336	11	Q80VG4	Q80vg4 mus musculu
42	235.5	15.2	800	5	Q86LF9	Q86lf9 drosophila
43	235.5	15.2	801	5	Q86LF8	Q86lf8 drosophila
44	212.5	13.7	551	5	Q8MSN7	Q8msn7 drosophila
45	212.5	13.7	956	5	Q9W4T9	Q9w4t9 drosophila

ALIGNMENTS

RESULT 1

Q9NQS3 PRELIMINARY; PRT; 549 AA.
AC Q9NQS3;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;

Query Match 97.8%; Score 1512; DB 4; Length 549;
Best Local Similarity 98.6%; Pred. No. 7.6e-126;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy	1	VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSGVQGEYQGRVLFKNYSLNDATI	60
Db	74	VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSGVQGEYQGRVLFKNYSLNDATI	133
Qy	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC	120
Db	134	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC	193

QY	121	IAATGKPVAHIDWEGDLGWESTTTTFPNETATIISQYKLFPTRFARGRRITCVWKHPAL	180
D6	194	IAATGKPVAHIDWEGDLGWESTTTTFPNETATIISQYKLFPTRFARGRRITCVWKHPAL	253
QY	181	EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVLNKCNDADANPPFKSVWSRLDGQWPD	240
D6	254	EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVLNKCNDADANPPFKSVWSRLDGQWPD	313
QY	241	GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSDDQVIYIISDVPPKQT	290
D6	314	GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSDDQVIYIISDPPTTTT	363

RESULT 2

Q9JLB7 PRELIMINARY; PRT; 438 AA.
Q9JLB7;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Cell adhesion molecule nectin-3 gamma.
PVRL3.
Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities.";
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195835; AAF63687.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;

RESULT 3

Q9JLB8	PRELIMINARY;	PRT;	510 AA.
AC	Q9JLB8;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Cell adhesion molecule nectin-3 beta.		
GN	PVRL3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20209403; PubMed=10744716;		
RA	SatoH-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,		
RA	Tachibana K., Mizoguchi A., Takai Y.;		
RT	"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules		
RT	that shows homophilic and heterophilic cell-cell adhesion		
RT	activities.";		
RL	J. Biol. Chem. 275:10291-10299 (2000).		
DR	EMBL; AF195834; AAF63686.1; --		
DR	MGI; MGI:1930171; Pvrl3.		
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.		
DR	GO; GO:0005194; F:cell adhesion molecule activity; IDA.		
DR	GO; GO:0005515; F:protein binding; IPI.		
DR	GO; GO:0007155; P:cell adhesion; IDA.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	Pfam; PF00047; ig; 2.		
DR	SMART; SM00409; IG; 1.		
DR	PROSITE; PS50835; IG_LIKE; 3.		
SO	SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;		

RESULT 4

Q9JLB9	PRELIMINARY;	PRT;	549 AA.
ID Q9JLB9			
AC Q9JLB9;			
DT 01-OCT-2000	(TREMBLrel. 15, Created)		
DT 01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)		
DE	Cell adhesion molecule nectin-3 alpha.		
GN	PVRL3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae		
OX	NCBI TaxID=10090;		


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RN
RP SEQUENCE FROM N.A.
RX MEDLINE=20209403; PubMed=10744716;
RA Satoh-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
RA Tachibana K., Mizoguchi A., Takai Y.;
RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
RT that shows homophilic and heterophilic cell-cell adhesion
RT activities."
RL J. Biol. Chem. 275:10291-10299(2000).
DR EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;

Query Match 95.7%; Score 1479; DB 11; Length 549;
Best Local Similarity 95.2%; Pred. No. 6.6e-123;
Matches 276; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFSGVQGEYQGRVLFKNYSLNDATI 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
74 VSLKCLIEVNETITQISWEKIHGKSTQTAVVHHHPQYGFSGVQGDYQGRVLFKNYSLNDATI 133
QY 61 TLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAIC 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
134 TLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAVC 193
QY 121 IAATGKPVVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
194 VAATGKPVQAIDWEGDLGEMESTTSPNETATIVSQYKLFPTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGNLKNADANPPPFKSVWSRLDGOWPD 240
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGNLKNADANPPPFKSVWSRLDGOWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYCKVTNSLQSRSDQKVIYISDVPEKQT 290
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
314 GLLASDNTLHFVHPLTFNYSGVYCKVTNSLQSRSDQKVIYISDPPTTTT 363

RESULT 5
Q9D006 PRELIMINARY; PRT; 549 AA.
ID Q9D006
AC Q9D006;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 2610301B19Rik protein.
GN PVRL3 OR 2610301B19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryo;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaudo I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
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RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1930171; Pvr13.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;

Query Match 92.8%; Score 1435; DB 11; Length 549;
Best Local Similarity 92.4%; Pred. No. 5.4e-119;
Matches 268; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHHPQYGFSGVQGEYQGRVLFKNYSLNDATI 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
74 VSLKCLIEVNETITQISWEKIHGKSTQTAVVHHHPQYGFSGVQGDYQGRVLFKNYSLNDATI 133
QY 61 TLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAIC 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
134 TLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSSIDGGNETVAAVC 193
QY 121 IAATGKPVVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
194 VSSTGKPVQAIDWEGDLGEREFSTISFLNETATIVSQYELFPTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGNLKNADANPPPFKSVWSRLDGOWPD 240
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGNLKNADANPPPFKSVWSRLDGOWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYCKVTNSLQSRSDQKVIYISDVPEKQT 290
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
314 GLLASDNTLHFVHPLTFNYSGVYCKVTNSLQSRSDQKVIYISDPPTTTT 363

RESULT 6
Q9Y412 PRELIMINARY; PRT; 407 AA.
ID Q9Y412
AC Q9Y412;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP566B0846.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
FT NON_TER 1
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SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;

Query Match 74.3%; Score 1149; DB 4; Length 407;
Best Local Similarity 98.2%; Pred. No. 1e-93;
Matches 217; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 70 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKPPVA 129
Db 1 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKPPVA 60

QY 130 HIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRRITCVVXHPALEKDIYSEFI 189
Db 61 HIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRRITCVVXHPALEKDIYSEFI 120

QY 190 LDIQYAPEVSVTGYDGNWFGVGRKGNLKCNDANANPPPFKSVWSRLDGQWPDGLLASDNTL 249
Db 121 LDIQYAPEVSVTGYDGNWFGVGRKGNLKCNDANANPPPFKSVWSRLDGQWPDGLLASDNTL 180

QY 250 HFVHPLTFNYSVGYVICKVTNSLQSRSDQKVIYISDVPFKQT 290
Db 181 HFVHPLTFNYSVGYVICKVTNSLQSRSDQKVIYISDVPFKQT 221

RESULT 7

Q8NC05 PRELIMINARY; PRT; 267 AA.

AC Q8NC05; Score 1149; DB 4; Length 407;
Best Local Similarity 98.2%; Pred. No. 1e-93;
Matches 217; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human CDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075105; BAC11404.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;

Query Match 73.0%; Score 1128; DB 4; Length 267;
Best Local Similarity 99.5%; Pred. No. 4.1e-92;
Matches 216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVHHPQYGFSGVQGEYQGRVLFKNYSLNDATI 60
Db 51 VSLKCLIEVNETITQISWEKIHGKSSQTAVHHPQYGFSGVQGEYQGRVLFKNYSLNDATI 110

QY 61 TLHNTGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 111 TLHNTGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 170

QY 121 IATGKPPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRRITCVVXHPAL 180
Db 171 IATGKPPVAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRRITCVVXHPAL 230

QY 181 EKDRIYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANANPPPFKSVWSRLDGQWPDGLLASDNTL 217
Db 231 EKDRIYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANANPPPFKSVWSRLDGQWPDGLLASDNTL 267

RESULT 8

Q9BVA9 PRELIMINARY; PRT; 304 AA.

AC Q9BVA9; Score 620; DB 4; Length 304;
Best Local Similarity 96.6%; Pred. No. 7.8e-47;
Matches 114; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Similar to nectin 3, DKFZP566B0846 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG-LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 304 AA; 34826 MW; 8BEACF94A6BA745 CRC64;

QY 173 CVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANANPPPFKSVWS 232
Db 1 CVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKCNDANANPPPFKSVWS 60

QY 233 RLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISDVPFKQT 290
Db 61 RLDGQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISDVPFKQT 118

RESULT 9

Q9ERF5 PRELIMINARY; PRT; 295 AA.

AC Q9ERF5; Score 533; DB 11; Length 295;
Best Local Similarity 39.4%; Pred. No. 4.1e-39;
Matches 109; Conservative 56; Mismatches 104; Indels 8; Gaps 5;

DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
DR EMBL; AF308634; AAG30283.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
FT NON_TER 1
FT NON_TER 295
SQ SEQUENCE 295 AA; 33112 MW; 03E5C4DCB5032E7F CRC64;

Query Match 34.5%; Score 533; DB 11; Length 295;
Best Local Similarity 39.4%; Pred. No. 4.1e-39;
Matches 109; Conservative 56; Mismatches 104; Indels 8; Gaps 5;

QY 13 ITQISWEKIHGSSQTAVVHHPQYGFSGVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGK 72
Db 21 ITQVTWQKATNGSKQNMAIYNPTMGVSVLPPYKRVFLRPSFIDGTIRLSHLEDEGM 80
QY 73 YICKAVTEPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDG---GNETVAAICIAATGKPV 128
Db 81 YICEFATFPGNRESQNLNLTVMKPT-NWIEGTQAVLRARKGQDDKVVVATCTSANGKPP 139
QY 129 AHIDWEGDL-GEMESTTSPNETATIIISQYKLPFTRFARRRITCVVKHPALEKDIRYS 187
Db 140 SVVSWETRLKGEABYQEIRPNPNTGTVVISRYRLVPSREAHQSLACIVNY-HLDR-FRES 197
QY 188 FILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPFKSVMSRLDGQWPDGLLASDN 247
Db 198 LTLNVQYEPEVTIEGFDGNWYLRQTDVXLTCKADANPPATEYHWTTLNGLSLPKGVEAQR 257
QY 248 TLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 284
Db 258 TLFFRGPIINYSLAGTYICEATNPIGTRSGQVEVNITE 294

RESULT 10
Q9GL74
ID Q9GL74 PRELIMINARY; PRT; 298 AA.
AC Q9GL74;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
DR EMBL; AF308635; AAG30284.1; -.
DR InterPro; IPR003599; IG.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 298
FT NON_TER 298
SQ SEQUENCE 298 AA; 33309 MW; AEA41842B8CA200 CRC64;

Query Match 34.1%; Score 526.5; DB 6; Length 298;
Best Local Similarity 38.6%; Pred. No. 1.6e-38;
Matches 108; Conservative 55; Mismatches 106; Indels 11; Gaps 5;
QY 13 ITQISWEKI---HGKSSQTAVVHHPQYGFSGVQGEYQGRVLFKNYSLNDATITLHNIGFSD 69
Db 21 ITQVTWQKITQATNGSKQNVAIYNPMSMGVSVLAPYRERVEFLRPSFTDGTIRLSRLEED 80
QY 70 SGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDG---GNETVAAICIAATG 125
Db 81 EGVYICEFATFPTGNRESQNLNLTVMKPT-NWIEGTQAVLRARKGQDDKVLVATCTSANG 139
QY 126 KPAHAIDWEGDL-GEMESTTSPNETATIIISQYKLPFTRFARRRITCVVKHPALEKDI 184
Db 140 KPSPVSVWETRLKGEABYQEIRPNPNTGTVVISRYRLVPSREAHQSLACIVNHYM--DRF 197
QY 185 RYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPFKSVMSRLDGQWPDGLLA 244
Db 198 KESLTINVQYEPEVTIEGFDGNWYLRQMDVKLTCKADANPPATEYHWTTLNGLSLPKGVEA 257

QY 245 SDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 284
Db 258 QNRILFEKGPISYSLAGTYICEATNPIGTRSGQVEVNITE 297
RESULT 11
Q9GL75
ID Q9GL75 PRELIMINARY; PRT; 295 AA.
AC Q9GL75;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
DR EMBL; AF308633; AAG30282.1; -.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON_TER 1
FT NON_TER 295
SQ SEQUENCE 295 AA; 33082 MW; 7C35D64022146AFA CRC64;

Query Match 34.0%; Score 526; DB 6; Length 295;
Best Local Similarity 39.8%; Pred. No. 1.7e-38;
Matches 111; Conservative 53; Mismatches 103; Indels 12; Gaps 7;
QY 13 ITQISWEKIHGSSQTAVVHHPQYGFSGVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGK 72
Db 21 ITQVTWQKATNGSKQNVAIYNPAMGVSVLAPYRERVEFLRPSFTDGTIRLSRLEDEGV 80
QY 73 YICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSLI---DGGNETV-AAICIAATGKPV 128
Db 81 YICEFATFPAAGNRESQNLNLTVMKPT-NWIEGTHAVLRARKGQDEKVLVATCTSANGKPP 139
QY 129 AHIDWEGDL-GEMESTTSPNETATIIISQYKLPFTRFARRRITCVVKHPALEKDIRY- 186
Db 140 SVVSWETRLKGEABYQEIRPNPNTGTVVISRYRLVPSREAHQSLACIVNY---HMD-RFW 195
QY 187 -SFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPFKSVMSRLDGQWPDGLLAS 245
Db 196 ESILTINVQYEPEVTIEGFDGNWYLRQMDVKLTCKADANPPATEYHWTTLNGLSLPKGVEAQ 255
QY 246 DNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 284
Db 256 NRTLFFRGPIINYSLAGTYICEATNPIGTRSGQVEVNITE 294

RESULT 12
Q96NY8
ID Q96NY8 PRELIMINARY; PRT; 510 AA.
AC Q96NY8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Nectin 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RT "Nectin4/PRR4: A new afadin-associated member of the nectin family
RT that trans-interacts with nectin1/PRR1 through V domain interaction.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF426163; AAL23958.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 510 AA; 55454 MW; DCF5E1D794F227FA CRC64;

Query Match 29.1%; Score 450.5; DB 4; Length 510;
Best Local Similarity 35.5%; Pred. No. 1.9e-31;
Matches 99; Conservative 55; Mismatches 116; Indels 9; Gaps 7;

QY 11 ETITQISWEKIH-GKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLN--DATITLHNIGF 67
Db EQVGQVAWARVDAGEGAQELALLHSKYGLHVSAPAYEGRVEQPPPNPLDGSVLLRNAVQ 119

QY 68 SDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKP 127
Db ADEGEYECRVSTFPAGSFQARLRRLRVLPPLPSLNPGP-ALEEGQGLTLAASC-TAEGSP 177

QY 128 VAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRRITCVVXHPALEKDIRYS 187
Db APSVTWDTVEKGTSSRSFKHSRSAAVTSEFHLVPSRMNGQPLTCVVSHPGLLQDQRIT 237

QY 188 FILDIOQYAPEVSVTGYDGN--WFGVRKGVNLKCNADANPPPKSVWSRLDGQWPDGLLAS 245
Db HILHVSFLAEASVRGLEQDNLWHIGREGAMLKCLSEGQPPPSYN-WTRLDGPLPSGVRVD 296

QY 246 DNTLHFVHPLTFNYSYGVYICKVTNSLQSRSDQKVIYISD 284
Db GDTLGF-PPLTTEHSGIYVCHVSNEFSRDSQVTVDVLD 334

RESULT 13
Q96K15
ID Q96K15 PRELIMINARY; PRT; 510 AA.
AC Q96K15;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ14847.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027753; BAB55344.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 510 AA; 55382 MW; 9B68CD50F086429E CRC64;

Query Match 29.1%; Score 450.5; DB 4; Length 510;
Best Local Similarity 35.5%; Pred. No. 1.9e-31;
Matches 99; Conservative 55; Mismatches 116; Indels 9; Gaps 7;

QY 11 ETITQISWEKIH-GKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLN--DATITLHNIGF 67
Db EQVGQVAWARVDAGEGAQELALLHSKYGLHVSAPAYEGRVEQPPPNPLDGSVLLRNAVQ 119

QY 68 SDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKP 127
Db ADEGEYECRVSTFPAGSFQARLRRLRVLPPLPSLNPGP-ALEEGQGLTLAASC-TAEGSP 177

QY 128 VAHIDWEGDLGEMESTTSPNETATIIISQYKLPFTRFARGRRITCVVXHPALEKDIRYS 187
Db APSVTWDTVEKGTSSRSFKHSRSAAVTSEFHLVPSRMNGQPLTCVVSHPGLLQDQRIT 237

QY 188 FILDIOQYAPEVSVTGYDGN--WFGVRKGVNLKCNADANPPPKSVWSRLDGQWPDGLLAS 245
Db HILHVSFLAEASVRGLEQDNLWHIGREGAMLKCLSEGQPPPSYN-WTRLDGPLPSGVRVD 296

QY 246 DNTLHFVHPLTFNYSYGVYICKVTNSLQSRSDQKVIYISD 284
Db GDTLGF-PPLTTEHSGIYVCHVSNEFSRDSQVTVDVLD 334

RESULT 14
Q9DBP8
ID Q9DBP8 PRELIMINARY; PRT; 483 AA.
AC Q9DBP8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 1200C17F15Rik protein.
GN PVRL4 OR 1200017F15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK004821; BAB23592.1; -.
DR MGD; MGI:1918990; Pvrl4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 483 AA; 53030 MW; F8F0466C000852E8 CRC64;

Query Match 28.0%; Score 432.5; DB 11; Length 483;

Best Local Similarity 34.7%; Pred. No. 7.2e-30;
Matches 102; Conservative 52; Mismatches 115; Indels 25; Gaps 9;

QY 10 NETITQISWEKIH-GKSSQTVAVHHPQYGFVSQGEYQGRV-----LFKNYSLNDA 59
Db 58 DEQVGQVAVARVDPNEGIRELALLHSKYGLHVNPAVEDRVEQPPPRDPL-----DGS 110

QY 60 ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAI 119
Db 111 VLLRNAVQADEGEYECRVSTFPAGSFQARMRLRVLPPLPSLNPGP-PLIEGQGLTLAAS 169

QY 120 CIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPA 179
Db 170 C-TAEGSPAPSVTWDTEVKGTQSSRSFTHPRSAAVTSEFHLVPSRSMNGQPLTCVVSHPG 228

QY 180 LEKDIRYSFILDIOYAPEVSVTYDGN--WFGVRKGVNLCNADANPPPFKSVWSRLDQG 237
Db 229 LLQDRRITHTLQVAFLAASVRGLEQNLWQVREGATLKCLSEGQPPP-KYNWTRLDGP 287

QY 238 WPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDV--PFKQ 289
Db 288 LPSGVRVKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQVTVEVLDPEDPGKQ 340

RESULT 15

Q8R007 PRELIMINARY; PRT; 508 AA.

AC Q8R007;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to poliovirus receptor-related 4 (Nectin 4).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21560925; PubMed=11544254;
RA Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RT "Nectin4/PRR4, a new afadin-associated member of the nectin family
RT that trans-interacts with nectini/PRR1 through V domain interaction.";
RL J. Biol. Chem. 276:43205-43215(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Reymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC024948; AAH24948.1; --
DR EMBL; AF472510; AAL79833.1; --
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 508 AA; 55657 MW; 24DAEBD21F22E376 CRC64;

Query Match 28.0%; Score 432.5; DB 11; Length 508;
Best Local Similarity 34.7%; Pred. No. 7.7e-30;
Matches 102; Conservative 52; Mismatches 115; Indels 25; Gaps 9;

QY 10 NETITQISWEKIH-GKSSQTVAVHHPQYGFVSQGEYQGRV-----LFKNYSLNDA 59
Db 58 DEQVGQVAVARVDPNEGIRELALLHSKYGLHVNPAVEDRVEQPPPRDPL-----DGS 110

QY 60 ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAI 119
Db 111 VLLRNAVQADEGEYECRVSTFPAGSFQARMRLRVLPPLPSLNPGP-PLIEGQGLTLAAS 169

QY 120 CIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPA 179
Db 170 C-TAEGSPAPSVTWDTEVKGTQSSRSFTHPRSAAVTSEFHLVPSRSMNGQPLTCVVSHPG 228

QY 180 LEKDIRYSFILDIOYAPEVSVTYDGN--WFGVRKGVNLCNADANPPPFKSVWSRLDQG 237
Db 229 LLQDRRITHTLQVAFLAASVRGLEQNLWQVREGATLKCLSEGQPPP-KYNWTRLDGP 287

QY 238 WPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDV--PFKQ 289
Db 288 LPSGVRVKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQVTVEVLDPEDPGKQ 340

Search completed: April 12, 2004, 09:45:10
Job time : 23.715 secs

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 35.2664 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-10_COPY_74_365
Perfect score: 1546
Sequence: 1 VSLKCLIEVNETITQISWEK.....QRSDQKVIYISDVPFKQTSS 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query Match		Score	Length	DB ID	Description
	Match	%				
1	1546	100.0	387	5	AAE23290	Aae23290 Human nec
2	1546	100.0	437	5	AAE23299	Aae23299 Human nec
3	1546	100.0	504	5	AAE23284	Aae23284 Human del
4	1546	100.0	510	5	AAE23285	Aae23285 Mouse nec
5	1546	100.0	510	5	AAE23286	Aae23286 Human nec
6	1546	100.0	595	5	AAE23288	Aae23288 Human nec
7	1512	97.8	426	5	AAE23289	Aae23289 Human nec
8	1512	97.8	542	5	AAE23281	Aae23281 Human del
9	1512	97.8	549	5	AAE23283	Aae23283 Human nec
10	1512	97.8	549	5	AAE23282	Aae23282 Mouse nec
11	1512	97.8	549	6	ABJ20222	Abj20222 Human IG
12	1512	97.8	555	4	AAM39143	Aam39143 Human pol
13	1512	97.8	634	5	AAE23287	Aae23287 Human nec
14	1500	97.0	438	4	AAG63984	Aag63984 Amino aci
15	1500	97.0	438	5	AAE23293	Aae23293 Mouse nec
16	1500	97.0	510	4	AAG63983	Aag63983 Amino aci
17	1500	97.0	510	5	AAE23292	Aae23292 Mouse nec
18	1479	95.7	549	4	AAG63982	Aag63982 Amino aci
19	1479	95.7	549	4	AAG63985	Aag63985 Amino aci
20	1479	95.7	549	5	AAE23291	Aae23291 Mouse nec
21	1444.5	93.4	559	4	AAM40929	Aam40929 Human pol
22	1128	73.0	267	4	AAM93536	Aam93536 Human pol
23	540	34.9	514	6	ABJ20237	Abj20237 Human IG
24	540	34.9	517	3	AAY32390	Aay32390 Herpesvir
25	540	34.9	517	5	AAE23294	Aae23294 Human nec

26	537	34.7	458	5	AAE23295	Aae23295 Human nec
27	517.5	33.5	518	5	ABG77170	Abg77170 Prostate
28	450.5	29.1	497	5	AAE23303	Aae23303 Human nec
29	450.5	29.1	510	4	AAB93365	Aab93365 Human pro
30	450.5	29.1	510	4	AAU00471	Aau00471 Human TAN
31	450.5	29.1	510	5	ABJ05562	Abj05562 Breast ca
32	450.5	29.1	510	6	ABJ20232	Abj20232 Human IG
33	450.5	29.1	510	6	ABR48229	Abri48229 Human bla
34	450.5	29.1	510	6	ABU56613	Abu56613 Lung canc
35	450.5	29.1	510	6	ABP97212	Abp97212 Tumour-as
36	450.5	29.1	510	7	ADB80512	Adb80512 Ovarian c
37	448.5	29.0	510	5	AAE23300	Aae23300 Human nec
38	448.5	29.0	510	6	ABJ20231	Abj20231 Human IG
39	446.5	28.9	498	5	AAE23305	Aae23305 Human nec
40	446.5	28.9	511	5	AAE23301	Aae23301 Human nec
41	446.5	28.9	580	5	AAE23302	Aae23302 Human nec
42	392	25.4	479	3	AAY32389	Aay32389 Herpesvir
43	392	25.4	479	5	AAE23296	Aae23296 Human nec
44	392	25.4	479	6	ABJ20239	Abj20239 Human IG
45	392	25.4	538	5	AAE23297	Aae23297 Human nec

ALIGNMENTS

RESULT 1
AAE23290
ID AAE23290 standard; protein; 387 AA.
XX
AC AAE23290;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta-FLAGpolyHis fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.

Key	Location/Qualifiers
Region	1..365
Region	/note= "Human nectin-3alpha protein"
Region	366..381
Region	/note= "FLAG peptide"
Region	382..387
Region	/note= "PolyHis tag"
WO200228902-A2.	
11-APR-2002.	
05-OCT-2001; 2001WO-US031392.	
05-OCT-2000; 2000US-0238557P.	
(IMMV) IMMUNEX CORP.	
Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;	
WPI; 2002-426103/45.	
Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, sepsis, stroke.	
Claim 9; Page 105-107; 141pp; English.	

```
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta-
CC FLAGpolyHis fusion protein
XX
SQ Sequence 387 AA;
Query Match 100.0%; Score 1546; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 5.3e-132;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSS 365
RESULT 2
AAE23299
ID AAE23299 standard; protein; 437 AA.
XX
AC AAE23299;
XX
XX 27-AUG-2002 (first entry)
XX
DE Human nectin-3gamma protein.
XX
KW Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
XX WO200228902-A2.
XX
XX 11-APR-2002.
XX
PD 05-OCT-2001; 2001WO-US031392.
XX
PF
XX 05-OCT-2000; 2000US-0238557P.
PR
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XX (IMMV ) IMMUNEX CORP.
XX PA
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37450.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX sepsis, stroke.
XX
XX Claim 1; Page 125-126; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
XX gamma and nectin-4 polypeptides and their corresponding polynucleotides.
XX Nectin DNA and protein are useful for treating a disease associated with
XX cell adhesion activity, adherens junction formation activity, epithelial
XX or endothelial barrier function activity, endothelial proliferation or
XX migration activity, viral polypeptide binding activity. The epithelial or
XX endothelial barrier function disorder which is treated by the above
XX mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
XX asthma, allergy, allograft rejection, metastasis of cancer cells,
XX paracellular transport disorders such as magnesium transport defects in
XX the kidney or inflammatory bowel disease. Nectin DNA is also useful for
XX inhibiting angiogenesis in a mammal and treating endothelial migration,
XX proliferation or angiogenic condition of a tissue or a subject, such as
XX ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
XX stroke, restenosis, tumour growth and treating herpesvirus infection.
XX Nectin is also useful for modulating proliferation or migration of an
XX endothelial cell, an epithelial cell or a smooth muscle cell (vascular
XX smooth muscle cell). The present sequence is human nectin-3gamma protein.
XX Human nectin-3gamma gene is located on chromosome 3
XX
SQ Sequence 437 AA;
Query Match 100.0%; Score 1546; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 6.2e-132;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSGVQGEYQGRVLFKNYSLNDAI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSS 365
RESULT 3
AAE23284
ID AAE23284 standard; protein; 504 AA.
XX
XX AAE23284;
XX
XX 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3beta protein.
XX
XX Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
```


KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX WO200228902-A2.
PN
XX
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMV) IMMUNEX CORP.
PA Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37443.
DR
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 89-91; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX
SQ Sequence 504 AA;

Query Match 100.0%; Score 1546; DB 5; Length 504;
Best Local Similarity 100.0%; Pred. NO. 7.6e-132;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db |||||
68 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 127
||
Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDSDLIDGNETVAAIC 120
Db |||||
128 TLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDSDLIDGNETVAAIC 187
||
Qy 121 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFARGRRITCVVKHPAL 180
Db |||||
188 IAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFARGRRITCVVKHPAL 247
||
Qy 181 EKDIRYSFILDIOYAPEVSVTYDGNWFVGRKGVNLCNADANPPPKSVWSRLDGQWPD 240
Db |||||
248 EKDIRYSFILDIOYAPEVSVTYDGNWFVGRKGVNLCNADANPPPKSVWSRLDGQWPD 307
||
Qy 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIIYISDVPFKQTSS 292

Db 308 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIIYISDVPFKQTSS 359
|||||
RESULT 4
AAE23285
ID AAE23285 standard; protein; 510 AA.
XX
AC AAE23285;
XX
DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin-3beta fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..6
FT /note= "Mouse nectin-3 pprotein"
FT Region 7..510
FT /note= "Human nectin-3beta protein"
FT
FT
XX WO200228902-A2.
XX 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37444.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 94-95; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.

CC	(Updated on 29-AUG-2003 to standardise OS field)					
XX						
SQ	Sequence	510	AA;			
	Query Match	100.0%;	Score 1546;	DB 5;	Length 510;	
	Best Local Similarity	100.0%;	Pred. No. 7.7e-132;			
	Matches 292;	Conservative	0;	Mismatches	0;	
				Indels	0;	
				Gaps	0;	
QY	1	VSLKCLIEVN	ETITQISWEKIHGSSQTVA	VHHPQGF	SVQGEYQGRVLFKNYS	LNDATI 60
Db	74	VSLKCLIEVN	ETITQISWEKIHGSSQTVA	VHHPQGF	SVQGEYQGRVLFKNYS	LNDATI 133
QY	61	TLHNIGFSD	SGKYICKAVTFPLGNAQ	SSTTVTVLVEPTVSLIKG	PDSLIDGNETVAAIC	120
Db	134	TLHNIGFSD	SGKYICKAVTFPLGNAQ	SSTTVTVLVEPTVSLIKG	PDSLIDGNETVAAIC	193
QY	121	IAATGKPV	AHIDWEGDLGEMESTT	TFPNETATIISQYKLP	PTTRFARGRRITCVVKHPAL	180
Db	194	IAATGKPV	AHIDWEGDLGEMESTT	TFPNETATIISQYKLP	PTTRFARGRRITCVVKHPAL	253
QY	181	EKDIRYS	FILDIQYAPEVSV	TGYDGNW	FVGRKGVNLKCNADANPP	PFKSVWSRLDGQWPD 240
Db	254	EKDIRYS	FILDIQYAPEVSV	TGYDGNW	FVGRKGVNLKCNADANPP	PFKSVWSRLDGQWPD 313
QY	241	GLLASD	NTLHFVHPLTFNYS	GVYICKVTNSLQ	RSDQKVIYISDVVPFKQTSS	292
Db	314	GLLASD	NTLHFVHPLTFNYS	GVYICKVTNSLQ	RSDQKVIYISDVVPFKQTSS	365

RESULT 5	
AAE23286	
ID	AAE23286 standard; protein; 510 AA.
XX	
XX	
AC	AAE23286;
XX	
DT	27-AUG-2002 (first entry)
XX	
DE	Human nectin-3beta protein.
XX	
KW	Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW	paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW	allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW	oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW	stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX	
OS	Homo sapiens.

Key	Location/Qualifiers
Modified-site	73
Domain	/note= "N-glycosylated"
Domain	74..152
Domain	/note= "Extracellular Ig domain"
Modified-site	83
Domain	/note= "N-glycosylated"
Modified-site	125
Domain	/note= "N-glycosylated"
Modified-site	186
Domain	/note= "N-glycosylated"
Domain	189..250
Domain	/note= "Extracellular Ig domain"
Modified-site	222
Domain	/note= "N-glycosylated"
Domain	287..342
Domain	/note= "Extracellular Ig domain"
Modified-site	331
Domain	/note= "N-glycosylated"
Domain	386..510
Domain	/note= "Intracellular C-terminal domain"

XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX

05-OCT-2001; 2001WO-US031392.
05-OCT-2000; 2000US-0238557P.
(IMMV) IMMUNEX CORP.
Baum ER, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
WPI; 2002-426103/45.
N-PSDB; AAD37445.
Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
sepsis, stroke.
Claim 1; Page 98-99; 141pp; English.
The invention relates to a substantially purified nectin3alpha, beta,
gamma and nectin-4 polypeptides and their corresponding polynucleotides.
Nectin DNA and protein are useful for treating a disease associated with
cell adhesion activity, adherens junction formation activity, epithelial
or endothelial barrier function activity, endothelial proliferation or
migration activity, viral polypeptide binding activity. The epithelial or
endothelial barrier function disorder which is treated by the above
mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
asthma, allergy, allograft rejection, metastasis of cancer cells,
paracellular transport disorders such as magnesium transport defects in
the kidney or inflammatory bowel disease. Nectin DNA is also useful for
inhibiting angiogenesis in a mammal and treating endothelial migration,
proliferation or angiogenic condition of a tissue or a subject, such as
ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
stroke, restenosis, tumour growth and treating herpesvirus infection.
Nectin is also useful for modulating proliferation or migration of an
endothelial cell, an epithelial cell or a smooth muscle cell (vascular
smooth muscle cell). The present sequence is human nectin-3beta protein.
Human nectin-3beta gene is located on chromosome 3
Sequence 510 AA;

Query Match	100.0%;	Score 1546;	DB 5;	Length 510;
Best Local Similarity	100.0%;	Pred. No. 7.7e-132;		
Matches 292;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0
QY	1	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDATI	60	
Db	74	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDATI	133	
QY	61	TLHNIGFSDSGKIYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDSLIDGGNETVAAIC	120	
Db	134	TLHNIGFSDSGKIYICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDSLIDGGNETVAAIC	193	
QY	121	IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFPFARGRRITCVVKKHPAL	180	
Db	194	IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFPFARGRRITCVVKKHPAL	253	
QY	181	EKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVLKCNADANPPFPKSVWSRLDGOWPD	240	
Db	254	EKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVLKCNADANPPFPKSVWSRLDGOWPD	313	
QY	241	GLLASDNTLHFVHPLTFENYSGVIYCKVTNSLQSRSDQKVIYISDVFPFKQTSS	292	
Db	314	CHIASDNTLHFVHPLTFENYSGVITCKVTNSLQSRSDQKVIYISDVFPFKQTSS	365	

RESULT 6
AAE23288
ID AAE23288 standard; protein; 595 AA.
XX
AC AAE23288;
XX
DT 27-AUG-2002 (first entry)
XX

DE Human nectin-3beta-IgG1Fc region fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
PR
XX (IMMV) IMMUNEX CORP.
PA
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX WPI; 2002-426103/45.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 102-104; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 595 AA;
Query Match 100.0%; Score 1546; DB 5; Length 595;
Best Local Similarity 100.0%; Pred. NO. 9.5e-132;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHFQYGFSGVQGEYQGRVLFKNYSLNDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHFQYGFSGVQGEYQGRVLFKNYSLNDATI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDLSLDGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDLSLDGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATISQYKLFPTFRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPFFKSVNSRLDQWPD 240

Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPFFKSVNSRLDQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQSDQKVYISDVFPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQSDQKVYISDVFPFKQTSS 365
RESULT 7
AAE23289
ID AAE23289 standard; protein; 426 AA.
XX
AC AAE23289;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-FLAGpolyHis fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
XX Key Location/Qualifiers
FH 1. .404
FT /note= "Human nectin-3alpha protein"
FT Region
FT 405. .420
FT /note= "FLAG peptide"
FT 421. .426
FT /note= "PolyHis tag"
FT
XX WO200228902-A2.
PN
XX 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX useful for treating or preventing heart failure, malaria,
XX glomerulonephritis, endometriosis, leukemia, asthma, edema,
XX sepsis, stroke.
XX
XX Claim 9; Page 104-105; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an

CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha-
CC FLAGpolyHis fusion protein
XX
SQ Sequence 426 AA;

Query Match 97.8%; Score 1512; DB 5; Length 426;
Best Local Similarity 98.6%; Pred. No. 7.5e-129;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSINDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSINDATI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVMSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVMSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVYIISDVPFKQT 290
Db 314 GLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVYIISDPTTTT 363

RESULT 8
AAE23281
ID AAE23281 standard; protein; 542 AA.
XX
AC AAE23281;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3alpha protein.

XX Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; chromosome 3; asthma.

XX Homo sapiens.
OS
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDE; AAD37440.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 76-78; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
gamma and nectin-4 polypeptides and their corresponding polynucleotides.

CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha protein
CC containing 7 amino acids deleted from the N-terminal end. Human nectin-
CC 3alpha gene is located on chromosome 3

XX
SQ Sequence 542 AA;

Query Match 97.8%; Score 1512; DB 5; Length 542;
Best Local Similarity 98.6%; Pred. No. 1e-128;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSINDATI 60
Db 67 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSINDATI 126
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 127 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSLIDGGNETVAAIC 186
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 187 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 246
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVMSRLDGQWPD 240
Db 247 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVMSRLDGQWPD 306
QY 241 GLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVYIISDVPFKQT 290
Db 307 GLLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVYIISDPTTTT 356

RESULT 9
AAE23283
ID AAE23283 standard; protein; 549 AA.
XX
AC AAE23283;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha protein.

XX Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.

XX Homo sapiens.
OS
XX
PH Key Location/Qualifiers
FT Modified-site 73 /note= "N-glycosylated"
FT Domain 74..152 /note= "Extracellular Ig domain"
FT Modified-site 83 /note= "N-glycosylated"
FT Modified-site 125 /note= "N-glycosylated"

FT Modified-site 186 /note= "N-glycosylated"
FT Domain 189. .250
FT /note= "Extracellular Ig domain"
FT Modified-site 222
FT /note= "N-glycosylated"
FT Domain 287. .342
FT /note= "Extracellular Ig domain"
FT Modified-site 331
FT /note= "N-glycosylated"
FT Domain 405. .424
FT /note= "Transmembrane domain"
FT Domain 425. .549
FT /note= "C-terminal domain"
XX WO200228902-A2.
PN 11-APR-2002.
XX
PD
XX
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37442.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 89-91; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is located on chromosome 3
CC Human nectin-3alpha gene is located on chromosome 3
XX
SQ Sequence 549 AA;

Query Match 97.8%; Score 1512; DB 5; Length 549;
Best Local Similarity 98.6%; Pred. No. 1.1e-128;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 60
Db
74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYSLNDATI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDLSLDGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDLSLDGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPTRFARGRITCVVKHPAL 180

Db 194 IAATGKPVAHIDWEGDLGEMESTTTSPNETATIISQYKLFPTRFARGRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDVPFKQT 290
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDPPTTT 363

RESULT 10
AAE23282
ID AAE23282 standard; protein; 549 AA.
XX
AC AAE23282;
XX
DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin 3alpha fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
KW chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .7
FT /note= "Mouse nectin-3 protein"
FT Region 8. .549
FT /note= "Human nectin-3alpha protein"
XX
WO200228902-A2.
PN 11-APR-2002.
XX
PD 05-OCT-2001; 2001WO-US031392.
PF 05-OCT-2000; 2000US-0238557P.
PR (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37441.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 80-82; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,

CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
CC alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 549 AA;

Query Match 97.8%; Score 1512; DB 5; Length 549;
Best Local Similarity 98.6%; Pred. No. 1.1e-128;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 TLHNIGFSDSGKICKAVTFPLGNAQSSITTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
134 TLHNIGFSDSGKICKAVTFPLGNAQSSITTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 193
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 IAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
194 IAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 253
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPEFKQT 290
314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPTTTT 363

RESULT 11
ABJ20222
ID ABJ20222 standard; protein; 549 AA.
XX
AC ABJ20222;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human IG gene related protein SEQ ID No 45.
XX
KW Breast cancer; p53 pathway modulating agent; IG; colon cancer;
KW kidney cancer; lung cancer; ovary cancer; human.
XX
OS Homo sapiens.
XX
PN WO200299040-A2.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017313.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 22-OCT-2001; 2001US-0338733P.
PR 15-FEB-2002; 2002US-0357253P.
PR 15-FEB-2002; 2002US-0357600P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Lioubin MN;
XX
DR WPI; 2003-148660/14.
XX
PT Identifying a candidate p53 pathway modulators that are useful as targets
PT for therapeutics or for diagnosing cancers associated with defective p53

PT function, by providing an assay system having a purified IG polypeptide
PT or nucleic acid.
XX
PS Claim 13; Page 206-209; 248pp; English.
XX
CC The invention relates to a novel method for identifying a candidate p53
CC pathway modulating agent. The method comprises providing an assay system
CC having a purified IG polypeptide or nucleic acid, or their functionally
CC active fragment or derivative. The method is useful for identifying
CC modulators of the p53 pathway, particularly for identifying agents for
CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
CC cancer or cancer of the ovary) associated with defective p53 function.
CC The identified modulators are useful as targets for novel therapeutics.
CC The method is also useful for diagnosing disorders associated with
CC defective p53 function. The IG proteins or nucleic acids are useful as
CC modifiers of the p53 pathway, and as therapeutic targets for disorders
CC associated with defective p53 function. This sequence represents a human
CC protein relating to the human IG genes used in the assay for identifying
CC modulators of the p53 pathway of the invention
XX
SQ Sequence 549 AA;

Query Match 97.8%; Score 1512; DB 6; Length 549;
Best Local Similarity 98.6%; Pred. No. 1.1e-128;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
61 TLHNIGFSDSGKICKAVTFPLGNAQSSITTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 120
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
134 TLHNIGFSDSGKICKAVTFPLGNAQSSITTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 193
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
121 IAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
194 IAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 253
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313
QY |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDVPEFKQT 290
314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISDPPTTTT 363

RESULT 12
AAM39143
ID AAM39143 standard; protein; 555 AA.
XX
AC AAM39143;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2288.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI58299.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
PT
XX
PS Example 4; SEQ ID NO 2288; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 555 AA;

Query Match 97.8%; Score 1512; DB 4; Length 555;
Best Local Similarity 98.6%; Pred. No. 1.1e-128;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSINDATI 60
Db 80 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSINDATI 139

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 140 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 199

QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 200 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 259

QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 260 EKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 319

QY 241 GLLASDNTLHFVHPLTFNYSVYICKVTNSLQSRSDQKVYIISDVFFKQT 290
Db 320 GLLASDNTLHFVHPLTFNYSVYICKVTNSLQSRSDQKVYIISDPPTTTT 369

RESULT 13
AAE23287
ID AAE23287 standard; protein; 634 AA.
XX
AC AAE23287;
XX
DT 27-AUG-2002 (first entry)

XX Human nectin-3alpha-IgG1Fc region fusion protein.
DE
XX Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
XX Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US0311392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 100-102; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 634 AA;

Query Match 97.8%; Score 1512; DB 5; Length 634;
Best Local Similarity 98.6%; Pred. No. 1.3e-128;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSINDATI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSINDATI 133

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC 193

QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 253

[illegible]

RESULT 14
AAG63984
ID AAG63984 standard; protein; 438 AA.

AC	AAG63984;
XX	
DT	26-NOV-2001 (first entry)
XX	
DE	Amino acid sequence of murine nectin-3.
XX	
KW	Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.
XX	
OS	Mus sp.

WO200166736-A1.

13-SEP-2001.

09-MAR-2001; 2001WO-JP001871.

09-MAR-2000: 2000JP-00065595.

PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.

Takahashi K, Takai Y, Nakanishi H, Sato K;

WPI; 2001-570771/64.
N-PSDB: AAH78181.

New protein family for diagnosing and treating tumor infiltration and metastasis comprises the mouse nectin-3 protein families and corresponding antibodies.

Claim 3: Page 53-55: 64pp: Japanese.

The present sequence represents a murine nectin-3 polypeptide. Nectin-3 is an immunoglobulin-like cell adhesion molecule that shows homophilic and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and polynucleotides are useful for investigating the mechanisms of cell adhesion, infiltration and metastasis of cancer cells, the diagnosis of malignancies of various cancers, and the development of methods for the treatment and prevention of cancer

Sequence 438 AA;

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Query Match          97.0%;   Score 1500;   DB 4;   Length 438;
Best Local Similarity 95.5%;   Pred. No. 9.6e-128;
Matches 279; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

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Db	74	VSLKCLIEVN	ETITQISWEKIHGKSTQTVAVHHPOYGFSVQGDYQGRVLFKNYS	LDAT	133
QY	61	TLHNIGFSD	SGKYICKAVTFPLGNAQSSTTTVLVEPTVSLIKGPD	SLIDGGNETVAAIC	120
Db	134	TLHNIGFSD	SGKYICKAVTFPLGNAQSSTTTVLVEPTVSLIKGPD	SLIDGGNETVAAVC	193

[illegible]

181 EKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGYNLKCNDADANPPFKSVWSRLDGQWPD 240

Db	254	EKDIRYSFILDIOQYAPEVSVTGYDGNWVFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD	313
QY	241	GLLASDNTLHFVPLTFNYSGVYICKVTNSLQORSDDQVYIYISDVPPFKQTSS	292
Db	314	GLLASDNTLHFVPLTFNYSGVYCKVNSLQORSDDQVYIYISDIPLTOTSS	365

RESULT 15
AAE23293

ID AAE23293 standard; protein; 438 AA.

AA
AC
AAE23:293;

DT 27-AUG-2002 (first entry)

XX
DE Mouse nectin-3gamma protein.

Mouse; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
paracellular transport disorder; kidney; diabetic retinopathy; allergy;
allograft rejection; metastasis; restenosis; inflammatory bowel disease;
oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
stroke; tumour; cancer; herpesvirus infection; asthma.

XX Mus musculus.

XX PN WO200228902-A2.

XX
PD
11-APR-2002

05-OCT-2001: 2001WO-US031392

05-OCT-2000: 2000US-0238557P:

AA
PA (IMMV) IMMUNEX CORP.

XX
PT Baum PR. Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX
DR WPI: 2002-426103/45.

Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
sepsis, stroke.

xx PG Disclosure: Page 111-112; 141pp; English.

The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is mouse nectin-3gamma protein

Sequence 438 AA:

Query Match 97.0%; Score 1500; DB 5; Length 438;
Best Local Similarity 95.5%; Pred. No. 9.6e-128;
Matches 279; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGEYQGRVLFKNYSLNDATI 60

Db	74	VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGDYQGRVLFKNYSLNDATI	133
QY	61	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAIC	120
Db	134	TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAVC	193
QY	121	IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISOYKLFPTRFARGRRITCVVKHPAL	180
Db	194	VAATGKPVAQIDWEGDLGEMESTTTSFPNETATIVSQYKLFPTRFARGRRITCVVKHPAL	253
QY	181	EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD	240
Db	254	EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD	313
QY	241	GLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGORSQDKVIYISDVPFKQTSS	292
Db	314	GLLASDNTLHFVHPLTFVNYSGVYVCKVNSLSGORSQDKVIYISDIPLTQTSS	365

Search completed: April 12, 2004, 09:38:33
Job time : 36.2664 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

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Run on:      April 12, 2004, 09:45:21 ; Search time 24.4035 Seconds
              (without alignments)
              3146.189 Million cell updates/sec
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Title: US-09-972-268-10_COPY_74_365
 Perfect score: 1546
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 s
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Database : Published_Applications_AA:*
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US05_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query %			DB	ID	Description
	Score	Match	Length			
1	1546	100.0	387	10	US-09-972-268-16	Sequence 16, Appl
2	1546	100.0	437	10	US-09-972-268-31	Sequence 31, Appl
3	1546	100.0	504	10	US-09-972-268-8	Sequence 8, Appl
4	1546	100.0	510	10	US-09-972-268-10	Sequence 10, Appl
5	1546	100.0	510	10	US-09-972-268-12	Sequence 12, Appl
6	1546	100.0	595	10	US-09-972-268-14	Sequence 14, Appl
7	1512	97.8	426	10	US-09-972-268-15	Sequence 15, Appl
8	1512	97.8	542	10	US-09-972-268-2	Sequence 2, Appl
9	1512	97.8	549	10	US-09-972-268-4	Sequence 4, Appl
10	1512	97.8	549	10	US-09-972-268-6	Sequence 6, Appl
11	1512	97.8	549	14	US-10-161-572-45	Sequence 45, Appl
12	1512	97.8	634	10	US-09-972-268-13	Sequence 13, Appl
13	1500	97.0	438	10	US-09-959-845-6	Sequence 6, Appl
14	1500	97.0	438	10	US-09-972-268-19	Sequence 19, Appl
15	1500	97.0	510	10	US-09-959-845-4	Sequence 4, Appl

ALIGNMENTS

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RESULT 1
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCL
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectrin
US-09-972-268-16

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Query Match      100.0%; Score 1546; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 3.3e-140;
Matches 292: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Dd	74	VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI	133
QY	61	TLHNIGFSDSGKYICKAVTFPLGNAOQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC	120
b	124	TIHNI GFSDSGKYICKAVTFPLIGNAOSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC	193

Qy 121 IAATGKPVVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 194 IAATGKPVVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 253
Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLCNADANPPPFKSVWSRLDGQWPD 313
Qy 241 GLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISDVVPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISDVVPFKQTSS 365

RESULT 2
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31

Query Match 100.0%; Score 1546; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 3.9e-140;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYSLNDAI 133
Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 193
Qy 121 IAATGKPVVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 194 IAATGKPVVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 253
Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLCNADANPPPFKSVWSRLDGQWPD 240
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RESULT 3
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T

; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8

Query Match 100.0%; Score 1546; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 4.8e-140;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 128 TLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDGGNETVAAIC 187
Qy 121 IAATGKPVVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 180
Db 188 IAATGKPVVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPTFRFARRRITCVVKHPAL 247
Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLCNADANPPPFKSVWSRLDGQWPD 240
Db 248 EKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLCNADANPPPFKSVWSRLDGQWPD 307
Qy 241 GLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISDVVPFKQTSS 292
Db 308 GLLASDNTLHFVHPLTFNYSVGYICKVTNSLGQRSDQKVIYISDVVPFKQTSS 359

RESULT 4
US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest ar
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10

Query Match 100.0%; Score 1546; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 4.9e-140;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYSLNDAI 60
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Db	134	TLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC	193
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Db	194	IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQKLFPTFRFARGRITCVVKHPAL	253
QY	181	EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVLKCNADANPPFKSVMSRLDGQWPD	240
Db	254	EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVLKCNADANPPFKSVMSRLDGQWPD	313
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RESULT 5
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US2003004893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-12

RESULT 6
US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.

```

; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

```

```

RESULT 7
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

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QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDAI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPPFKQT 290
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPPFKQT 363

RESULT 8

US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match 97.8%; Score 1512; DB 10; Length 542;
Best Local Similarity 98.6%; Pred. No. 9.9e-137;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDAI 60
Db 67 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDAI 126
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 127 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGGNETVAAIC 186
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
Db 187 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 246
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 247 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 306
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPPFKQT 290
Db 307 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPPFKQT 356

RESULT 9

US-09-972-268-4

; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are f:
; OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match 97.8%; Score 1512; DB 10; Length 549;
Best Local Similarity 98.6%; Pred. No. 1e-136;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNYSLNDAI 133
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGGNETVAAIC 193
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRITCVVKHPAL 253
QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313
QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPPFKQT 290
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPPFKQT 363

RESULT 10

US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-6

Query Match 97.8%; Score 1512; DB 10; Length 549;
Best Local Similarity 98.6%; Pred. No. 1e-136;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133

Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 193

Qy 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253

Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313

Qy 241 GLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQRSDQKVIYISDPFKQT 290
Db 314 GLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQRSDQKVIYISDPFKQT 363

RESULT 11
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 97.8%; Score 1512; DB 14; Length 549;
Best Local Similarity 98.6%; Pred. No. 1e-136;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133

Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 193

Qy 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253

Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313

Qy 241 GLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQRSDQKVIYISDPFKQT 290
Db 314 GLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQRSDQKVIYISDPFKQT 363

RESULT 12
US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match 97.8%; Score 1512; DB 10; Length 634;
Best Local Similarity 98.6%; Pred. No. 1.2e-136;
Matches 286; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133

Qy 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSSTTVTLVEPTVSLIKGPDSDLIDGNETVAAIC 193

Qy 121 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 180
Db 194 IAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRITCVVKHPAL 253

Qy 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPD 313

Qy 241 GLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQRSDQKVIYISDPFKQT 290
Db 314 GLLASDNTLHFVHPLTFENYSGVYICKVTNSLGQRSDQKVIYISDPFKQT 363

RESULT 13
US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595

;; PRIOR FILING DATE: 2000-03-09
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 438
;; TYPE: PRT
;; ORGANISM: Mouse
US-09-959-845-6

Query Match 97.0%; Score 1500; DB 10; Length 438;
Best Local Similarity 95.5%; Pred. No. 1.1e-135;
Matches 279; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAVC 193

QY 121 IAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARRRITCVVKHPAL 180
Db 194 VAATGKPVQAIDWEGDLGEMESSTTSPFNETATIVSQYKLPFTRFARRRITCVVKHPAL 253

QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 313

QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDIPLTQTSS 365

RESULT 14
US-09-972-268-19
;; Sequence 19, Application US/09972268
;; Publication No. US20030044893A1
;; GENERAL INFORMATION:
;; APPLICANT: Baum, Peter R.
;; APPLICANT: Fanslow, William C.
;; APPLICANT: Lofton, Timothy E.
;; APPLICANT: Sorensen, Eric A.
;; APPLICANT: Youakim, Adel
;; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
;; FILE REFERENCE: 3101-A
;; CURRENT APPLICATION NUMBER: US/09/972,268
;; CURRENT FILING DATE: 2001-10-05
;; PRIOR APPLICATION NUMBER: 60/238,557
;; PRIOR FILING DATE: 2000-10-05
;; NUMBER OF SEQ ID NOS: 39
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 19
;; LENGTH: 438
;; TYPE: PRT
;; ORGANISM: mus musculus
US-09-972-268-19

Query Match 97.0%; Score 1500; DB 10; Length 438;
Best Local Similarity 95.5%; Pred. No. 1.1e-135;
Matches 279; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAVC 193

QY 121 IAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARRRITCVVKHPAL 180
Db 194 VAATGKPVQAIDWEGDLGEMESSTTSPFNETATIVSQYKLPFTRFARRRITCVVKHPAL 253

QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 313

QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDIPLTQTSS 365

RESULT 15
US-09-959-845-4
;; Sequence 4, Application US/09959845
;; Publication No. US20030008334A1
;; GENERAL INFORMATION:
;; APPLICANT: Yoshimi TAKAI
;; APPLICANT: Hiroyuki NAKANISHI
;; APPLICANT: Keiko SATO
;; APPLICANT: Kenichi TAKAHASHI
;; TITLE OF INVENTION: Protein Nectin-3
;; FILE REFERENCE: 2001-1678A/LC/00653
;; CURRENT APPLICATION NUMBER: US/09/959,845
;; CURRENT FILING DATE: 2001-12-31
;; PRIOR APPLICATION NUMBER: PCT/JP01/01871
;; PRIOR FILING DATE: 2001-03-09
;; PRIOR APPLICATION NUMBER: JP 2000-065595
;; PRIOR FILING DATE: 2000-03-09
;; NUMBER OF SEQ ID NOS: 14
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 4
;; LENGTH: 510
;; TYPE: PRT
;; ORGANISM: Mouse
US-09-959-845-4

Query Match 97.0%; Score 1500; DB 10; Length 510;
Best Local Similarity 95.5%; Pred. No. 1.3e-135;
Matches 279; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 60
Db 74 VSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFSVQGEYQGRVLFKNYSLNDAI 133

QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAIC 120
Db 134 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDGGNETVAAVC 193

QY 121 IAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLPFTRFARRRITCVVKHPAL 180
Db 194 VAATGKPVQAIDWEGDLGEMESSTTSPFNETATIVSQYKLPFTRFARRRITCVVKHPAL 253

QY 181 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 240
Db 254 EKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVWSRLDGQWPD 313

QY 241 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDVPFKQTSS 292
Db 314 GLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDIPLTQTSS 365

Search completed: April 12, 2004, 10:25:26
Job time : 25.4035 secs

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 9.63898 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-10_COPY_74_365
Perfect score: 1546
Sequence: 1 VSLKCLIEVNETITQISWEK.....QRSDQKVIYISDVFPFKQTSS 292

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	540	34.9	517	4	US-09-723-368-4
2	534	34.5	458	4	US-09-435-956A-1
3	517.5	33.5	518	4	US-09-919-172-20
4	392	25.4	479	4	US-09-723-368-2
5	359	23.2	408	4	US-09-724-864-62
6	258.5	16.7	440	4	US-09-866-028-61
7	258.5	16.7	442	4	US-09-778-510-20
8	258.5	16.7	442	4	US-09-930-803-1
9	255.5	16.5	423	4	US-09-778-510-22
10	212	13.7	398	4	US-09-778-510-4
11	209	13.5	421	2	US-08-659-984A-1
12	209	13.5	421	3	US-08-660-531-1
13	209	13.5	444	2	US-08-659-984A-5
14	209	13.5	444	3	US-08-660-531-5
15	202	13.1	398	4	US-09-778-510-6
16	202	13.1	398	4	US-09-907-794A-84
17	202	13.1	398	4	US-09-905-125A-84
18	202	13.1	398	4	US-09-902-775A-84
19	202	13.1	432	4	US-09-778-510-2
20	190.5	12.3	227	4	US-09-205-258-947
21	187.5	12.1	274	4	US-09-570-367C-19
22	187.5	12.1	274	4	US-09-915-524-19
23	158.5	10.3	278	4	US-09-570-367C-2
24	158.5	10.3	278	4	US-09-915-524-2
25	155.5	10.1	278	4	US-09-570-367C-21
26	155.5	10.1	278	4	US-09-915-524-21
27	153.5	9.9	642	1	US-08-217-299-1

28	153.5	9.9	698	2	US-08-602-725-36	Sequence 36, Appl
29	153.5	9.9	734	2	US-08-389-459A-17	Sequence 17, Appl
30	153.5	9.9	734	3	US-08-987-867A-17	Sequence 17, Appl
31	149.5	9.7	467	3	US-09-046-736-2	Sequence 2, Appli
32	147	9.5	477	2	US-08-432-016-3	Sequence 3, Appli
33	147	9.5	477	2	US-08-684-594-3	Sequence 3, Appli
34	145	9.4	1101	3	US-08-986-485-2	Sequence 2, Appli
35	142	9.2	1651	3	US-09-540-245A-18	Sequence 18, Appl
36	140	9.1	643	5	PCT-US93-00031-19	Sequence 19, Appl
37	140	9.1	644	5	PCT-US93-00031-21	Sequence 21, Appl
38	140	9.1	647	4	US-09-009-490A-91	Sequence 91, Appl
39	140	9.1	647	4	US-08-482-073-5	Sequence 5, Appli
40	140	9.1	647	5	PCT-US93-00031-11	Sequence 11, Appl
41	140	9.1	647	5	PCT-US93-00031-23	Sequence 23, Appl
42	136.5	8.8	486	2	US-08-432-016-6	Sequence 6, Appli
43	136.5	8.8	486	2	US-08-684-594-6	Sequence 6, Appli
44	133	8.6	313	4	US-09-700-397-4	Sequence 4, Appli
45	133	8.6	344	4	US-09-700-397-3	Sequence 3, Appli

ALIGNMENTS

RESULT 1
US-09-723-368-4
; Sequence 4, Application US/097233368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match	34.9%	Score	540	DB	4	Length	517
Best Local Similarity	38.6%	Pred. No.	1.1e-46				
Matches	108	Conservative	55	Mismatches	109	Indels	8
						Gaps	4
QY	13	ITQISWEKIHGSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATITLHNIGFSDSGK	72				
Db	62	ITQVTWQKSTNGSKONVAIYNPSMGVSLAPRERVEFLRPSFTDGTIRLSRLEDEGV	121				
QY	73	YICKAVTFPLGNAQSSTVTVLVEPTVSLIKGPDSDLIDG----GNETVAACIAATGKPV	128				
Db	122	YICEFATFTGNRESQNLTVMAKPT-NWIEGTQAVLRAKKGDDKVLVATCTSANGKPP	180				
QY	129	AHIDWEGDL-GEMESITTSFPNETATIIISQKLPFTRFARRRITCVVKKHPALEKDIRYS	187				
Db	181	SVVSWETRLKGEAEYQIRNPNGTIVTISRVLVPSREAHQQSLACIVNYHM--DRFKES	238				
QY	188	FILDIOYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPFKSVWSRLDQGWPDGLLASDN	247				

Db 239 LTLNVQYEPEVTIEGDFGNWYLQRMVDVKLTCKADANPPATEYHWTTLNGLSLPKGVAEQNR 298
QY 248 TLHFVHPLTFNYSQVYICKVTNSLQGRSDQKVYIYISDVPE 287
Db 299 TLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPY 338

RESULT 2
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: Higr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Higr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 34.5%; Score 534; DB 4; Length 458;
Best Local Similarity 38.7%; Pred. No. 3.7e-46;
Matches 109; Conservative 53; Mismatches 112; Indels 8; Gaps 4;
QY 13 ITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATITLHNIGFSDSGK 72
Db 62 ITQVTWQKSTNGSKQNVAIYNPMSGVSLAPYRERVEFLRPSFTDGTIRLSRLEDEGV 121
QY 73 YICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG----GNETVAAICIAATGKPV 128
Db 122 YICGFATPPTGNRESQNLNLTVMAKPT--NWIEGTQAVLRAKKGQDDKVLVATCTSANGKPP 180
QY 129 AHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTREARGRRITCVVKHPALEKDIRYS 187
Db 181 SVVSWETRLKGEAEYQEIERNPNTGTVTVISRYRLVPSREAHQQSLACIVNYEM--DRFKES 238
QY 188 FILDQYAPEVSVTGYDGNWVFGKGNLKNADANPPFPKSVWSRLDGQWPDGILLASDN 247
Db 239 LTLNVQYEPEVTIEGDFGNWYLQRMVDVKLTCKADANPPATEYHWTTLNGLSLPKGVAEQNR 298
QY 248 TLHFVHPLTFNYSQVYICKVTNSLQGRSDQKVYIYISDVPEPKQ 289
Db 299 TLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEKPRPQ 340

RESULT 3
US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20
Query Match 33.5%; Score 517.5; DB 4; Length 518;
Best Local Similarity 36.3%; Pred. No. 2.2e-44;
Matches 105; Conservative 55; Mismatches 104; Indels 25; Gaps 5;
QY 13 ITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDATITLHNIGFSDSGK 72
Db 62 ITQVTWQKSTNGSKQNVAIYNPMSGVSLAPYRERVEFLRPSFTDGTIRLSRLEDEGV 121
QY 73 YICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG----GNETVAAICIAATGKPV 128
Db 122 YICEFATPPTGNRESQNLNLTVMAKPT--NWIEGTQAVLRAKKGQDDKVLVATCTSANGKPP 180
QY 129 AHIDWE-----GDLGEMESTTTSFPNETATIIISQYKLFPTREARGRRITCVVKHP 178
Db 181 SVVSWETRLKGEARVPGDSGT-----PMAPVTVISRYRLVPSREAHQQSLACIVNYH 232
QY 179 ALEKDIRVSPILDIQYAPEVSVTGYDGNWVFGKGNLKNADANPPFPKSVWSRLDGQW 238
Db 233 M--DRFKESLTLNVQYEPEVTIEGDFGNWYLQRMVDVKLTCKADANPPATEYHWTTLNGLSL 290
QY 239 PDGLLASDNTLHFVHPLTFNYSQVYICKVTNSLQGRSDQKVYIYISDVPE 287
Db 291 PKGVEAQNRITLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPY 339

RESULT 4
US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Mo'gyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match 25.4%; Score 392; DB 4; Length 479;
Best Local Similarity 29.3%; Pred. No. 1.4e-31;
Matches 88; Conservative 56; Mismatches 116; Indels 40; Gaps 8;
QY 13 ITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEYQG--RVLF-----KNYSLNDAT 59

Db 65 ISLVTPQRPDAPANHQNVAAFHPKMGESFPSPKPGSERLSFVSAKQSTGQDTEAELQDAT 124
QY 60 ITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVLEP-----TVSLIKGPDSLIDGG 112
Db 125 LALHGLTVEDEGNYTCEFATFPKGSVRGWTWLRVIAKPKNAQEAQKVTFSDP----- 177
QY 113 NETVAAICIAATGKPVVAHI-----DWEGLGEMESTTTSFPNETATILISQYKLFPTTREA 166
Db 178 --TTVALCISKEGRPPARISWLSSLDWEAKETQVSGTLAG-----TVTTSRFTLVPSGRA 231
QY 167 RGRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGKGVNLCNADANPPP 226
Db 232 DGVTVCKVEHESFEPEPALIPVTLVSRYPPEVSGYDDNWYLGRTDATLSCDVRSNPEP 291
QY 227 FKSWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVP 286
Db 292 TGYDWTSTGTFPTSAVAQGSQ-L-VIHAVDLSLFTNTFVCTVTNAVGMGRAEQVIFVRETP 350

RESULT 5
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
; ORGANISM: Mouse
US-09-724-864-62

Query Match 23.2%; Score 359; DB 4; Length 408;
Best Local Similarity 32.8%; Pred. No. 2.7e-28;
Matches 98; Conservative 49; Mismatches 130; Indels 22; Gaps 10;
QY 2 SLKCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSLNDA 58
Db 47 TLHCSLTSNENVTITQITWMKKDSGGSHALVAFHPKKGNPNIKEPERVKFLAAQQDLRNA 106
QY 59 TITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVLEP--TVSLIKGPDSLI--DGGNE 114
Db 107 SLAISNLSVEDEGIYECQIATFPRGSRSTNAWLKVQARPKNTAEALPSPFTLILQD---- 162
QY 115 TVAAICIAATGKPVVAHIW-----EGDLGEMESTTTSFPNETATILISQYKLFPTTREFARR 170
Db 163 --VAKCISANGHPGGRISWPSNVNGSHREMK-PGSQPG-TTIVTSYLSMVPSPQADGKN 218
QY 171 ITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWVFGKGVNLCNADANPPPFKS 229
Db 219 ITCVHEHESLQELDQLLVLSQYPPPENVSISGYDGNWVGLTNLTLTCEAHSKPADMA 278
QY 230 --VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISDVP 286
Db 279 GYNWSTNTGDFPNSVKRQGNMLLISTVEDGLNNTVIVCEVTNALGSGQGVHIIIVKEP 337

RESULT 6
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMERANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548PIC1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61
Query Match 16.7%; Score 258.5; DB 4; Length 440;
Best Local Similarity 28.7%; Pred. No. 6.2e-18;
Matches 70; Conservative 48; Mismatches 107; Indels 19; Gaps 8;
QY 52 NYSLNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVLEPTVSLIK-GPDSLID 110
Db 99 NFSSELKVSLTNVSIISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMDIQKDTAVE 156
QY 111 GGNETVAAICIAATGKPVVAHIW-EGDL-----GEMESTTTSFPNETATILISQYKLFPTTR 164
Db 157 G--EEIEVNVCTAMASKPATITIRFKGNTELKKGSEVEEWSDMY-----TSTSOLMLKVHK 209
QY 165 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGKGVNLCNADA 222
Db 210 EDDGVPVICQVEHPAVTGNLQTRYLEVQYKPOVHIQMTYPLQGLTREGDALELTCEAIG 269
QY 223 NPPPFKSWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYI 282
Db 270 KPQPMVMTVVRVDDDEMPQHAVLSGNL-FINNLNKTDNGTYRCEASNIVGKAHSDYMLYV 328
QY 283 SDVP 286
Db 329 YDPP 332
RESULT 7
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien

Db 46 VVLKQVCKDHED--SSLQWS---NPAQOTL-----YFGEKRALRDNRIQLVSSSTPHELSI 95
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEPTVSLIKGPDLSLIDGNETVAAIC 120
Db 96 SISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REKETATLNC 152
QY 121 IAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTFRFARGRRITCVVK 176
Db 153 QSSGSKPAAQLTWRKGQELHGDQTRIQEDPNGKTFVSSSVSFQVTRDDGANIVCSVN 212
QY 177 HPALE-KDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLD 235
Db 213 HESLKGADRSTSQRIEVLTYPTAMIRPEPAHPREGQK-LLLHCEGRGNPVPQQVYVVK-E 270
QY 236 GOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISD-VPFKQTSS 292
Db 271 GSEPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYTAYFTLNVDNPSVPFSSSS 327

RESULT 11
US-08-659-984A-1
; Sequence 1, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-984A-1

Query Match 13.5%; Score 209; DB 2; Length 421;
Best Local Similarity 23.6%; Pred. No. 6.9e-13;
Matches 70; Conservative 61; Mismatches 132; Indels 34; Gaps 13;
QY 3 LKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNSLNDATITL 62
Db 28 LTRVDQNDN-TSLQWS---NPAQOTL-----YFDDKKALRDNRIELVRASWHELSISV 77

QY 63 HNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLE-PTVSLIKGPDLSLIDGNETVAAICI 121
Db 78 SDVLSDEGQYTCISLFTMPVKTSKAYLTVLGVPEKPKQISGFSSP--VMEG--DLMLQLTCK 133
QY 122 AATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATIIISQYKLFPTFRFARGRRITCVVKH 177
Db 134 TSGSKPAADIRWFKNDEIKDKVYLKEEDANRKTFTVSSLTDFRVDRSDDGVAVICRVDH 193
QY 178 PALEKDIRYSF-IIDIOYAPEVSVT-----GYDGNWFVGRKGVNLKCNADANPPPFKSVW 231
Db 194 ESLNATPOVAMQVLEIHYTPSVKIIIPSTPFPQEGQPLI-----LTCESKGKPLPEPVLW 247
QY 232 SRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVIYISDVP 286
Db 248 TKDGGELPDPRMVSVSGRELNILF-LNKTDNGTYRCEATNTIGQSSAEYVLIVHDVP 303

RESULT 12
US-08-660-531-1
; Sequence 1, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-531-1

Query Match 13.5%; Score 209; DB 3; Length 421;
Best Local Similarity 23.6%; Pred. No. 6.9e-13;
Matches 70; Conservative 61; Mismatches 132; Indels 34; Gaps 13;
QY 3 LKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNSLNDATITL 62
Db 28 LTRVDQNDN-TSLQWS---NPAQOTL-----YFDDKKALRDNRIELVRASWHELSISV 77
QY 63 HNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLE-PTVSLIKGPDLSLIDGNETVAAICI 121

Db 78 SDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSSP--VMEG--DLMQLTCK 133
QY 122 AATGKPVAHIDW---EGDLGEMESTTTSPFN-ETATIIISQYKLFPRFARGRRITCVVKH 177
Db 134 TSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLDFRVDSDDGVAVICRVDH 193
QY 178 PALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWVFVGRKGVNLKCNADANPPPFKSVW 231
Db 194 ESLNATPQVAMQVLEIHVTPSVKIIIPSTPPQEGQPLI-----LTCESKGKPLPEPVLW 247
QY 232 SRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 286
Db 248 TKDGGELPDPDRMVVSGRELNILF-LNKTDNGTYRCEATNTIGQSSAEYVLIIVHDVP 303

RESULT 13
US-08-659-984A-5
; Sequence 5, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/659,984A
FILING DATE: 07-JUN-1996
CLASSIFICATION: 436
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,152
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002810US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-659-984A-5

Query Match 13.5%; Score 209; DB 2; Length 444;
Best Local Similarity 23.6%; Pred. No. 7.5e-13;
Matches 70; Conservative 61; Mismatches 132; Indels 34; Gaps 13;
QY 3 LKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSINDATITL 62
Db 51 LTCRVDQNDN-TSLQWS---NPAQQTLL-----YFDDKKALRDNRIELVRASWHELSISV 100
QY 63 HNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVE-PTVSLIKGPDSDLIDGNETVAACI 121
Db 101 SDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSSP--VMEG--DLMQLTCK 156

QY 122 AATGKPVAHIDW---EGDLGEMESTTTSPFN-ETATIIISQYKLFPRFARGRRITCVVKH 177
Db 157 TSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKTFTVSSTLDFRVDSDDGVAVICRVDH 216
QY 178 PALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWVFVGRKGVNLKCNADANPPPFKSVW 231
Db 217 ESLNATPQVAMQVLEIHVTPSVKIIIPSTPPQEGQPLI-----LTCESKGKPLPEPVLW 270
QY 232 SRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQSDQKVIYISDVP 286
Db 271 TKDGGELPDPDRMVVSGRELNILF-LNKTDNGTYRCEATNTIGQSSAEYVLIIVHDVP 326

RESULT 14
US-08-660-531-5
; Sequence 5, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/660,531
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/480,498
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Heslin, James M.
REGISTRATION NUMBER: 29,541
REFERENCE/DOCKET NUMBER: 15270-002210US
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-660-531-5

Query Match 13.5%; Score 209; DB 3; Length 444;
Best Local Similarity 23.6%; Pred. No. 7.5e-13;
Matches 70; Conservative 61; Mismatches 132; Indels 34; Gaps 13;
QY 3 LKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYSINDATITL 62
Db 51 LTCRVDQNDN-TSLQWS---NPAQQTLL-----YFDDKKALRDNRIELVRASWHELSISV 100
QY 63 HNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVE-PTVSLIKGPDSDLIDGNETVAACI 121
Db 101 SDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFSSP--VMEG--DLMQLTCK 156
QY 122 AATGKPVAHIDW---EGDLGEMESTTTSPFN-ETATIIISQYKLFPRFARGRRITCVVKH 177

Db 157 TSGSKPAADIRWFKNDKEIKDKYLKEEDANRKFTVSSSTLDFRVDRSDDGVAVICRVDH 216
QY 178 PALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWFVGRKGVLNLCNADANPPPFKSVW 231
Db 217 ESLNATPQVAMQVLEIHVTPSVKIIPTSTPPQEGQPLI-----LTCEKKGKPLPEPVLW 270
QY 232 SRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVVICKVTNSLGQSRSDQKVIYISDVP 286
Db 271 TKDGGELPDPDRMVVSGRELNILF-LNKTDNGTYRCEATNTIGQSSAEYVLIVHDVP 326

RESULT 15

US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 13.1%; Score 202; DB 4; Length 398;
Best Local Similarity 25.5%; Pred. No. 3.3e-12;
Matches 76; Conservative 53; Mismatches 147; Indels 22; Gaps 12;

QY 1 VSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGSFVQGEYQGRVLFKNYSLNDATI 60
Db 46 VVLKQVQKDHED-SSLQWS---NPAQOTL-----YFGEKRALRDNRIQLVTSSTPHELSI 95
QY 61 TLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGGNETVAAIC 120
Db 96 SISNVALADEGEYTCISIFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REKDTATLNC 152
QY 121 IAATGKPVAHIDWEGDLGEMESTTSF---PN-ETATIIISQYKLPFTRFARGRRITCVVK 176
Db 153 QSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFTVSSSVTFQVTRDDGASIVCSVN 212
QY 177 HPALE-KDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVLNLCNADANPPPFKSVWSRLD 235
Db 213 HESLKGADRSTSQRIEVLXTPTAMIRPDPPHPREGQK-LLHCEGRGNPVPQQYLWEK-E 270
QY 236 GQWPDGLLASDNTLHFVHPLTFNYSGVVICKVTNSLGQSRSDQKVIYISD-VPFKQTSS 292
Db 271 GSVFPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYKAYYTLNVNDPSPVPSSSS 327

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 7.54126 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-2_COPY_58_342
Perfect score: 1520
Sequence: 1 HVTAVMGKNVSLKCLIEVNE.....FNYSGVYICKVTNSLQGRSD 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1104	72.6	407	2 T08732	hypothetical prote
2	502	33.0	518	2 JC4024	poliovirus recepto
3	394	25.9	467	1 HLMSP3	poliovirus recepto
4	394	25.9	530	2 A53437	poliovirus recepto
5	379.5	25.0	392	2 B44194	poliovirus recepto
6	379.5	25.0	417	2 A44194	poliovirus recepto
7	372	24.5	478	2 I53960	PRR2 alpha - human
8	372	24.5	538	2 I68093	PRR2 delta - human
9	368.5	24.2	392	1 RWHUPD	poliovirus recepto
10	368.5	24.2	417	1 RWHUPA	poliovirus recepto
11	305.5	20.1	416	2 A54017	colon carcinoma-as
12	207	13.6	764	2 A49448	irregular chiasm C
13	187.5	12.3	274	2 A47639	OX-2 membrane glyco
14	178.5	11.7	4391	2 A38096	perlecan precursor
15	173.5	11.4	5175	2 T20992	hypothetical prote
16	173.5	11.4	5198	2 T43290	hemikentatin precurs
17	166.5	11.0	853	1 IJBONC	neural cell adhesi
18	166	10.9	588	2 JH0506	adhesion molecule
19	166	10.9	588	2 A45254	surface glycoprote
20	163.5	10.8	626	1 A61084	myelin-associated
21	163.5	10.8	637	2 B33785	myelin-associated
22	162.5	10.7	278	1 TDRTOX	OX-2 membrane glyco
23	161.5	10.6	582	1 BNRT3S	myelin-associated
24	161.5	10.6	626	1 BNRT3	myelin-associated
25	161.5	10.6	1896	2 T08851	Down syndrome cell
26	161	10.6	765	2 C42632	cell adhesion mole
27	161	10.6	812	2 B42632	cell adhesion mole
28	161	10.6	932	2 A42632	cell adhesion mole
29	159.5	10.5	7962	2 I38346	elastic titin - hu

30	154	10.1	587	2 JH0464	DM-GRASP precursor
31	154	10.1	702	2 A36319	carcinoembryonic a
32	152.5	10.0	858	1 IJRTNC	neural cell adhesi
33	152	10.0	761	1 IJHUNG	neural cell adhesi
34	147	9.7	344	2 I56551	neurotrimin - rat
35	147	9.7	739	2 JN0581	vascular cell adhe
36	145.5	9.6	345	2 S03199	opioid-binding pro
37	143.5	9.4	725	1 IJMSNG	neural cell adhesi
38	143.5	9.4	1115	1 IJMSNL	neural cell adhesi
39	143	9.4	1091	1 IJCHNL	neural cell adhesi
40	139	9.1	3707	2 S18252	heparan sulfate pr
41	138.5	9.1	458	2 S23969	cell-adhesion mole
42	138.5	9.1	847	2 JH0371	B-cell adhesion pr
43	137	9.0	583	2 I39428	alcam - human
44	136.5	9.0	345	2 JC4025	opioid-binding cel
45	136.5	9.0	1018	2 A54744	contactin 1 precur

ALIGNMENTS

RESULT 1

T08732

hypothetical protein DKFZp566B0846.1 - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C:Accession: T08732

R:Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A:Reference number: Z16474

A:Accession: T08732

A:Molecule type: mRNA

A:Residues: 1-407 <OTT>

A:Cross-references: EMBL:AL050071

A:Experimental source: fetal kidney; clone DKFZp566B0846

C:Genetics:

A:Note: DKFZp566B0846.1

Query Match 72.6%; Score 1104; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 3.9e-78;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	79	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKPVA	138
Db	1	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKPVA	60
QY	139	HIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARRRITCVVKHPALEKDRIYSFI	198
Db	61	HIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARRRITCVVKHPALEKDRIYSFI	120
QY	199	LDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTL	258
Db	121	LDIQYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVWSRLDGQWPDGLLASDNTL	180
QY	259	HFVHPLTFNYSGVYICKVTNSLGQRSD	285
Db	181	HFVHPLTFNYSGVYICKVTNSLGQRSD	207

RESULT 2

JC4024

poliovirus receptor-related protein precursor - human

C:Species: Homo sapiens (man)

C:Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999

C:Accession: JC4024

R:Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Bardin, F.; Maroc, C.; Dubr

Gene 155, 261-265, 1995

A:Title: Complementary DNA characterization and chromosomal localization of a human gene

A:Reference number: JC4024; MUID:95237621; PMID:7721102

A:Accession: JC4024

A:Molecule type: mRNA

A:Residues: 1-518 <LOP>

A:Cross-references: EMBL:X76400; NID:g7332795; PIDN:CAA53980.1; PID:g732796

C;Genetics:
A;Gene: GDB:PVRR1
A;Cross-references: GDB:583951
A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: Glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;356-379/Domain: transmembrane #status predicted <TM>
F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 33.0%; Score 502; DB 2; Length 518;
Best Local Similarity 35.9%; Pred. No. 2.6e-31;
Matches 106; Conservative 53; Mismatches 108; Indels 28; Gaps 6;

QY 7 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYS 63
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRERVEFLRPS 103
QY 64 LNDATITLHNIGFSDSGKYCKAVTFEPLGNAQSSTTVTLVVEPTVSLIKGPDLSLDG--- 120
Db 104 FTDGTLRLSRLEDEGVVCEFAFTEPTGNRESQLNLTVMAKPT-NWIEGTQAVLRKKG 162
QY 121 -GNETVAAICIAATGKPVAHIDWE-----GDIGEMESTTTSFPNETATISQYKL 169
Db 163 QDDKVLVATCTSANGKPPSVSWETRLKGEARVPDGSCT-----PMAPVTVISRYRL 214
QY 170 FPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCN 229
Db 215 VPSREAHQQLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRLMDVKLTCKA 272
QY 230 DANPPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS 284
Db 273 DANPPATEYHWTTLNGSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRS 327

RESULT 3
HLMSP3
poliovirus receptor homolog precursor - mouse
C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A38211
R;Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A;Title: Molecular cloning and expression of a murine homolog of the human poliovirus re
A;Reference number: A38211; MUID:92219365; PMID:1560525
A;Accession: A38211
A;Molecule type: DNA
A;Residues: 1-467 <MOR>
A;Cross-references: GB:M80206; NID:G199785; PIDN:AAA39734.1; PID:G199786
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F;26-354/Domain: extracellular #status predicted <EXT>
F;47-133/Domain: immunoglobulin homology <IMM1>
F;167-231/Domain: immunoglobulin homology <IMM2>
F;267-322/Domain: immunoglobulin homology <IMM3>
F;355-374/Domain: transmembrane #status predicted <TMN>
F;375-467/Domain: intracellular #status predicted <INT>
F;54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.9%; Score 394; DB 1; Length 467;
Best Local Similarity 32.1%; Pred. No. 5.4e-23;
Matches 94; Conservative 45; Mismatches 124; Indels 30; Gaps 9;

QY 7 GKNVSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEY--QGRVLF--- 59
Db 47 GGTVELPCHELLPPTTERVSRVQVTWQRLDG---TVVAAFHPSPGVDFFNSQFSKDRLSFVRA 103
QY 60 ---KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP-----TVSLI 111
Db 104 RPETNADLRDATLAFRGLRVEDEGNYTCEFAFPNGTRRRGVTWLRVIAQPENHAEAEQV 163
QY 112 KGPDSLIDGNETVAAICIAATGKPVAHIDWEGLGEMESTTTSFPN---ETATISQYK 168
Db 164 IGPOSV-----AVARCVSTGGRPPARITWISSLG-BAKDTQEPGIQAGTVTISRYS 215
QY 169 LFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCN 228
Db 216 LVPVGRADGVKVTCTRVEHSPPEEPILLPVTLSVRYPPEVSIISGYDDNWYLGSRSEAILTCD 275
QY 229 ADANPPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 276 VRSNPEPTDYDWSTTSGVFPASAVAQSQL-LVHSVDRMVNTTICTATNAV 327

poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Molecule type: DNA

Db 104 RPETNADLRDATLAFRGLRVEDEGNYTCEFAFPNGTRRRGVTWLRVIAQPENHAEAEQV 163
QY 112 KGPDSLIDGNETVAAICIAATGKPVAHIDWEGLGEMESTTTSFPN---ETATISQYK 168
Db 164 IGPOSV-----AVARCVSTGGRPPARITWISSLG-BAKDTQEPGIQAGTVTISRYS 215
QY 169 LFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCN 228
Db 216 LVPVGRADGVKVTCTRVEHSPPEEPILLPVTLSVRYPPEVSIISGYDDNWYLGSRSEAILTCD 275
QY 229 ADANPPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 276 VRSNPEPTDYDWSTTSGVFPASAVAQSQL-LVHSVDRMVNTTICTATNAV 327

RESULT 4
A53437
poliovirus receptor mpVR - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A53437
R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with I
A;Reference number: A53437; MUID:94179228; PMID:8132569
A;Accession: A53437
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-530 <AOK>
A;Cross-references: GB:D26107; NID:G475017; PIDN:BAA05103.1; PID:G825507
A;Experimental source: C57/BL6, brain
A;Note: sequence extracted from NCBI backbone (NCBI:146664, NCBIP:146667)
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IMM>

Query Match 25.9%; Score 394; DB 2; Length 530;
Best Local Similarity 32.1%; Pred. No. 6.3e-23;
Matches 94; Conservative 45; Mismatches 124; Indels 30; Gaps 9;

QY 7 GKNVSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEY--QGRVLF--- 59
Db 47 GGTVELPCHELLPPTTERVSRVQVTWQRLDG---TVVAAFHPSPGVDFFNSQFSKDRLSFVRA 103
QY 60 ---KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP-----TVSLI 111
Db 104 RPETNADLRDATLAFRGLRVEDEGNYTCEFAFPNGTRRRGVTWLRVIAQPENHAEAEQV 163
QY 112 KGPDSLIDGNETVAAICIAATGKPVAHIDWEGLGEMESTTTSFPN---ETATISQYK 168
Db 164 IGPOSV-----AVARCVSTGGRPPARITWISSLG-BAKDTQEPGIQAGTVTISRYS 215
QY 169 LFPTRFARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLKCN 228
Db 216 LVPVGRADGVKVTCTRVEHSPPEEPILLPVTLSVRYPPEVSIISGYDDNWYLGSRSEAILTCD 275
QY 229 ADANPPPPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 276 VRSNPEPTDYDWSTTSGVFPASAVAQSQL-LVHSVDRMVNTTICTATNAV 327

poliovirus receptor (clone AGM-delta-1) - green monkey
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
C;Accession: B44194
R;Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.
J. Virol. 66, 7059-7066, 1992
A;Title: A second gene for the African green monkey poliovirus receptor that has no puta
A;Reference number: A44194; MUID:93059651; PMID:1331508
A;Accession: B44194
A;Status: preliminary
A;Molecule type: DNA

Db 158 ---GEPVPMARCVSTGGRPPAQITWHSDLGMENTSQVPGFLSGTIVTSLWILVPSSQV 214

QY 176 RGRITCVVKHDALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPP 235

Db 215 DGKNTCKVEHSEKPOLLTVNLTVYYPPEVSIISGYDNNWYLGQNEATLTCDARSNPEP 274

QY 236 FKSWSRLDGQWPDGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQOR 283

Db 275 TGYNSTTGMPLPPFAVQAQL-LIRPVDKPEINTLICNVTNALGAR 321

RESULT 11

A54017

colon carcinoma-associated antigen pE4 precursor - rat

N;Alternate names: pE4 protein

C;Species: Rattus norvegicus (Norway rat)

C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 01-Dec-1995

C;Accession: A54017; A61206

R;Chadeneau, C.; LeMouillac, B.; Denis, M.G.

J. Biol. Chem. 269, 15601-15605, 1994

A;Title: A novel member of the immunoglobulin gene superfamily expressed in rat carcinoma

A;Reference number: A54017; MUID:94253144; PMID:8195207

A;Accession: A54017

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-416 <CHA>

A;Cross-references: GB:L12025

R;Chadeneau, C.; Denis, M.G.; Blottiere, H.M.; Gregoire, M.; Douillard, J.Y.; Meflah, K.

Int. J. Cancer 47, 903-908, 1991

A;Title: Characterization, isolation and amino terminal sequencing of a rat colon carcin

A;Reference number: A61206; MUID:91184910; PMID:2010233

A;Accession: A61206

A;Molecule type: protein

A;Residues: 34-41,'X',43-53 <CH2>

A;Note: the residue at position 9 is suggested to be glycosylated asparagine

C;Comment: This 66K protein is detected by monoclonal antibody E4 on colon carcinoma cel

C;Keywords: glycoprotein; membrane protein

Query Match 20.1%; Score 305.5; DB 2; Length 416;

Best Local Similarity 29.7%; Pred. No. 3.4e-16;

Matches 86; Conservative 45; Mismatches 142; Indels 17; Gaps 8;

QY 3 TAVWGKNVSLKCLI--EVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLF- 59

Db 44 TGFLGGSTVLHCSLASKDNVTITQLTWMKRDGSPFRACLPPQEGPSISDPERVKPLVA 103

QY 60 KNY-SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEP--TVSLIKGPD 116

Db 104 KYEDLRNASLAISNLRVEDEGIECQIATFTPTGSKSANVWLKVFPKNTAEALPSPT 163

QY 117 LIDGNETVAAICIAATGKPVAHIDW----EGDLGEMESTTSPFPNETATIIISQYKLPPT 172

Db 164 LMPQD----VAKCISADGHPGGRITWSSNVNGSYREMKETGSSRAPPQLSATSPWCLLAR 219

QY 173 RFARGRRITCVVKHDALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADAN 232

Db 220 QMARTSPAQWNMK--ASRSRTSRPLILSLPYPPPEVSIISGYEGNWIYGLTNVNLTCERSK 277

QY 233 PPPFKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSYGVYICKVTNSLQ 281

Db 278 PPPTNYSWSTATGPLPNSHTFQENGSHLLISTVDDLNTTIFVCKAINALG 327

RESULT 12

A49448

irregular chiasm C-roughest precursor - fruit fly (Drosophila melanogaster)

N;Alternate names: irregC-roughest protein

C;Species: Drosophila melanogaster

C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 07-May-1999

C;Accession: A49448; S34129

R;Ramos, R.G.P.; Igloi, G.L.; Lichte, B.; Baumann, U.; Maier, D.; Schneider, T.; Brandst

Genes Dev. 7, 2533-2547, 1993

A;Title: The irregular chiasm C-roughest locus of Drosophila, which affects axonal proje

A;Reference number: A49448; MUID:94102535; PMID:7503814

A;Accession: A49448

A;Status: preliminary

A;Molecule type: DNA; mRNA

A;Residues: 1-764 <RAM>

A;Cross-references: GB:L11040; NID:g304790; PID:g304791; EMBL:Z21641; NID:g312985; PID:g

C;Genetics:

A;Gene: FlyBase:rst

A;Cross-references: FlyBase:FBgn0003285

C;Keywords: transmembrane protein

Query Match 13.6%; Score 207; DB 2; Length 764;

Best Local Similarity 24.1%; Pred. No. 3.2e-08;

Matches 78; Conservative 52; Mismatches 128; Indels 66; Gaps 15;

QY 3 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 62

Db 38 TAVVGARVTLPCRVI--INKQGT-LQWTK-----DDFGLGTSRDLG---FERY 79

QY 63 SL-----NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT---VTVLVEPTVSLIKG 113

Db 80 AMVGSDEEGDYSLDIYPVMDLDDARYQCQVSPGEGQPAIRSTEAGLIVLPPEAPKITQ 139

QY 114 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLG-----EMESTTTSFPNETA-TIISQY 167

Db 140 GDVIYATADRKVEIECVSVGKPAAEITWIDGLGNVLTDNIEYTVIPLPDQRRTAKSVL 199

QY 168 KLFPTFRFARRRITCVVKHDALEKDIRYSFI-LDIQYAPEVSVT-----GYDGNWFFV 219

Db 200 RLTPKKEHNTNFSQAQNTA-DRTYRSAKIRVEVKYAPKVKVNVVMGSLPGGAGS--VG 256

QY 220 RKG-----VNLKNADANPPPKSVWSRLDGQWPDGLASDNTLHFVH 262

Db 257 GAGGGSVHMSTGSRIVEHSQVRLECRADANPSDVRVRFIND----EPIIGGQKTEMVIR 312

QY 263 PLTFNYSYGVYI-CKVTNSLQGRSD 285

Db 313 NVTRKFHDAIVKCEVQNSVGKSED 336

RESULT 13

A47639

OX-2 membrane glycoprotein precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Jun-2000

C;Accession: A47639

R;McCaughan, G.W.; Clark, M.J.; Barclay, A.N.

Immunogenetics 25, 329-335, 1987

A;Title: Characterization of the human homolog of the rat MRC OX-2 membrane glycoprotein

A;Reference number: A47639; MUID:87192943; PMID:3032785

A;Accession: A47639

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-274 <MCC>

A;Cross-references: GB:X05323; NID:g34742; PIDN:CAA28943.1; PID:g1335216; GB:M17226; GB:

C;Superfamily: MRC OX-2 antigen; immunoglobulin homology

C;Keywords: glycoprotein; membrane protein

F;40-119/Domain: immunoglobulin homology <IMM>

Query Match 12.3%; Score 187.5; DB 2; Length 274;

Best Local Similarity 24.8%; Pred. No. 2.9e-07;

Matches 52; Conservative 36; Mismatches 97; Indels 25; Gaps 4;

QY 11 SLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKYNLNDATIT 70

Db 44 SLKCSLQNAQAEALIVTWQKKKAVSPENMVTFSENHGVVIQPAYKDKINITQLGLQNSTIT 103

QY 71 LHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSL-IGPDSLIDGGNETVAAIC 129

Db 104 FWNITLEDGECYMCLENTFGFGKISGTACTLVYVQPIVSLHYKFSSEHNLN-----IT 155

QY 130 IAATGKPVAHIDWEGDLGEMESTT--SFPNETATIIISQYKLPFPFARGRRITCVVKHP 187

A;Residues: 1-5175 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: CESP:F15G9.4a
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3;
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/

Query Match 11.4%; Score 173.5; DB 2; Length 5175;
Best Local Similarity 26.0%; Pred. No. 0.00013;
Matches 79; Conservative 39; Mismatches 123; Indels 63; Gaps 17;

QY 8 KNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLEKKNYSLND 67
Db 808 RQVTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG-----NLLITDA 854

QY 68 TITLHNIGFSDSGKYICKAVTFPLGNAQSST--VTVLVEPTVSLIKGPDSLIDGGNETV 125
Db 855 QI-----EDQGQFTCIARN-TYQQQSQSTTLMVTGLVSPVLGHVPPEEQLIEGQDLTL 906

QY 126 AAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQKLFPTRFARGR---RITC 182
Db 907 S--CVVVLGTPKPSIVWIKDDKPVEE-----GPTIKIEGGGSLRLRGGNPKDEGKYTC 958

QY 183 VVKHPALEKDIRYSFIL---DIQYAPE-----VSVTGYDGNW-----FVGRKGV 223
Db 959 IAVSPAGNSTLHINVLIKKPEFVYKPEGGIVFKPTISGMDEKHVAVVNSTHDVLDGEF 1018

QY 224 NLKCNADANPPPKSVWSRLDGQWP-----DGLLASDNTLHFVHPLTFNYSGVYICKVT 277
Db 1019 AIPCWVSGTTPPI-ITW-YLDGR-PITPNSRDEFTVTADNTL-IVRKADKSYSGVYTCQAT 1074

QY 278 NSLG 281
Db 1075 NSAG 1078

Search completed: April 12, 2004, 09:47:01
Job time : 8.54126 secs

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 4.55462 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-2_COPY_58_342
Perfect score: 1520
Sequence: 1 HVTAVWGKNVSLKCLIEVNE.....FNYSGVYICKVTNSLGQRSD 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	532.5	35.0	515	1 PVR1_MOUSE	Q9jkf6 mus musculu
2	524.5	34.5	517	1 PVR1_HUMAN	Q15223 homo sapien
3	520.5	34.2	515	1 PVR1_PIG	Q9gl76 sus scrofa
4	394	25.9	530	1 PVR2_MOUSE	P32507 mus musculu
5	379.5	25.0	417	1 PVR_CERAE	P32506 cercopithec
6	372	24.5	538	1 PVR2_HUMAN	Q92692 homo sapien
7	368.5	24.2	417	1 PVR_HUMAN	P15151 homo sapien
8	207	13.6	764	1 ICCR_DROME	Q08180 drosophila
9	187.5	12.3	278	1 OX2G_HUMAN	P41217 homo sapien
10	183.5	12.1	837	1 NCM2_MOUSE	O35136 mus musculu
11	178.5	11.7	4391	1 PGBM_HUMAN	P98160 homo sapien
12	166.5	11.0	853	1 NCAL_BOVIN	P31836 bos taurus
13	166	10.9	588	1 C166_CHICK	P42292 gallus gall
14	163.5	10.8	626	1 MAG_HUMAN	P20916 homo sapien
15	163.5	10.8	626	1 MAG_MOUSE	P20917 mus musculu
16	162.5	10.7	278	1 OX2G_MOUSE	O54901 mus musculu
17	162.5	10.7	278	1 OX2G_RAT	P04218 rattus norv
18	161.5	10.6	626	1 MAG_RAT	P07722 rattus norv
19	161.5	10.6	2012	1 DSCA_HUMAN	O60469 homo sapien
20	158.5	10.4	509	1 SHS1_RAT	P97710 r protein-t
21	154	10.1	702	1 CEAS_HUMAN	P06731 homo sapien
22	154	10.1	837	1 NCM2_HUMAN	O15394 homo sapien
23	153	10.1	353	1 CEPU_CHICK	Q90773 gallus gall
24	152.5	10.0	858	1 NCAL_RAT	P13596 rattus norv
25	152	10.0	761	1 NCA2_HUMAN	P13592 homo sapien
26	152	10.0	848	1 NCAL_HUMAN	P13591 homo sapien
27	147	9.7	344	1 NTRI_MOUSE	Q99pj0 mus musculu
28	147	9.7	344	1 NTRI_RAT	Q62718 rattus norv
29	147	9.7	739	1 VCA1_MOUSE	P29533 mus musculu
30	147	9.7	1709	1 SN_HUMAN	Q9bzz2 mus musculu
31	145.5	9.6	345	1 OPCM_BOVIN	P11834 bos taurus
32	145	9.5	337	1 OPCM_CHICK	Q98892 gallus gall
33	144	9.5	344	1 NTRI_HUMAN	Q9p121 homo sapien

34	143.5	9.4	725	1 NCA2_MOUSE	P13594 mus musculu
35	143.5	9.4	1115	1 NCA1_MOUSE	P13595 mus musculu
36	143	9.4	1091	1 NCA1_CHICK	P13590 gallus gall
37	142	9.3	569	1 SILF_MOUSE	Q920g3 mus musculu
38	141	9.3	359	1 LACH_DROME	Q24372 drosophila
39	140	9.2	332	1 CD22_PANPA	Q9nie5 pan paniscu
40	140	9.2	332	1 CD22_PANTR	Q9nie6 pan troglod
41	139.5	9.2	271	1 OX2V_KSHV	P88963 kaposi's sa
42	139.5	9.2	467	1 SIL7_HUMAN	Q9y286 homo sapien
43	139	9.1	583	1 C166_MOUSE	Q61490 mus musculu
44	139	9.1	3707	1 PGBM_MOUSE	Q05793 mus musculu
45	138.5	9.1	330	1 CD22_PONPY	Q9nie3 pongo pygma

ALIGNMENTS

RESULT 1					
PVR1_MOUSE					
ID	PVR1_MOUSE	STANDARD;	PRT;	515 AA.	
AC	Q9JKF6; Q9ERL5; Q9JIL7;				
DT	16-OCT-2001 (Rel. 40, Created)				
DT	16-OCT-2001 (Rel. 40, Last sequence update)				
DT	15-MAR-2004 (Rel. 43, Last annotation update)				
DE	Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (HvEC) (Nectin 1).				
GN	PVRL1 OR PRR1 OR HVEC.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxID=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-20243787; PubMed-10781093;				
RA	Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J.,				
RA	Lecocq E., Dubreuil P., Campadelli-Fiume G.;				
RT	"The murine homolog of human nectin1 delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gp.";				
RT	Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE-20541977; PubMed-11090177;				
RA	Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;				
RT	"Striking similarity of murine nectin-lalpha to human nectin-lalpha (Hvec) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";				
RT	J. Virol. 74:11773-11781(2000).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=Swiss Webster;				
RA	Zhan J., Wimmer E.;				
RT	"Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development.";				
RT	Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.				
RL	-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAPERPEPVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.				
CC	-!- SUBUNIT: Interacts with HSV glycoprotein D (gp).				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.				
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).				
CC	-----				
CC	EMBL; AF239762; AAF60333.1; -.				

DR	EMBL; AF270977; AAF76195.1; -.	DE	(CD111 antigen).
DR	EMBL; AF297665; AAG22808.1; -.	GN	PVRL1 OR PRR1 OR HVEC.
DR	MGD; MGI:1926483; Pvr11.	OS	Homo sapiens (Human).
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DR	GO; GO:0005515; F:protein binding; IPI.	OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
DR	GO; GO:0004872; F:receptor activity; IDA.	OX	NCBI_TaxID=9606;
DR	InterPro; IPR007110; IG-like.	RN	[1]
DR	InterPro; IPR003599; IG.	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
DR	Pfam; PF00047; IG; 2.	RX	MEDLINE=95237621; PubMed=7721102;
DR	SMART; SM00409; IG; 2.	RA	Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
DR	PROSITE; PS50835; IG LIKE; 2.	RA	Dubreuil P.;
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;	RT	"CDNA characterization and chromosomal localization of a gene related
KW	Repeat; Glycoprotein; Signal.	RT	to the poliovirus receptor gene.";
FT	SIGNAL 1 30	RL	Gene 155:261-265(1995).
FT	CHAIN 31 515	RN	[2]
FT	DOMAIN 31 354	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
FT	TRANSMEM 355 375	RX	MEDLINE=98279152; PubMed=9616127;
FT	DOMAIN 376 515	RA	Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
FT	DOMAIN 31 141	RA	Spear P.G.;
FT	DOMAIN 145 243	RT	"Entry of alphaherpesviruses mediated by poliovirus receptor-related
FT	DOMAIN 247 334	RT	protein 1 and poliovirus receptor.";
FT	DOMAIN 436 442	RL	Science 280:1618-1620(1998).
FT	DOMAIN 443 447	RN	[3]
FT	DISULFID 51 124	RP	SEQUENCE FROM N.A. (ISOFORM GAMMA).
FT	DISULFID 172 226	RX	MEDLINE=21256041; PubMed=11356977;
FT	DISULFID 269 316	RA	Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
FT	CARBOHYD 36 36	RA	Campadelli-Fjume G., Dubreuil P.;
FT	CARBOHYD 72 72	RT	"Novel, soluble isoform of the herpes simplex virus (HSV) receptor
FT	CARBOHYD 139 139	RT	nectini (or prr1-HIGR-Hvec) modulates positively and negatively
FT	CARBOHYD 202 202	RT	susceptibility to hsv infection.";
FT	CARBOHYD 286 286	RL	J. Virol. 75:5684-5691(2001).
FT	CARBOHYD 297 297	RN	[4]
FT	CARBOHYD 332 332	RP	SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
FT	CONFLICT 138 138	RX	MEDLINE=20392396; PubMed=10932188;
FT	CONFLICT 165 165	RA	Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
FT	CONFLICT 342 342	RA	Helms J.A., Spritz R.A.;
FT	CONFLICT 428 428	RT	"Mutations of PVRL1, encoding a cell-cell adhesion
FT	SEQUENCE 515 AA; 57064 MW; FFF608EB5FFB7A0F CRC64;	RT	molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
		RT	dysplasia.";
		RL	Nat. Genet. 25:427-430(2000).
		CC	-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
		CC	ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
		CC	CELLS.
		CC	-!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
		CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
		CC	delta). Secreted (isoform gamma).
		CC	-!- ALTERNATIVE PRODUCTS:
		CC	Event=Alternative splicing; Named isoforms=3;
		CC	Name=Delta;
		CC	Isoid=Q15223-1; Sequence=Displayed;
		CC	Name=Alpha;
		CC	Isoid=Q15223-2; Sequence=VSP_002626, VSP_002627;
		CC	Name=Gamma;
		CC	Isoid=Q15223-3; Sequence=VSP_002624, VSP_002625;
		CC	DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
		CC	ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is
		CC	responsible for allelic forms known as Margarita island ectodermal
		CC	dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
		CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
		CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
		CC	-!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
		CC	WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
		CC	-----
		CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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		CC	or send an email to license@isb-sib.ch).
		CC	-----
		DR	EMBL; X76400; CAA53980.2; ALT_INIT.
		DR	EMBL; AF060231; AAC23798.1; -.

DR	EMBL; AF270977; AAF76195.1; -.	DE	(CD111 antigen).
DR	EMBL; AF297665; AAG22808.1; -.	GN	PVRL1 OR PRR1 OR HVEC.
DR	MGD; MGI:1926483; Pvr11.	OS	Homo sapiens (Human).
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DR	GO; GO:0005515; F:protein binding; IPI.	OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
DR	GO; GO:0004872; F:receptor activity; IDA.	OX	NCBI_TaxID=9606;
DR	InterPro; IPR007110; IG-like.	RN	[1]
DR	InterPro; IPR003599; IG.	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
DR	Pfam; PF00047; IG; 2.	RX	MEDLINE=95237621; PubMed=7721102;
DR	SMART; SM00409; IG; 2.	RA	Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
DR	PROSITE; PS50835; IG LIKE; 2.	RA	Dubreuil P.;
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;	RT	"CDNA characterization and chromosomal localization of a gene related
KW	Repeat; Glycoprotein; Signal.	RT	to the poliovirus receptor gene.";
FT	SIGNAL 1 30	RL	Gene 155:261-265(1995).
FT	CHAIN 31 515	RN	[2]
FT	DOMAIN 31 354	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
FT	TRANSMEM 355 375	RX	MEDLINE=98279152; PubMed=9616127;
FT	DOMAIN 376 515	RA	Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
FT	DOMAIN 31 141	RA	Spear P.G.;
FT	DOMAIN 145 243	RT	"Entry of alphaherpesviruses mediated by poliovirus receptor-related
FT	DOMAIN 247 334	RT	protein 1 and poliovirus receptor.";
FT	DOMAIN 436 442	RL	Science 280:1618-1620(1998).
FT	DOMAIN 443 447	RN	[3]
FT	DISULFID 51 124	RP	SEQUENCE FROM N.A. (ISOFORM GAMMA).
FT	DISULFID 172 226	RX	MEDLINE=21256041; PubMed=11356977;
FT	DISULFID 269 316	RA	Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
FT	CARBOHYD 36 36	RA	Campadelli-Fjume G., Dubreuil P.;
FT	CARBOHYD 72 72	RT	"Novel, soluble isoform of the herpes simplex virus (HSV) receptor
FT	CARBOHYD 139 139	RT	nectini (or prr1-HIGR-Hvec) modulates positively and negatively
FT	CARBOHYD 202 202	RT	susceptibility to hsv infection.";
FT	CARBOHYD 286 286	RL	J. Virol. 75:5684-5691(2001).
FT	CARBOHYD 297 297	RN	[4]
FT	CARBOHYD 332 332	RP	SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
FT	CONFLICT 138 138	RX	MEDLINE=20392396; PubMed=10932188;
FT	CONFLICT 165 165	RA	Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
FT	CONFLICT 342 342	RA	Helms J.A., Spritz R.A.;
FT	CONFLICT 428 428	RT	"Mutations of PVRL1, encoding a cell-cell adhesion
FT	SEQUENCE 515 AA; 57064 MW; FFF608EB5FFB7A0F CRC64;	RT	molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
		RT	dysplasia.";
		RL	Nat. Genet. 25:427-430(2000).
		CC	-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
		CC	ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
		CC	CELLS.
		CC	-!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
		CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
		CC	delta). Secreted (isoform gamma).
		CC	-!- ALTERNATIVE PRODUCTS:
		CC	Event=Alternative splicing; Named isoforms=3;
		CC	Name=Delta;
		CC	Isoid=Q15223-1; Sequence=Displayed;
		CC	Name=Alpha;
		CC	Isoid=Q15223-2; Sequence=VSP_002626, VSP_002627;
		CC	Name=Gamma;
		CC	Isoid=Q15223-3; Sequence=VSP_002624, VSP_002625;
		CC	DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
		CC	ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is
		CC	responsible for allelic forms known as Margarita island ectodermal
		CC	dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
		CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
		CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
		CC	-!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
		CC	WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
		CC	-----
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		CC	or send an email to license@isb-sib.ch).
		CC	-----
		DR	EMBL; X76400; CAA53980.2; ALT_INIT.
		DR	EMBL; AF060231; AAC23798.1; -.

DR	EMBL; AF270977; AAF76195.1; -.	DE	(CD111 antigen).
DR	EMBL; AF297665; AAG22808.1; -.	GN	PVRL1 OR PRR1 OR HVEC.
DR	MGD; MGI:1926483; Pvr11.	OS	Homo sapiens (Human).
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DR	GO; GO:0005515; F:protein binding; IPI.	OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
DR	GO; GO:0004872; F:receptor activity; IDA.	OX	NCBI_TaxID=9606;
DR	InterPro; IPR007110; IG-like.	RN	[1]
DR	InterPro; IPR003599; IG.	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
DR	Pfam; PF00047; IG; 2.	RX	MEDLINE=95237621; PubMed=7721102;
DR	SMART; SM00409; IG; 2.	RA	Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
DR	PROSITE; PS50835; IG LIKE; 2.	RA	Dubreuil P.;
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;	RT	"CDNA characterization and chromosomal localization of a gene related
KW	Repeat; Glycoprotein; Signal.	RT	to the poliovirus receptor gene.";
FT	SIGNAL 1 30	RL	Gene 155:261-265(1995).
FT	CHAIN 31 515	RN	[2]
FT	DOMAIN 31 354	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
FT	TRANSMEM 355 375	RX	MEDLINE=98279152; PubMed=9616127;
FT	DOMAIN 376 515	RA	Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
FT	DOMAIN 31 141	RA	Spear P.G.;
FT	DOMAIN 145 243	RT	"Entry of alphaherpesviruses mediated by poliovirus receptor-related
FT	DOMAIN 247 334	RT	protein 1 and poliovirus receptor.";
FT	DOMAIN 436 442	RL	Science 280:1618-1620(1998).
FT	DOMAIN 443 447	RN	[3]
FT	DISULFID 51 124	RP	SEQUENCE FROM N.A. (ISOFORM GAMMA).
FT	DISULFID 172 226	RX	MEDLINE=21256041; PubMed=11356977;
FT	DISULFID 269 316	RA	Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
FT	CARBOHYD 36 36	RA	Campadelli-Fjume G., Dubreuil P.;
FT	CARBOHYD 72 72	RT	"Novel, soluble isoform of the herpes simplex virus (HSV) receptor
FT	CARBOHYD 139 139	RT	nectini (or prr1-HIGR-Hvec) modulates positively and negatively
FT	CARBOHYD 202 202	RT	susceptibility to hsv infection.";
FT	CARBOHYD 286 286	RL	J. Virol. 75:5684-5691(2001).
FT	CARBOHYD 297 297	RN	[4]
FT	CARBOHYD 332 332	RP	SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
FT	CONFLICT 138 138	RX	MEDLINE=20392396; PubMed=10932188;
FT	CONFLICT 165 165	RA	Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
FT	CONFLICT 342 342	RA	Helms J.A., Spritz R.A.;
FT	CONFLICT 428 428	RT	"Mutations of PVRL1, encoding a cell-cell adhesion
FT	SEQUENCE 515 AA; 57064 MW; FFF608EB5FFB7A0F CRC64;	RT	molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
		RT	dysplasia.";
		RL	Nat. Genet. 25:427-430(2000).
		CC	-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
		CC	ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO
		CC	CELLS.
		CC	-!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
		CC	-!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
		CC	delta). Secreted (isoform gamma).
		CC	-!- ALTERNATIVE PRODUCTS:
		CC	Event=Alternative splicing; Named isoforms=3;
		CC	Name=Delta;
		CC	Isoid=Q15223-1; Sequence=Displayed;
		CC	Name=Alpha;
		CC	Isoid=Q15223-2; Sequence=VSP_002626, VSP_002627;
		CC	Name=Gamma;
		CC	Isoid=Q15223-3; Sequence=VSP_002624, VSP_002625;
		CC	DISEASE: Defects in PVRL1 are a cause of cleft lip/palate-
		CC	ectodermal dysplasia syndrome (CLPEDI) [MIM:225000]. CLPEDI is
		CC	responsible for allelic forms known as Margarita island ectodermal
		CC	dysplasia [MIM:225060] and Zlotogora-Ogur syndrome.
		CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
		CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
		CC	-!- DATABASE: NAME=PROW; NOTE=PROW 2:45-49(2001);
		CC	WWW="http://www.ncbi.nlm.nih.gov/prow/guide/2005693930_g.htm".
		CC	-----
		CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration
		CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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		CC	use by non-profit institutions as long as its content is in no way
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		CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
		CC	or send an email to license@isb-sib.ch).
		CC	-----
		DR	EMBL; X76400; CAA53980.2; ALT_INIT.
		DR	EMBL; AF060231; AAC23798.1; -.

DR	EMBL; AF270977; AAF76195.1; -.	DE	(CD111 antigen).
DR	EMBL; AF297665; AAG22808.1; -.	GN	PVRL1 OR PRR1 OR HVEC.
DR	MGD; MGI:1926483; Pvr11.	OS	Homo sapiens (Human).
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.	OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
DR	GO; GO:0005515; F:protein binding; IPI.	OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
DR	GO; GO:0004872; F:receptor activity; IDA.	OX	NCBI_TaxID=9606;
DR	InterPro; IPR007110; IG-like.	RN	[1]
DR	InterPro; IPR003599; IG.	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
DR	Pfam; PF00047; IG; 2.	RX	MEDLINE=95237621; PubMed=7721102;
DR	SMART; SM00409; IG; 2.	RA	Lopez M., Eberle F., Mattei M.-G., Gabert J., Bardin F., Maroc C.,
DR	PROSITE; PS50835; IG LIKE; 2.	RA	Dubreuil P.;
KW	Cell adhesion; Immunoglobulin domain; Receptor; Transmembrane;	RT	"CDNA characterization and chromosomal localization of a gene related
KW	Repeat; Glycoprotein; Signal.	RT	to the poliovirus receptor gene.";
FT	SIGNAL 1 30	RL	Gene 155:261-265(1995).
FT	CHAIN 31 515	RN	[2]
FT	DOMAIN 31 354	RP	SEQUENCE FROM N.A. (ISOFORM DELTA).
FT	TRANSMEM 355 375	RX	MEDLINE=98279152; PubMed=9616127;
FT	DOMAIN 376 515	RA	Geraghty R.J., Krummenacher C., Cohen G.H., Eisenberg R.J.,
FT	DOMAIN 31 141	RA	Spear P.G.;
FT	DOMAIN 145 243	RT	"Entry of alphaherpesviruses mediated by poliovirus receptor-related
FT	DOMAIN 247 334	RT	protein 1 and poliovirus receptor.";
FT	DOMAIN 436 442	RL	Science 280:1618-1620(1998).
FT	DOMAIN 443 447	RN	[3]
FT	DISULFID 51 124	RP	SEQUENCE FROM N.A. (ISOFORM GAMMA).
FT	DISULFID 172 226	RX	MEDLINE=21256041; PubMed=11356977;
FT	DISULFID 269 316	RA	Lopez M., Cocchi F., Avitabile E., Leclerc A., Adelaide J.,
FT	CARBOHYD 36 36	RA	Campadelli-Fjume G., Dubreuil P.;
FT	CARBOHYD 72 72	RT	"Novel, soluble isoform of the herpes simplex virus (HSV) receptor
FT	CARBOHYD 139 139	RT	nectini (or prr1-HIGR-Hvec) modulates positively and negatively
FT	CARBOHYD 202 202	RT	susceptibility to hsv infection.";
FT	CARBOHYD 286 286	RL	J. Virol. 75:5684-5691(2001).
FT	CARBOHYD 297 297	RN	[4]
FT	CARBOHYD 332 332	RP	SEQUENCE OF 28-517 FROM N.A. (ISOFORMS ALPHA AND DELTA), AND DISEASE.
FT	CONFLICT 138 138	RX	MEDLINE=20392396; PubMed=10932188;
FT	CONFLICT 165 165	RA	Suzuki K., Hu D., Bustos T., Zlotogora J., Richieri-Costa A.,
FT	CONFLICT 342 342	RA	Helms J.A., Spritz R.A.;
FT	CONFLICT 428 428	RT	"Mutations of PVRL1, encoding a cell-cell adhesion
FT	SEQUENCE 515 AA; 57064 MW; FFF608EB5FFB7A0F CRC64;	RT	molecule/herpesvirus receptor, in cleft lip/palate-ectodermal
		RT	dysplasia.";
		RL	Nat. Genet. 25:427-430(2000).
		CC	-!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR
		CC	ALPHAHERPESVIRUS (HSV-1, HSV-2

FT	DOMAIN	437	443	POLY-GLU.
FT	DOMAIN	444	447	POLY-GLY.
FT	DISULFID	51	124	BY SIMILARITY.
FT	DISULFID	172	226	BY SIMILARITY.
FT	DISULFID	269	316	BY SIMILARITY.
FT	CARBOHYD	36	36	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	72	72	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	202	202	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	286	286	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	297	297	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	307	307	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	515 AA;	57047 MW;	BFAB00320DDE3785 CRC64;
Query Match 34.2%; Score 520.5; DB 1; Length 515;				
Best Local Similarity 38.1%; Pred. No. 2.5e-35;				
Matches 109; Conservative 51; Mismatches 115; Indels 11; Gaps 5;				
QY	7	GKNVSLKCLIE---	VNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLFKNYS	63
Db	44	GTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPAMGVSVLAPYRERVEFLRPS	103	
QY	64	LNDATTTLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDSLIDG---	120	
Db	104	FTDGTIRLSRLELEDEGVYICEFATFPAGNRESQNLNLTVMKFT-NWIEGTQAVLRAKKG	162	
QY	121	-GNETVAICIAATGKPVAHIDWEGDL-GEMESTTTTSFPNETATITISQYKLFPTRFARGR	178	
Db	163	KDDKVLVATCTSANGKPPSVSVSWETHLKGAEYQEIRNPNGTIVISRYRLVPSREDHRQ	222	
QY	179	RITCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNFVGRKGVLNLCNADANPPPFKS	238	
Db	223	SLACIVNYHM--DRPRESLTNLVQYEPEVTIEGFDGNWYLRQMDVKLTCKADANPPATEY	280	
QY	239	VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS	284	
Db	281	HWTTLNGSLPKGVEAQNRTLFFRGPIINYSMAGTYICEATNPIGTRS	326	
RESULT 4				
PVR2_MOUSE	STANDARD;	PRT;	530 AA.	
AC	P32507; Q62096;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Poliovirus receptor related protein 2 precursor (Murine herpesvirus entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).			
GN	PVRL2 OR PVS OR PVR OR MPH.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=92219365; PubMed=1560525;			
RA	Morrison M.E., Racaniello V.R.;			
RT	"Molecular cloning and expression of a murine homolog of the human poliovirus receptor gene."			
RL	J. Virol. 66:2807-2813(1992).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM BETA).			
RC	STRAIN=C57BL/6; TISSUE=Brain;			
RX	MEDLINE=94179228; PubMed=8132569;			
RA	Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;			
RT	"Amino acid residues on human poliovirus receptor involved in interaction with poliovirus."			
RL	J. Biol. Chem. 269:8431-8438(1994).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM BETA).			
RC	STRAIN=FVB/N; TISSUE=Colon;			
RX	MEDLINE=22388257; PubMed=12477932;			

RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F., Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RA	CHARACTERIZATION.			
RP	MEDLINE=99214397; PubMed=10196354;			
RX	Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;			
RA	"The murine homolog (Mph) of human herpesvirus entry protein B (HvEB) mediates entry of pseudorabies virus but not herpes simplex virus types 1 and 2."			
RT	J. Virol. 73:4493-4497 (1999).			
RL	FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (SUCH AS MURINE HSV) ENTRY INTO CELLS.			
CC	SUBCELLULAR LOCATION: Type I membrane protein.			
CC	ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=Beta;			
CC	Isoid=P32507-1; Sequence=Displayed;			
CC	Name=Alpha;			
CC	Isoid=P32507-2; Sequence=VSP 002630, VSP 002631;			
CC	TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and liver.			
CC	SIMILARITY: Contains 1 immunoglobulin-like V-type domain.			
CC	SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.			
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CC	EMBL; M80206; AAA39734.1; -.			
DR	EMBL; D26107; BAA05103.1; -.			
DR	EMBL; BC059941; AAH59941.1; -.			
DR	PIR; A38211; HLMSP3.			
DR	PIR; A53437; A53437.			
DR	MGD; MGI:97822; Pvrl2.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; ig; 3.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 3.			
DR	Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal; Repeat; Alternative splicing.			
KW	SIGNAL	1	31	POTENTIAL.
KW	CHAIN	32	530	POLIOVIRUS RECEPTOR RELATED PROTEIN 2.
FT	DOMAIN	32	351	EXTRACELLULAR (POTENTIAL).
FT	DOMAIN	352	372	POTENTIAL.
FT	TRANSMEM	373	530	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	32	147	IG-LIKE V-TYPE.
FT	DOMAIN	153	247	IG-LIKE C2-TYPE 1.
FT	DOMAIN	252	337	IG-LIKE C2-TYPE 2.
FT	DISULFID	54	131	BY SIMILARITY.
FT	DISULFID	174	229	BY SIMILARITY.


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FT DISULFID 274 320 BY SIMILARITY.
FT CARBOHYD 128 128 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 339 467 ESPATAGATGGIIGIIAIIATAVAGTILICRQORKE
FT VARSPLIC 339 467 ORLQAADEEEELGPPSYKPTPKAKLEPEMPSQLFTLGA
FT SEHSPVKTPYFDAGVSCADQEMPRYHELPLEERSGPLLGL
FT ATGLGP -> DTPQASRDVGLVWGVGGTLLVLLAGGFL
FT ALILLRGRRRKSPGGGNDGRSDYDPKTVFGNGGPFVFW
FT RSASPEPMRDPGREDEEEEMKAEGLMLPPHESPDDM
FT ESHLDGSLISRRVAVV (in isoform Alpha).
FT /FTid=VSP 002630.
FT Missing (in isoform Alpha).
FT /FTid=VSP 002631.
FT SEQUENCE 530 AA; 57317 MW; 0ED71BFA2B231BBE CRC64;

Query Match 25.9%; Score 394; DB 1; Length 530;
Best Local Similarity 32.1%; Pred. No. 6.5e-25;
Matches 94; Conservative 45; Mismatches 124; Indels 30; Gaps 9;

QY 7 GKNVSLKC--LIEVNETITQISWEKIHGKSSQTVAHHHPQYGFVSQGEY--QGRVLF--- 59
Db 47 GGTVELPCHLLPPTTTERVSQVTWQRLDG---TVVAAHFPSFGVDFFPNSQFSKDRLSFVRA 103
QY 60 ---KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP-----TVSLI 111
Db 104 RPETNADLRDATLAFRGLRVEDEGNYTCEFATFPNGTRRGVTWLRVIAQDENHAEAEVET 163
QY 112 KSPDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTSFPN---ETATIIISQYK 168
Db 164 IGQSV-----AVARCVSTGGRPPARITWISSLGG-EAKDTQEPGIAQGTVTIISRY 215
QY 169 LFPTRFARRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNFWFVGRKGVNLKCN 228
Db 216 LVFVGRADGVKVTCTRVEHESFEPEILLPVTLVSRYPPEVSGYDDNWNWYLGSRSEAILTCD 275
QY 229 ADANPPPKSVWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLG 281
Db 276 VRSNPEPTDYDWSTTSQVFPASAVAQSQL-LVHSVDRMVNTTICTATNAV 327

RESULT 5
PVR CERAE
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AC P32506;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor.
GN PVR OR PVS.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND DELTA).
RC TISSUE=Kidney;
RX MEDLINE=93059651; PubMed=1331508;
RA Koike S., Ise I., Sato Y., Yonekawa H., Gotoh O., Nomoto A.;
RT "A second gene for the African green monkey poliovirus receptor that
RT has no putative N-glycosylation site in the functional N-terminal
RT immunoglobulin-like domain."
RL J. Virol. 66:7059-7066(1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoform alpha).
CC Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P32506-1; Sequence=Displayed;
CC Name=Beta;
```

```
CC IsoId=P32506-3; Sequence=Not described;
CC Name=Gamma;
CC IsoId=P32506-4; Sequence=Not described;
CC Name=Delta;
CC IsoId=P32506-2; Sequence=VSP 002622, VSP 002623;
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC -----
CC EMBL; D12611; BAA02136.1; -.
CC EMBL; D12612; BAA02137.1; -.
CC PIR; A44194; A44194.
CC PIR; B44194; B44194.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG_LIKE; 3.
CC Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
CC Repeat; Alternative splicing.
CC SIGNAL 1 20 POTENTIAL.
CC CHAIN 21 417 POLIOVIRUS RECEPTOR.
CC DOMAIN 21 343 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 344 367 POTENTIAL.
CC DOMAIN 368 417 CYTOPLASMIC (POTENTIAL).
CC DOMAIN 24 139 IG-LIKE V-TYPE.
CC DOMAIN 145 237 IG-LIKE C2-TYPE 1.
CC DOMAIN 244 328 IG-LIKE C2-TYPE 2.
CC DISULFID 49 123 BY SIMILARITY.
CC DISULFID 166 221 BY SIMILARITY.
CC DISULFID 266 312 BY SIMILARITY.
CC CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 120 120 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 237 237 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 278 278 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC CARBOHYD 313 313 N-LINKED (GLCNAC. . .) (POTENTIAL).
CC VARSPLIC 386 392 EHASASA -> HHQSCHN (in isoform Delta).
CC /FTid=VSP 002622.
CC Missing (in isoform Delta).
CC /FTid=VSP 002623.
CC SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6E1F CRC64;

Query Match 25.0%; Score 379.5; DB 1; Length 417;
Best Local Similarity 32.3%; Pred. No. 7.5e-24;
Matches 93; Conservative 50; Mismatches 126; Indels 19; Gaps 9;

QY 7 GKNVSLKCLIEV--NET-ITQISWEKIHGKSSQTVAHH---POYGFVSQGEYQGRVLF 59
Db 42 GDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGPYSEPKRLEFVAARL- 99
QY 60 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP--TVSLIKGPD 117
Db 100 -GTELRDASLRMFGRLVEDEGNYTCLFVTFPPQGSRSVDIWLRLVLAKEPQNTAEVQKVLT- 157
QY 118 IDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTTS--FPNETATIIISQYKLFPT 175
Db 158 ---GKPVVARCVSTGGRPPAHITWHSDLGCMPTSQAPGFLSGTIVTSLWILVPS 214
QY 176 RGRRTICVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNFWFVGRKGVNLKCNADANPPP 235
Db 215 DGKSVTCVKEHESFEKPOLLTVNLTVVYYPEVSVISGYDNNWYLSQNEATLTCDARSNPEP 274
QY 236 FKSWSRLDGQWPDGGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLG 283
```


Db 65 ISLVTWQRPDAPANHQNVAAPFKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDAT 124
QY 69 ITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP-----TVSLIKGPDSDLIDGG 121
Db 125 LALHGLTVEDEGNYTCEFAFPFKGSGVRGMTWLRVIAKPKNAQAEAKVTFSQDP----- 177
QY 122 NETVAAICIAATGKPVVHI-----DWEGLGEMESITTSFPNETATIISQYKLFPTTREA 175
Db 178 --TTVALCISKEGRPPARISWLSLSDWEAKETQVSGTLAG---TVTTSRFTLVPSGRA 231
QY 176 RGRRTCVVKKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFVGRKGVNLCNADANPPP 235
Db 232 DGVTVTCKVEHESFEPEPALIPVTLVSVRYPPEVSIISGDDNWYLGRTDATALSCDVRSNPEP 291
QY 236 FKSVMWSRLDQWPPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 292 TGYDWSSTSGTFTPTSAVAQSQL-VIHAVDLSLFTTTFVCTVTNAVG 336

RESULT 7

PVR_HUMAN
ID PVR_HUMAN STANDARD; PRT; 417 AA.
AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. PubMed=2538245;
RX MEDLINE=89168426; PubMed=2538245;
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
RT sequence, and expression of a new member of the immunoglobulin
RT superfamily.";
RL Cell 56:855-865(1989).
RN [2]
RP REVISIONS.
RA Racaniello V.R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91006015; PubMed=2170108;
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RA Takeuchi K., Takegami T., Nomoto A.;
RT "The poliovirus receptor protein is produced both as membrane-bound
RT and secreted forms.";
RL EMBO J. 9:3217-3224(1990).
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyianni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
RA Shannon M., Brower A., Olsen A.S., Smith L.M.;
RT "Sequence analysis of a 1Mb region in 19ql3.2 containing a zinc finger
RT gene cluster.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS.
RX MEDLINE=91239515; PubMed=1851992;
RA Koike S., Ise I., Nomoto A.;
RT "Functional domains of the poliovirus receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108(1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N glycosylation of the virus binding domain is not essential for
RT function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373(1992).

CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
CC cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
CC delta). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=4;
CC Name=Alpha;
CC IsoId=P15151-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=P15151-2; Sequence=VSP_002617;
CC Name=Gamma;
CC IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
CC Name=Delta;
CC IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC -!- MISCCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
CC VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
CC -----
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CC -----
CC EMBL; M24407; AAA36461.1; -
CC EMBL; M24406; AAA36462.1; -
CC EMBL; X64116; CAA45478.1; -
CC EMBL; X64117; CAA45478.1; JOINED.
CC EMBL; X64118; CAA45478.1; JOINED.
CC EMBL; X64119; CAA45478.1; JOINED.
CC EMBL; X64120; CAA45478.1; JOINED.
CC EMBL; X64121; CAA45478.1; JOINED.
CC EMBL; X64122; CAA45478.1; JOINED.
CC EMBL; X64123; CAA45478.1; JOINED.
CC EMBL; X64116; CAA45479.1; -
CC EMBL; X64117; CAA45479.1; JOINED.
CC EMBL; X64118; CAA45479.1; JOINED.
CC EMBL; X64119; CAA45479.1; JOINED.
CC EMBL; X64120; CAA45479.1; JOINED.
CC EMBL; X64121; CAA45479.1; JOINED.
CC EMBL; X64122; CAA45479.1; JOINED.
CC EMBL; X64123; CAA45479.1; JOINED.
CC EMBL; X64116; CAA45480.1; -
CC EMBL; X64117; CAA45480.1; JOINED.
CC EMBL; X64118; CAA45480.1; JOINED.
CC EMBL; X64119; CAA45480.1; JOINED.
CC EMBL; X64120; CAA45480.1; JOINED.
CC EMBL; X64121; CAA45480.1; JOINED.
CC EMBL; X64122; CAA45480.1; JOINED.
CC EMBL; X64123; CAA45480.1; JOINED.
CC EMBL; AC068948; AAF69803.1; -
CC PIR; A43024; RWHUPD.
CC PIR; S12048; RWHUPA.
CC Genew; HGNC:9705; PVR.
CC MIM; 173850; -
CC GO; GO:0005737; C:cytoplasm; TAS.
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0016021; C:integral to membrane; TAS.
CC GO; GO:0004872; F:receptor activity; TAS.
CC GO; GO:0007125; P:invasive growth; TAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; ig; 3.
CC SMART; SM00406; IGv; 1.
CC PROSITE; PS0835; IG_LIKE; 3.
KW Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Antigen; Alternative splicing; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 417
FT POLIOVIRUS RECEPTOR.


```
RESULT 10
NCM2 MOUSE
ID NCM2_MOUSE STANDARD; PRT; 837 AA.
AC O35136; O35962;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2) (RB-8 neural cell
adhesion molecule) (R4B12).
GN NCAM2 OR OCAM OR RNCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS LONG AND SHORT).
RC STRAIN=BALB/c; TISSUE=Olfactory neuroepithelium;
RX MEDLINE=97368238; PubMed=9221781;
RA Yoshihara Y., Kawasaki M., Tamada A., Fujita H., Hayashi H.,
RA Kagamiyama H., Mori K.;
RT "OCAM: A new member of the neural cell adhesion molecule family
related to zone-to-zone projection of olfactory and vomeronasal
axons.";
RL J. Neurosci. 17:5830-5842(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM SHORT).
RC STRAIN=C57BL/6J; TISSUE=Olfactory epithelium;
RX MEDLINE=97476194; PubMed=9334170;
RA Alenius M., Bohm S.;
RT "Identification of a novel neural cell adhesion molecule-related gene
with a potential role in selective axonal projection.";
RL J. Biol. Chem. 272:26083-26086(1997).
CC -!- FUNCTION: May play important roles in selective fasciculation and
zone-to-zone projection of the primary olfactory axons.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (long isoform) and
attached to the membrane by a GPI-anchor (short isoform).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=O35136-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=O35136-2; Sequence=VSP_002590;
CC -!- TISSUE SPECIFICITY: Expressed in subsets of both olfactory and
vomeronasal neurons in a zone-specific manner.
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
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EMBL; AF001287; AAB69125.1; -.
EMBL; AF001286; AAB69124.1; -.
EMBL; AF016619; AAC53375.1; -.
DR MGD; MGI:97282; Ncam2.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_C2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Transmembrane; Glycoprotein; Repeat;
KW Immunoglobulin domain; Signal; GPI-anchor; Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 837 NEURAL CELL ADHESION MOLECULE 2.
FT DOMAIN 20 697 EXTRACELLULAR (POTENTIAL).
```

FT	TRANSMEM	698	718	POTENTIAL.
FT	DOMAIN	719	837	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	21	108	IG-LIKE C2-TYPE 1.
FT	DOMAIN	113	202	IG-LIKE C2-TYPE 2.
FT	DOMAIN	208	297	IG-LIKE C2-TYPE 3.
FT	DOMAIN	302	396	IG-LIKE C2-TYPE 4.
FT	DOMAIN	401	491	IG-LIKE C2-TYPE 5.
FT	DOMAIN	482	581	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	594	678	FIBRONECTIN TYPE-III 2.
FT	DISULFID	42	93	PROBABLE.
FT	DISULFID	136	186	PROBABLE.
FT	DISULFID	232	281	PROBABLE.
FT	DISULFID	322	380	PROBABLE.
FT	DISULFID	422	475	PROBABLE.
FT	CARBOHYD	177	177	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	219	219	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	309	309	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	419	419	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	445	445	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	474	474	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	562	562	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPPLIC	694	837	TFNLGLGLGAIIGLGVAAALLILVVDVSCFFIROCGLLMC
FT				ITRRMCKGKSSGSGKEEGKAAVLDGSGKEPIVEMRTE
FT				DERITNHEDGSPVNEPNETTPTLPEKPLKEENGKEVLNA
FT				ETIEIKVSDIIQSKEDDIKA -> NCCEANKGNGGQSWH
FT				LNAVGFVTITMSLSCLF (in isoform Short).
FT				/FTId=VSP_002590.
SQ	SEQUENCE	837 AA; 93203 MW; 70473B053A2D65A5 CRC64;		

Query Match 12.1%; Score 183.5; DB 1; Length 837;

Best Local Similarity 24.9%; Pred. No. 2.3e-07;

Matches 81; Conservative 41; Mismatches 102; Indels 101; Gaps 17;

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QY 1 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFSGVEYQGRVLFK 60
Db 219 NATAEERGEEMTLTCKASGPDPT-ISWFR-----NGKLIIE 253

QY 61 N--YSL--NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPD 116
Db 254 NEKYILKGSNTELTVRNIINKDGGSYVCKA-TNKAGEDQKQAFLOVFPVPHILQLK--- 308

QY 117 LIDGGNET-----VAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIISQYKL 169
Db 309 -----NETTSENGHVTLC-EAEGEPVPEITWKRAIDGVMFSEGDKSPDGRIEVKGQH-- 360

QY 170 FPTRFARGRRITCVVKHPALEKDIRY-----SFILDIQYAP-----EVSVTG 211
Db 361 -----GRSSLHIRDVKLSDSGRYDCEAASRIGHQSRMHLDIEYAPKFSVNQTMYS 412

QY 212 YDGNWFVGRKGVNLKNADANPPFKSV-WSRLDGQWPDGLLASDNTLHF----- 260
Db 413 WEGN-----PINISCDVTANPP--ASIHWR-----EKLLLPKNTTTLKTHSVGRKMI 459

QY 261 --VHPLTFNYSGVYICKVTNSLGQR 283
Db 460 LEIAPTSNDNDFGRYNTATNRIGTR 484

RESULT 11
PGBM HUMAN
ID PGBM_HUMAN STANDARD; PRT; 4391 AA.
AC P98160; Q16287; Q9H3V5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Basement membrane-specific heparan sulfate proteoglycan core
DE protein precursor (HSPG) (Perlecan) (PLC).
GN HSPG2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
```


RN SEQUENCE FROM N.A.
RX MEDLINE=92112994; PubMed=1730768;
RA Kallunki P., Tryggvason K.;
RT "Human basement membrane heparan sulfate proteoglycan core protein: a
RT 467-kD protein containing multiple domains resembling elements of the
RT low density lipoprotein receptor, laminin, neural cell adhesion
RT molecules, and epidermal growth factor.";
RL J. Cell Biol. 116:559-571(1992).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=Colon, and skin;
RX MEDLINE=92235084; PubMed=1569102;
RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;
RT "Primary structure of the human heparan sulfate proteoglycan from
RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple
RT domains homologous to the low density lipoprotein receptor, laminin,
RT neural cell adhesion molecules, and epidermal growth factor.";
RL J. Biol. Chem. 267:8544-8557(1992).
RN [3]
RN SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.
RX MEDLINE=20553141; PubMed=11101850;
RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,
RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,
RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,
RA Hentati F., Fontaine B.;
RT "perlecan, the major proteoglycan of basement membranes, is altered in
RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";
RL Nat. Genet. 26:480-483(2000).
RN [4]
RN SEQUENCE OF 1016-1470 FROM N.A.
RC TISSUE=Colon;
RX MEDLINE=91365376; PubMed=1679749;
RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,
RA Yi H.F., Iozzo R.V.;
RT "Heparan sulfate proteoglycan of human colon: partial molecular
RT cloning, cellular expression, and mapping of the gene (HSPG2) to the
RT short arm of human chromosome 1.";
RL Genomics 10:673-680(1991).
RN [5]
RN SEQUENCE OF 890-1396 FROM N.A.
RC TISSUE=Fibrosarcoma;
RX MEDLINE=92120660; PubMed=1685141;
RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,
RA Tryggvason K.;
RT "Cloning of human heparan sulfate proteoglycan core protein,
RT assignment of the gene (HSPG2) to 1p36.1--p35 and identification of
RT a BamHI restriction fragment length polymorphism.";
RL Genomics 11:389-396(1991).
RN [6]
RN SEQUENCE OF 1-21 FROM N.A.
RX MEDLINE=94052171; PubMed=8234307;
RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;
RT "Structural characterization of the complete human perlecan gene and
RT its promoter.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).
RN [7]
RN CARBOHYDRATE-LINKAGE SITE ASN-2121.
RX MEDLINE=22660472; PubMed=12754519;
RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;
RT "Identification and quantification of N-linked glycoproteins using
RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";
RL Nat. Biotechnol. 21:660-666(2003).
CC -!- FUNCTION: This protein is an integral component of basement
CC membranes. It is responsible for the fixed negative electrostatic
CC charge and is involved in the charge-selective ultrafiltration
CC properties. It serves as an attachment substrate for cells.
CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in
CC dimers or stellate structures. It interacts with other basement
CC membrane components such as laminin, prolargin and collagen type
CC IV.
CC -!- SUBCELLULAR LOCATION: Extracellular.
CC -!- TISSUE SPECIFICITY: Found in the basement membranes.

CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED
CC AND O-LINKED OLIGOSACCHARIDES.
CC -!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel
CC syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder
CC characterized by permanent myotonia (prolonged failure of muscle
CC relaxation) and skeletal dysplasia, resulting in reduced stature,
CC kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.
CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.
CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 3 laminin IV domains.
CC -!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 3 laminin G-like domains.
CC -!- SIMILARITY: Contains 4 EGF-like domains.
CC -!- SIMILARITY: Contains 1 SEA domain.
CC -----
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CC -----
CC EMBL; X62515; CAA44373.1; -.
CC EMBL; M85289; AAAS2700.1; -.
CC EMBL; AL445795; CAC18534.1; -.
CC EMBL; M64283; AAAS2699.1; -.
CC EMBL; S76436; AAB21121.2; -.
CC EMBL; L22078; -; NOT_ANNOTATED_CDS.
CC PIR; A38096; A38096.
CC HSSP; P00740; IEDM.
CC Siena-2DPAGE; P98160; -.
CC Genew; HGNC:5273; HSPG2.
CC MIM; 142461; -.
CC MIM; 255800; -.
CC InterPro; IPR008985; ConA_like_lect_g1.
CC InterPro; IPR000742; EGF_2.
CC InterPro; IPR006209; EGF_like.
CC InterPro; IPR006210; IEGF.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003599; Ig.
CC InterPro; IPR003598; Ig_c2.
CC InterPro; IPR003596; Ig_v.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR002172; LDL_receptor_A.
CC InterPro; IPR000082; SEA_domain.
CC Pfam; PF00008; EGF; 4.
CC Pfam; PF00047; ig; 22.
CC Pfam; PF00052; laminin_B; 3.
CC Pfam; PF00053; laminin_EGF; 7.
CC Pfam; PF00054; laminin_G; 3.
CC Pfam; PF00057; ldl_recept_a; 4.
CC Pfam; PF01390; SEA; 1.
CC PRINTS; PR00261; LDLRECEPTOR.
CC PRODOM; PD003031; Laminin_B; 3.
CC SMART; SM00181; EGF; 15.
CC SMART; SM00180; EGF_Lam; 12.
CC SMART; SM00409; IG; 22.
CC SMART; SM00408; IGC2; 21.
CC SMART; SM00406; IGV; 7.
CC SMART; SM00281; LamB; 3.
CC SMART; SM00282; LamG; 3.
CC SMART; SM00192; LDLa; 4.
CC SMART; SM00200; SEA; 1.
CC PROSITE; PS00022; EGF_1; 9.
CC PROSITE; PS01186; EGF_2; 6.
CC PROSITE; PS50026; EGF_3; 4.
CC PROSITE; PS50835; IG_LIKE; 22.
CC PROSITE; PS50025; LAM_G_DOMAIN; 3.
CC PROSITE; PS01248; LAMININ_TYPE_EGF; 11.
CC PROSITE; PS01209; LDLa_1; 4.

DR PROSITE; PSS0068; LDLRA.2; 4.
DR PROSITE; PSS0024; SEA; 1.
KW Signal; Basement membrane; Proteoglycan; Repeat; Glycoprotein;
KW Heparan sulfate; Laminin EGF-like domain; Immunoglobulin domain;
KW Extracellular matrix; EGF-like domain; Disease mutation.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 4391 BASEMENT MEMBRANE-SPECIFIC HEPARAN
SULFATE PROTEOGLYCAN CORE PROTEIN.
SEA.
FT DOMAIN 80 194 LDL-RECEPTOR CLASS A 1.
FT DOMAIN 198 235 LDL-RECEPTOR CLASS A 2.
FT DOMAIN 284 320 LDL-RECEPTOR CLASS A 3.
FT DOMAIN 324 360 LDL-RECEPTOR CLASS A 4.
FT DOMAIN 367 404 IG-LIKE C2-TYPE 1.
FT DOMAIN 405 504 LAMININ EGF-LIKE 1 (N-TERMINAL).
FT DOMAIN 521 530 LAMININ DOMAIN IV 1 (DOMAIN III A).
FT DOMAIN 531 730 LAMININ EGF-LIKE 1 (C-TERMINAL).
FT DOMAIN 731 763 LAMININ EGF-LIKE 2.
FT DOMAIN 764 813 LAMININ EGF-LIKE 3.
FT DOMAIN 814 871 LAMININ EGF-LIKE 4 (INCOMPLETE).
FT DOMAIN 879 923 LAMININ EGF-LIKE 5 (N-TERMINAL).
FT DOMAIN 924 933 LAMININ EGF-LIKE 5 (C-TERMINAL).
FT DOMAIN 934 1125 LAMININ EGF-LIKE 6.
FT DOMAIN 1126 1158 LAMININ EGF-LIKE 7.
FT DOMAIN 1159 1208 LAMININ EGF-LIKE 8.
FT DOMAIN 1209 1265 LAMININ EGF-LIKE 9 (N-TERMINAL).
FT DOMAIN 1275 1324 LAMININ EGF-LIKE 9 (C-TERMINAL).
FT DOMAIN 1325 1334 LAMININ EGF-LIKE 10.
FT DOMAIN 1335 1529 LAMININ EGF-LIKE 11.
FT DOMAIN 1530 1562 LAMININ EGF-LIKE 12.
FT DOMAIN 1563 1612 LAMININ EGF-LIKE 13.
FT DOMAIN 1613 1670 LAMININ EGF-LIKE 14.
FT DOMAIN 1677 1771 IG-LIKE C2-TYPE 1.
FT DOMAIN 1772 1865 IG-LIKE C2-TYPE 2.
FT DOMAIN 1866 1955 IG-LIKE C2-TYPE 3.
FT DOMAIN 1956 2051 IG-LIKE C2-TYPE 4.
FT DOMAIN 2052 2151 IG-LIKE C2-TYPE 5.
FT DOMAIN 2152 2244 IG-LIKE C2-TYPE 6.
FT DOMAIN 2245 2340 IG-LIKE C2-TYPE 7.
FT DOMAIN 2341 2436 IG-LIKE C2-TYPE 8.
FT DOMAIN 2437 2533 IG-LIKE C2-TYPE 9.
FT DOMAIN 2534 2629 IG-LIKE C2-TYPE 10.
FT DOMAIN 2630 2726 IG-LIKE C2-TYPE 11.
FT DOMAIN 2727 2823 IG-LIKE C2-TYPE 12.

Query Match 11.7%; Score 178.5; DB 1; Length 4391;
Best Local Similarity 24.2%; Pred. No. 4.6e-06;
Matches 72; Conservative 47; Mismatches 123; Indels 55; Gaps 14;

QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAHHHPQYGSVQGEYQGRVLFK 60
Db 2935 HVTE--GQTLDLNCVVP-GQAHQVTVYKRG-----SLPARHQTHG----- 2973
QY 61 NYSLNDAITLHNGFSDSGKYICKAVTFPLGNAQSSTTVTV-----LVEPTVSLI 111
Db 2974 -----SQLRLHLVSPADSGEYVCRASGPGPEQASFTVTPPSEGSSYRLRSPVIS-I 3026
QY 112 KGPDSLIDGGNETVAATCIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLEP 171
Db 3027 DPSSSTVQQGD-ASFCLIHGDAAPISLEWKTNRQLEDNVHISPN--GSIIT---IVG 3080
QY 172 TRFARGRRITCVVHKPALEKDIRYSFI-LDIQVAPESVVTGYDGNWFVGRKGVNLCNAD 230
Db 3081 TRPSNHGTYRCVASN---AYGVAQSVNLSVHGPPVSVLPPEGVVWVKVAVTLEC-VS 3136
QY 231 ANEPFPKSVWSRLDG-----QWPDGLLASDNTLHFVHPLTFNYSVGVYICKVNTSLG 281
Db 3137 ACEPSSARWTRISSTPAKLEQRTYGLMDSHAVLQ-ISSAKPSDAGTYVCLQAQNALG 3192

RESULT 12
NCAL_BOVIN
ID NCAL_BOVIN STANDARD; PRT; 853 AA.
AC P31836;
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 1, 140 kDa isoform precursor (N-CAM 140)
DE (NCAM-140).
GN NCAM1 OR NCAM.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Brain cortex;
RX MEDLINE=89378239; PubMed=2776887;
RA Lipkin V.M., Khrantsov N.V., Andreeva S.G., Moshnyakov M.V.,
RA Petukhova G.V., Rakitina T.V., Feshchenko E.A., Ishchenko K.A.,
RA Mirzoeva S.F., Chernova M.N., Dranytsyna S.M.;
RT "Calmodulin-independent bovine brain adenylate cyclase. Amino acid
sequence and nucleotide sequence of the corresponding cDNA.";
RL FEBS Lett. 254:69-73 (1989).
RN [2]
RP SEQUENCE OF 20-36.
RX MEDLINE=86140120; PubMed=3512556;
RA Rougon G., Marshak D.R.;
RT "Structural and immunological characterization of the amino-terminal
domain of mammalian neural cell adhesion molecules.";
RL J. Biol. Chem. 261:3396-3401 (1986).
RN [3]
RP IDENTIFICATION AS N-CAM.
RX MEDLINE=92111748; PubMed=1765159;
RA Premont R.T.;
RT "A bovine brain cDNA purported to encode calmodulin-insensitive
adenylate cyclase has extensive identity with neural cell adhesion
molecules (N-CAMs).";
RL FEBS Lett. 295:230-231 (1991).
CC -!- FUNCTION: This protein is a cell adhesion molecule involved in
neuron-neuron adhesion, neurite fasciculation, outgrowth of
neurites, etc.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=1;
Comment=A number of isoforms are produced;
Name=1;
CC IsoId=P31836-1; Sequence=Displayed;
CC -!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 fibronectin type III domains.
CC -!- CAUTION: Was originally (Ref.1) thought to be a calmodulin-
independent adenylate cyclase.
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or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X16451; CAA34470.1; --
CC PIR; A32976; IJBONC.
CC HSSP; P40189; IBQU.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00041; fn3; 2.
CC Pfam; PF00047; ig; 5.
CC SMART; SM00060; FN3; 2.
CC SMART; SM00408; IGC2; 5.
CC PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal.
FT SIGNAL 1 19
FT CHAIN 20 853 NEURAL CELL ADHESION MOLECULE 1, 140 kDa

FT	DOMAIN	20	719	ISOFORM.	
FT	TRANSMEM	720	737	EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN	738	853	POTENTIAL.	
FT	DOMAIN	20	111	CYTOPLASMIC (POTENTIAL).	
FT	DOMAIN	116	205	IG-LIKE C2-TYPE 1.	
FT	DOMAIN	212	300	IG-LIKE C2-TYPE 2.	
FT	DOMAIN	307	412	IG-LIKE C2-TYPE 3.	
FT	DOMAIN	415	500	IG-LIKE C2-TYPE 4.	
FT	DOMAIN	527	604	IG-LIKE C2-TYPE 5.	
FT	DOMAIN	633	700	FIBRONECTIN TYPE-III 1.	
FT	DOMAIN	152	156	FIBRONECTIN TYPE-III 2.	
FT	DOMAIN	161	165	HEPARIN-BINDING (POTENTIAL).	
FT	DISULFID	41	96	HEPARIN-BINDING (POTENTIAL).	
FT	DISULFID	139	189	BY SIMILARITY.	
FT	DISULFID	235	286	BY SIMILARITY.	
FT	DISULFID	328	394	BY SIMILARITY.	
FT	DISULFID	435	488	BY SIMILARITY.	
FT	CARBOHYD	222	222	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	314	314	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	346	346	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	432	432	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	458	458	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD	487	487	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE	853 AA; 93893 MW; E12FD49231A7A368	CRC64;		
Query Match					11.0%; Score 166.5; DB 1; Length 853;
Best Local Similarity					23.6%; Pred. No. 5.9e-06;
Matches					74; Conservative 51; Mismatches 122; Indels 67; Gaps 16;
QY	1	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLPK	60		
Db	222	NATANLQSVTLVCNAEGFPEPT-VSWTK-----DGEIENEDEKYLFS	265		
QY	61	NYSINDATITLHNIGFSDSGKICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDG	120		
Db	266	D---DSSELTIRKVDKNDKDEAEYVCIAEN-KAGEQDASIHKLVFAKPKITYVENQTAM--E	319		
QY	121	GNETVAACIAATGKPVAHIDWE---GDLGEMESTTTSFPNETATI-----ISQ	166		
Db	320	LEEQTILTC-EASGDPIPSITWTSTRNISSEKASWTREKQETLDGHMVVRSHARVSS	378		
QY	167	YKLFTRFARGRRITCVVHKPALEKDIRYSFILDIOYAPE----VSVTGYDGNWFVGRKG	222		
Db	379	LTLKSIQYTDAGEYVCTASN-TIGQDSQ-SMYLEVQYAPKLGQPVAVYTWEGN-----Q	430		
QY	223	VNLKCNADANPPPKSVWSRLDQWPDCLLASDNLHF-----VHPLTFNYSG	270		
Db	431	VNITCEVAYPSATIS-WFR-DGQ---LLPSSNYSNIKIYNTSPASYLEVTPDSENDFG	484		
QY	271	VYICKVTNSLQGRS	284		
Db	485	NYNCTAVNRIGQES	498		
RESULT 13					
CI66	CHICK	STANDARD;	PRT;	588	AA.
ID	CI66	CHICK			
AC	P42292;				
DT	01-NOV-1995	(Rel. 32, Created)			
DT	01-NOV-1995	(Rel. 32, Last sequence update)			
DT	10-OCT-2003	(Rel. 42, Last annotation update)			
DE	CD166	antigen precursor (SC1 glycoprotein) (BEN glycoprotein) (DM-			
DE	GRASP	protein) (JC7 protein).			
OS	Gallus	gallus (Chicken).			
OC	Eukaryota;	Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria;	Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;			
OC	Gallus.				
OX	NCBI_TaxID=9031;				
RN	[1]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.				
RC	TISSUE=Embryo;				
RX	MEDLINE=92030150; PubMed=1931049;				

RA	Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,				
RA	McFarland K.C., Kehr B., Lee A., Phillips H.S., Shelton D.L.;				
RT	"Molecular cloning and expression of a novel adhesion molecule, SC1.;"				
RL	Neuron 7:535-545(1991).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=91337449; PubMed=1873027;				
RA	Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,				
RA	Chang S.;				
RT	"DM-GRASP, a novel immunoglobulin superfamily axonal surface protein				
RT	that supports neurite extension.;"				
RL	Neuron 7:209-220(1991).				
RN	[3]				
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.				
RC	TISSUE=Bursa of fabricius;				
RX	MEDLINE=92302224; PubMed=1608932;				
RA	Pourquie O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;				
RT	"BEN, a surface glycoprotein of the immunoglobulin superfamily, is				
RT	expressed in a variety of developing systems.;"				
RL	Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).				
RN	[4]				
RP	POSSIBLE FUNCTION.				
RX	MEDLINE=92211411; PubMed=1313497;				
RA	Pourquie O., Hallonet M.E.R., le Douarin N.M.;				
RT	"Association of BEN glycoprotein expression with climbing fiber				
RT	axonogenesis in the avian cerebellum.;"				
RL	J. Neurosci. 12:1548-1557(1992).				
CC	-!- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING				
CC	FIBER AXONEMESIS. SUPPORTS NEURITE EXTENSION.				
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.				
CC	-!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.				
CC	WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL				
CC	FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN				
CC	EPITHELIA, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH				
CC	DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS				
CC	OF BEN.				
CC	-!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC				
CC	DEVELOPMENT.				
CC	-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.				
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; S63276; AAB20170.1; -.				
DR	EMBL; M76678; AAA48602.1; -.				
DR	EMBL; X64301; CAA45579.1; -.				
DR	PIR; A45254; A45254.				
DR	PIR; JH0464; JH0464.				
DR	PIR; JH0506; JH0506.				
DR	HSSP; Q13740; 1KJC.				
DR	InterPro; IPR007110; Ig-like.				
DR	InterPro; IPR003599; Ig.				
DR	InterPro; IPR003006; Ig_MHC.				
DR	Pfam; PF00047; ig; 5.				
DR	SMART; SM00409; IG; 3.				
DR	PROSITE; PS50835; IG LIKE; 4.				
DR	PROSITE; PS00290; IG_MHC; FALSE NEG.				
KW	Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;				
KW	Repeat; Signal.				
FT	SIGNAL	1	33		
FT	CHAIN	34	588		CD166 ANTIGEN.
FT	DOMAIN	34	532		EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	533	553		POTENTIAL.
FT	DOMAIN	554	588		CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	42	126		IG-LIKE V-TYPE 1.
FT	DOMAIN	131	240		IG-LIKE V-TYPE 2.
FT	DOMAIN	251	333		IG-LIKE C2-TYPE 1.

```
FT DOMAIN 338 414 IG-LIKE C2-TYPE 2.
FT DOMAIN 421 501 IG-LIKE C2-TYPE 3.
FT DISULFID 49 119 POTENTIAL.
FT DISULFID 163 226 POTENTIAL.
FT DISULFID 276 319 POTENTIAL.
FT DISULFID 359 397 POTENTIAL.
FT DISULFID 440 490 POTENTIAL.
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 271 271 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 312 312 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 462 462 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 485 485 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 504 504 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 1 10 MMEPPAAAAR -> MEPPRRRP (IN REF. 3).
FT CONFLICT 25 25 A -> S (IN REF. 3).
FT CONFLICT 112 113 SD -> RH (IN REF. 3).
FT CONFLICT 329 329 A -> T (IN REF. 2).
FT CONFLICT 401 402 LQ -> HK (IN REF. 2).
SQ SEQUENCE 588 AA; 65726 MW; 2A28612D0164531E CRC64;

Query Match 10.9%; Score 166; DB 1; Length 588;
Best Local Similarity 22.0%; Pred. No. 4.1e-06;
Matches 67; Conservative 62; Mismatches 126; Indels 50; Gaps 14;

QY 2 VTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQ---GEYQGRV 57
Db 37 VNAVYGDITMPCRLVDPDGLMFGKWKYEMPNPSPVFIAPRSSTKKNVQYDDVPDYKDR 96

QY 58 -LFKNYSILNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSFTVTVLVEPTVSLIKGPD 116
Db 97 SLSENY-----TSLIKNARISDEKRFVCMVLTED-DVSEEPVVKVFKQPSQPEILHQAD 150

QY 117 LIDGNETVAAICIAATGKPVAHIDW--EG-----DLGEMESTTTSFPNETAT 162
Db 151 FLETEKLMKGECVWRDSYPEGNTWYKNGRVLQPVVEVVINLRKVENRSTGL----FT 206

QY 163 IISQYKLFPTFRPARGRRITCVVKH--PALEKDIRYS-FILDIQYAPE-----VSVTG 211
Db 207 MTSSLQYMPTEKEDANAKFTCIIVTHGPGSQKTIQSEPVVDFVHYPTKVTIRVLSQSS 266

QY 212 YDGNWVGRKGVLNKNADANPPPKSVWSRLDQWPDGLASDNTLHFVHLPTFNKSGV 271
Db 267 KEGD-----NVTLCGSGNGNPPPPQBELF-YIPGE-TEGIRSSDT--YVMTDVRNRNATGE 316

QY 272 YICKV 276
Db 317 YKCSL 321

RESULT 14
MAG_HUMAN STANDARD; PRT; 626 AA.
AC P20916;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Myelin-associated glycoprotein precursor (Siglec-4a).
GN MAG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89392063; PubMed=2476987;
RA Sato S., Fujita N., Kurihara T., Kuwano R., Sakimura K., Takahashi Y.,
RA Miyatake T.;
RT "cDNA cloning and amino acid sequence for human myelin-associated
RT glycoprotein.";
RL Biochem. Biophys. Res. Commun. 163:1473-1480(1989).
```

```
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Adamson A.W., Burkhardt-Schultz K.,
RA Kyle A., Ramirez M., Stilwagen S.A., Garnes J., Danganan L.,
RA Bruce R., Quan G., Montgomery M., Ow D., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Adhesion molecule in postnatal neural development that
CC mediates sialic-acid dependent cell-cell interactions between
CC neuronal and myelinating cells. Preferentially binds to alpha2,3-
CC linked sialic acid (By similarity).
CC -!- SUBUNIT: Binds to RTN4R (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC
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CC
CC -----
CC EMBL; M29273; AAA59545.1; -;
CC EMBL; AC002132; AAB58805.1; -;
CC EMBL; BC053347; AAH53347.1; -;
CC PIR; A61084; A61084.
CC HSSP; Q62230; IQFP.
CC Genew; HGNC:6783; MAG.
CC MIM; 159460; -;
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00047; ig; 2.
CC SMART; SM00408; IGC2; 2.
CC PROSITE; PS50835; IG_LIKE; 3.
CC Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat; Palmitate; Lipoprotein.
FT SIGNAL 1 19
FT CHAIN 20 626 MYELIN-ASSOCIATED GLYCOPROTEIN.
FT DOMAIN 20 516 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 517 536 POTENTIAL.
FT DOMAIN 537 626 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 22 120 IG-LIKE V-TYPE.
FT DOMAIN 139 237 IG-LIKE C2-TYPE 1.
FT DOMAIN 241 325 IG-LIKE C2-TYPE 2.
FT DOMAIN 327 412 IG-LIKE C2-TYPE 3.
```


FT	DOMAIN	413	508	IG-LIKE C2-TYPE 4.
FT	DISULFID	37	165	BY SIMILARITY.
FT	DISULFID	42	100	BY SIMILARITY.
FT	DISULFID	159	217	BY SIMILARITY.
FT	DISULFID	261	305	BY SIMILARITY.
FT	DISULFID	347	392	BY SIMILARITY.
FT	DISULFID	421	430	BY SIMILARITY.
FT	DISULFID	432	488	BY SIMILARITY.
FT	CARBOHYD	99	99	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	223	223	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	246	246	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	315	315	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	332	332	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	406	406	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	450	450	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	454	454	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	LIPID	531	531	S-palmitoyl cysteine (By similarity).
SQ	SEQUENCE	626 AA;	69068 MW;	ED2D36B24F21CAA CRC64;
Query Match 10.8%; Score 163.5; DB 1; Length 626;				
Best Local Similarity 24.4%; Pred. No. 7e-06;				
Matches 77; Conservative 44; Mismatches 129; Indels 65; Gaps 16;				
QY	2	VTAVWGNVSLKCLIEVNETITQISWEKIHGK-----SSQTVAVHHPOY	45	
Db	30	ISAFEGTCVSI PCRFDFPD--ELRPVVHGVWYFNSPYPKNYPVPVFKSRTQVWHE---	83	
QY	46	GFSVQGEYQGRV-LFKNYSLNDAITITLHNIGFSDSGKYICKAVTFPLG--NAQSSTITTV	102	
Db	84	-----SFQGRSRLLDGLRNCITLLSNVSPELGGKYFRG---DLGGYNQYTFSEHSV	134	
QY	103	L-VEPTVSLIKGPDLSLDGGNETVAAICIAATGKPV--AHIDWEGDLGEMESTTTSFPNE	159	
Db	135	LDIVNTNIVVPE--VVAGTE-VEVSCMVDPDNCPELRPELSWLGHGEPVGLRLRE	191	
QY	160	---TATISQYKLFPTFRFARRRITCVVKHPALEKDIRYSFILDIOYAPEV-----SVTG	211	
Db	192	DEGTWQVSLHFPVPTREANGHRLGCGASFPNTTLQFEGYASMDVKYPPVIVEMNSSVEA	251	
QY	212	YDGNWVFGRKGNLKNADANPPPKSVWSRLDGQWPDGLL-----ASDNTLHFVHPLTFN	267	
Db	252	IEGS-----HVSLLCGADSNPPPLLT-WNR-----DGTVLRREAVAESLLELEEVTPA	298	
QY	268	YSGVYICKVTNSLGQ	282	
Db	299	EDGVYACLAENAYGQ	313	
RESULT 15				
MAG MOUSE STANDARD; PRT; 626 AA.				
ID	MAG_MOUSE			
AC	P20917; P16880;			
DT	01-AUG-1990 (Rel. 15, Created)			
DT	15-JUL-1998 (Rel. 36, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Myelin-associated glycoprotein precursor (Siglec-4a).			
GN	MAG.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORMS L-MAG AND S-MAG).			
RX	MEDLINE=90121220; PubMed=2482022;			
RA	Fujita N., Sato S., Kurihara T., Kuwano R., Sakimura K., Inuzuka T.,			
RA	Takahashi Y., Miyatake T.;			
RT	"CDNA cloning of mouse myelin-associated glycoprotein: a novel			
RT	alternative splicing pattern.";			
RL	Biochem. Biophys. Res. Commun. 165:1162-1169(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM S-MAG).			
RC	TISSUE=Brain;			
RX	MEDLINE=91298961; PubMed=1712586;			

RA	Nakano R., Fujita N., Sato S., Inuzuka T., Sakimura K.,
RA	Ishiguro H., Mishina M., Miyatake T.;
RT	"Structure of mouse myelin-associated glycoprotein gene.";
RL	Biochem. Biophys. Res. Commun. 178:282-290(1991).
RN	[3]
RP	TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX	MEDLINE=91366725; PubMed=1716323;
RA	Pedraza L., Frey A.B., Hempstead B.L., Colman D.R., Salzer J.L.;
RT	"Differential expression of MAG isoforms during development.";
RL	J. Neurosci. Res. 29:141-148(1991).
RN	[4]
RP	SIALIC ACID BINDING.
RX	MEDLINE=95179521; PubMed=7533044;
RA	Kelm S., Pelz A., Schauer R., Filbin M.T., Tang S., de Bellard M.E.;
RA	Schnaar R.L., Mahoney J.A., Hartnell A., Bradfield P., Crocker P.R.;
RT	"Sialoadhesin, myelin-associated glycoprotein and CD22 define a new
RT	family of sialic acid-dependent adhesion molecules of the
RT	immunoglobulin superfamily.";
RL	Curr. Biol. 4:965-972(1994).
RN	[5]
RP	FUNCTION, AND TISSUE SPECIFICITY.
RX	MEDLINE=20090811; PubMed=10625334;
RA	Schachner M., Bartsch U.;
RT	"Multiple functions of the myelin-associated glycoprotein MAG
RL	(siglec-4a) in formation and maintenance of myelin.";
RN	Glia 29:154-165(2000).
RN	[6]
RP	INTERACTION WITH RTN4R.
RX	MEDLINE=22171378; PubMed=12089450;
RA	Liu B.P., Fournier A., GrandPre T., Strittmatter S.M.;
RT	"Myelin-associated glycoprotein as a functional ligand for the Nogo-66
RT	receptor.";
RL	Science 297:1190-1193(2002).
CC	-!- FUNCTION: Adhesion molecule in postnatal neural development that
CC	mediates sialic-acid dependent cell-cell interactions between
CC	neuronal and myelinating cells. Preferentially binds to alpha2,3-
CC	linked sialic acid. Isoform L-MAG is critical for the formation of
CC	myelin in the CNS, whereas isoform S-MAG is sufficient to maintain
CC	the integrity of myelin in PNS.
CC	-!- SUBUNIT: Binds to RTN4R.
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-!- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=L-MAG;
CC	isoId=P20917-1; Sequence=Displayed;
CC	Name=S-MAG;
CC	isoId=P20917-2; Sequence=VSP_002527, VSP_002528;
CC	-!- TISSUE SPECIFICITY: Expressed by myelinating glial cells in the
CC	central and peripheral nervous system. Detected in oligodendrocyte
CC	processes before formation of compact myelin. Restricted to the
CC	periaxonal space after myelination. Isoform S-MAG is the
CC	predominant isoform in CNS and PNS of the adult.
CC	-!- DEVELOPMENTAL STAGE: In CNS isoform L-MAG is the major form
CC	synthesized early in development, and it persists as a significant
CC	proportion of the MAG present in the adult. In the PNS isoform L-
CC	MAG is expressed at modest levels during development; it is absent
CC	in the adult.
CC	-!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC	(sialic acid binding Ig-like lectin) family.
CC	-!- SIMILARITY: Contains 4 immunoglobulin-like C2-type domains.
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC	-----
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; M31811; AAA39487.1; -.
DR	EMBL; M74793; AAA91743.1; -.
DR	EMBL; M74783; AAA91743.1; JOINED.

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 23.1465 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-2_COPY_58_342
Perfect score: 1520
Sequence: 1 HVTAVWGKNVSLKCLIEVNE.....FNYSGVYICKVTNSLQGRSD 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rodent: *
12: sp_virus: *
13: sp_vertebrate: *
14: sp_unclassified: *
15: sp_rvirus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1520	100.0	549	4 Q9NQS3	Q9nqs3 homo sapien
2	1487	97.8	438	11 Q9JLB7	Q9jlb7 mus musculus
3	1487	97.8	510	11 Q9JLB8	Q9jlb8 mus musculus
4	1487	97.8	549	11 Q9JLB9	Q9jlb9 mus musculus
5	1443	94.9	549	11 Q9D006	Q9d006 mus musculus
6	1181	77.7	267	4 Q8NC05	Q8nc05 homo sapien
7	1104	72.6	407	4 Q9Y412	Q9y412 homo sapien
8	575	37.8	304	4 Q9BVA9	Q9bva9 homo sapien
9	526.5	34.6	295	11 Q9ERF5	Q9erf5 mesocricetu
10	520	34.2	298	6 Q9GL74	Q9gl74 cercopithec
11	519.5	34.2	295	6 Q9GL75	Q9gl75 bos taurus
12	459.5	30.2	510	4 Q96NY8	Q96ny8 homo sapien
13	459.5	30.2	510	4 Q96K15	Q96k15 homo sapien
14	439.5	28.9	483	11 Q9DBP8	Q9dbp8 mus musculus
15	439.5	28.9	508	11 Q8R007	Q8r007 mus musculus
16	439.5	28.9	508	11 Q8CED8	Q8ced8 mus musculus

17	394	25.9	467	11 Q91VT9	Q91vt9 mus musculu
18	394	25.9	467	11 Q8C6F2	Q8c6f2 mus musculu
19	394	25.9	530	11 Q80XJ5	Q80xj5 mus musculu
20	379	24.9	412	11 Q9RIE1	Q9rie1 rattus norv
21	377	24.8	403	6 Q8HY15	Q8hy15 lemur catta
22	374	24.6	412	11 Q63611	Q63611 rattus norv
23	373.5	24.6	400	6 Q8HY16	Q8hy16 cebus apell
24	372	24.5	449	4 Q9UEI6	Q9uei6 homo sapien
25	368.5	24.2	417	4 Q96BJ1	Q96bj1 homo sapien
26	363	23.9	408	11 Q91WP1	Q91wp1 mus musculu
27	361	23.8	408	11 Q8BVF6	Q8bvf6 mus musculu
28	361	23.8	408	11 Q8K094	Q8k094 mus musculu
29	355.5	23.4	401	6 Q08835	Q08835 cercopithe
30	337	22.2	412	6 Q8HY14	Q8hy14 oryctolagus
31	322	21.2	415	11 Q60977	Q60977 mus musculu
32	252	16.6	394	13 Q7ZXX1	Q7zxx1 xenopus lae
33	247.5	16.3	333	4 Q86WB8	Q86wb8 homo sapien
34	247.5	16.3	443	4 Q8N2F4	Q8n2f4 homo sapien
35	246.5	16.2	442	4 Q9BY67	Q9by67 homo sapien
36	244.5	16.1	336	11 Q9D6E7	Q9d6e7 mus musculu
37	244.5	16.1	336	11 Q80VG4	Q80vg4 mus musculu
38	244.5	16.1	417	11 Q7TNL1	Q7tnl1 mus musculu
39	244.5	16.1	445	11 Q8K3T6	Q8k3t6 mus musculu
40	244.5	16.1	445	11 Q8R4L1	Q8r4l1 mus musculu
41	244.5	16.1	456	11 Q8R5M8	Q8r5m8 mus musculu
42	240	15.8	800	5 Q86LF9	Q86lf9 drosophila
43	240	15.8	801	5 Q86LF8	Q86lf8 drosophila
44	217.5	14.3	396	11 Q99N28	Q99n28 mus musculu
45	216	14.2	551	5 Q8MSN7	Q8msn7 drosophila

ALIGNMENTS

RESULT 1

Q9NQS3
ID Q9NQS3 PRELIMINARY; PRT; 549 AA.
AC Q9NQS3;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.;
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterFro; IPR003599; Ig.
DR InterFro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;

Query Match 100.0%; Score 1520; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 6.4e-127;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSGVQGEYQGRVLFK 60
Db	65	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOYGFSGVQGEYQGRVLFK 124
QY	61	NYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db	125	NYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184

QY	121	GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI	180
Db	185	GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI	244
QY	181	TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVW	240
Db	245	TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVW	304
QY	241	SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD	285
Db	305	SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD	349
RESULT 2			
Q9JLB7 PRELIMINARY; PRT; 438 AA.			
ID	Q9JLB7		
AC	Q9JLB7;		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Cell adhesion molecule nectin-3 gamma.		
GN	PVRL3.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20209403; PubMed=10744716;		
RA	SatoH-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,		
RA	Tachibana K., Mizoguchi A., Takai Y.;		
RT	"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules		
RT	that shows homophilic and heterophilic cell-cell adhesion		
RT	activities.";		
RL	J. Biol. Chem. 275:10291-10299(2000).		
DR	EMBL; AF195835; AAF63687.1; -.		
DR	MGD; MGI:1930171; Pvr13.		
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.		
DR	GO; GO:0005194; F:cell adhesion molecule activity; IDA.		
DR	GO; GO:0005515; F:protein binding; IPI.		
DR	GO; GO:0007155; P:cell adhesion; IDA.		
DR	InterPro; IPR003599; Ig.		
DR	InterPro; IPR007110; Ig-like.		
DR	Pfam; PF00047; ig; 2.		
DR	SMART; SM00409; IG; 1.		
DR	PROSITE; PS50835; IG LIKE; 3.		
SQ	SEQUENCE 438 AA; 47261 MW; 2A0A4416E5B02FEF CRC64;		
Query Match 97.8%; Score 1487; DB 11; Length 438;			
Best Local Similarity 96.5%; Pred. No. 4.1e-124;			
Matches 275; Conservative 8; Mismatches 2; Indels 0; Gaps 0;			
QY	1	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLEK	60
Db	65	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSGVQGEYQGRVLEK	124
QY	61	NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG	120
Db	125	NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG	184
QY	121	GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI	180
Db	185	GNETVAAVCVAATGKPVQAIDWEGDLGEMESTTTSFPNETATIVSQYKLFPTFRFARGRRI	244
QY	181	TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVW	240
Db	245	TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVW	304
QY	241	SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD	285
Db	305	SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD	349

RESULT 3				
Q9JLB8				
ID	Q9JLB8	PRELIMINARY;	PRT;	510 AA.
AC	Q9JLB8;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Cell adhesion molecule nectin-3 beta.			
GN	PVRL3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20209403; PubMed=10744716;			
RA	SatoH-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,			
RA	Tachibana K., Mizoguchi A., Takai Y.;			
RT	"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules			
RT	that shows homophilic and heterophilic cell-cell adhesion			
RT	activities.";			
RL	J. Biol. Chem. 275:10291-10299(2000).			
DR	EMBL; AF195834; AAF63686.1; --			
DR	MGD; MGI:1930171; Pvr13.			
DR	GO; GO:0005913; C:cell-cell adherens junction; IDA.			
DR	GO; GO:0005194; F:cell adhesion molecule activity; IDA.			
DR	GO; GO:0005515; F:protein binding; IPI.			
DR	GO; GO:0007155; P:cell adhesion; IDA.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	Pfam; PF00047; ig; 2.			
DR	SMART; SM00409; IG; 1.			
DR	PROSITE; PS50835; IG LIKE; 3.			
SQ	SEQUENCE 510 AA; 55811 MW; 45CFE6EF78454864 CRC64;			
Query Match 97.8%; Score 1487; DB 11; Length 510;				
Best Local Similarity 96.5%; Pred. No. 5.1e-124;				
Matches 275; Conservative 8; Mismatches 2; Indels 0; Gaps 0;				
QY	1	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFK	60	
Db	65	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFSGVQGEYQGRVLFK	124	
QY	61	NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG	120	
Db	125	NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG	184	
QY	121	GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI	180	
Db	185	GNETVAAVCVAATGKPVQAIDWEGDLGEMESTTTSFPNETATIVSQYKLFPTFRFARGRRI	244	
QY	181	TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPKSVW	240	
Db	245	TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPKSVW	304	
QY	241	SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD	285	
Db	305	SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD	349	
RESULT 4				
Q9JLB9				
ID	Q9JLB9	PRELIMINARY;	PRT;	549 AA.
AC	Q9JLB9;			
DT	01-OCT-2000 (TrEMBLrel. 15, Created)			
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)			
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)			
DE	Cell adhesion molecule nectin-3 alpha.			
GN	PVRL3.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			

RN SEQUENCE FROM N.A.
 RP MEDLINE=20209403; PubMed=10744716;
 RX SatoH-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
 RA Tachibana K., Mizoguchi A., Takai Y.;
 RT "Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
 RT that shows homophilic and heterophilic cell-cell adhesion
 RT activities.";
 RL J. Biol. Chem. 275:10291-10299(2000).
 DR EMBL; AF195833; AAF63685.1; -.
 DR MGD; MGI:1930171; Pvr13.
 DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
 DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
 DR GO; GO:0005515; P:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 3.
 SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;
 Query Match 97.8%; Score 1487; DB 11; Length 549;
 Best Local Similarity 96.5%; Pred. No. 5.7e-124;
 Matches 275; Conservative 8; Mismatches 2; Indels 0; Gaps 0;
 QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
 Db 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGEYQGRVLFK 124
 QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG 120
 Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG 184
 QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRI 180
 Db 185 GNETVAAVCVSAATGKPVQAIDWEGDLGEMESTTTSFPNETATIVSQYKLPFTRFARGRI 244
 QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPFKSVW 240
 Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPFKSVW 304
 QY 241 SRLDGQWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSD 285
 Db 305 SRLDGQWPDGILLASDNTLHFVHPLTFNYSGVYCKVNSLQGRSD 349
 RESULT 5
 Q9D006 PRELIMINARY; PRT; 549 AA.
 ID Q9D006;
 AC Q9D006;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 2610301B19Rik protein.
 GN PVR13 OR 2610301B19RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK011949; BAB27933.1; -.
 DR MGD; MGI:1930171; Pvr13.
 DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
 DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
 DR GO; GO:0005515; F:protein binding; IPI.
 DR GO; GO:0007155; P:cell adhesion; IDA.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; IG; 1.
 DR PROSITE; PS50835; IG LIKE; 3.
 SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;
 Query Match 94.9%; Score 1443; DB 11; Length 549;
 Best Local Similarity 93.7%; Pred. No. 4.8e-120;
 Matches 267; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
 QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
 Db 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPQYGFVSQGEYQGRVLFK 124
 QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG 120
 Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSSIDG 184
 QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTRFARGRI 180
 Db 185 GNETVAAVCVSVSTGKPVQAIDWEGDLGEREFSTISFLNETATIVSQYELFPTRFARGRI 244
 QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPFKSVW 240
 Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPFKSVW 304
 QY 241 SRLDGQWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSD 285
 Db 305 SRLDGQWPDGILLASDNTLHFVHPLTFNYSGVYCKVNSLQGRSD 349
 RESULT 6
 Q8NC05 PRELIMINARY; PRT; 267 AA.
 ID Q8NC05
 AC Q8NC05;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Hypothetical protein FLJ90624.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
 RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
 RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
 RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK075105; BAC11404.1; -.
 DR InterPro; IPR003599; Ig.

QY 7 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYS 63
Db 3 GTDVVLHCSFANPLPSVKITQVTWQKATNGSKQNMAIYNPTMGVSVLPPEYKRVERFLRPS 62
QY 64 LNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG--- 120
Db 63 FIDGTIRLSHLEDEGMWICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRARKG 121
QY 121 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSPNETATIISQYKLPPTRFARGR 178
Db 122 QDDKVVATCTSANGKPPSVVSWETRLKGEAEYQEIIRNPNGTIVISRYRLVPSREAHQ 181
QY 179 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKS 238
Db 182 SLACIVNY-HLDR-FRESLTNLNVQYEPEVTIEGFDGNWYLQRTDVKLTCKADANPPATEY 239
QY 239 VWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS 284
Db 240 HWTTLNGLSLPKGVEAQNRITLFFRGPINYSLAGTYICEATNPIGTRS 285

RESULT 10
Q9GL74
ID Q9GL74 PRELIMINARY; PRT; 298 AA.
AC Q9GL74;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
DR EMBL; AF308635; AAG30284.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG-LIKE; 2.
FT NON_TER 1
FT NON_TER 298
SQ SEQUENCE 298 AA; 33309 MW; AEAD41842B8CA200 CRC64;

Query Match 34.2%; Score 520; DB 6; Length 298;
Best Local Similarity 38.1%; Pred. No. 4.5e-38;
Matches 110; Conservative 54; Mismatches 111; Indels 14; Gaps 6;
QY 7 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFK 60
Db 3 GTDVVLHCSFANPLPSVKITQVTWQKATNGSKQNMAIYNPMSMGVSVLPYRVERVEFL 62
QY 61 NYSLNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db 63 RPSFTDGTIRLSRLEDEGMWICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRA 121
QY 121 ----GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSPNETATIISQYKLPPTRFA 175
Db 122 KKGQDDKVLVATCTSANGKPPSVVSWETRLKGEAEYQEIIRNPNGTIVISRYRLVPSREA 181
QY 176 RGRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPP 235
Db 182 HQQSLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPA 239

QY 236 FKSWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS 284
Db 240 TEYHWTTLNGLSLPKGVEAQNRITLFFKGPISYSLAGTYICEATNPIGTRS 288
RESULT 11
Q9GL75
ID Q9GL75 PRELIMINARY; PRT; 295 AA.
AC Q9GL75;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
DR EMBL; AF308633; AAG30282.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
FT NON_TER 1
FT NON_TER 295
SQ SEQUENCE 295 AA; 33082 MW; 7C35D64022146AFA CRC64;

Query Match 34.2%; Score 519.5; DB 6; Length 295;
Best Local Similarity 39.2%; Pred. No. 4.9e-38;
Matches 113; Conservative 51; Mismatches 109; Indels 15; Gaps 8;
QY 7 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYS 63
Db 3 GTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPAMGVSVLPYRVERVEFLRPS 62
QY 64 LNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLI---DG 120
Db 63 FTDGTIRLSRLEDEGMWICEFATFPAGNRESQNLNLTVMAKPT-NWIEGTHAVLRARKG 121
QY 121 GNETV-AAICIAATGKPVAHIDWEGDL-GEMESTTTSPNETATIISQYKLPPTRFARGR 178
Db 122 QDEKVLVATCTSANGKPPSVVSWETRLKGEAEYQEIIRNPNGTIVISRYRLVPSREAHQ 181
QY 179 RITCVVKHPALEKDIRY--SFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPF 236
Db 182 SLACIVNY---HMD-RFWESLTNLNVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPAT 237
QY 237 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS 284
Db 238 EYHWTTLNGLSLPKGVEAQNRITLFFRGPINYSLAGTYICEATNPIGTRS 285

RESULT 12
Q96NY8
ID Q96NY8 PRELIMINARY; PRT; 510 AA.
AC Q96NY8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Nectin 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 34.421 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-2_COPY_58_342
Perfect score: 1520
Sequence: 1 HVTAVWGKNVSLKCLIEVNE.....FNYSGVYICKVTNSLGQRSD 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1520	100.0	387	5	AAE23290	Aae23290 Human nec
2	1520	100.0	426	5	AAE23289	Aae23289 Human nec
3	1520	100.0	437	5	AAE23299	Aae23299 Human nec
4	1520	100.0	504	5	AAE23284	Aae23284 Human del
5	1520	100.0	510	5	AAE23285	Aae23285 Mouse nec
6	1520	100.0	510	5	AAE23286	Aae23286 Human nec
7	1520	100.0	542	5	AAE23281	Aae23281 Human del
8	1520	100.0	549	5	AAE23283	Aae23283 Human nec
9	1520	100.0	549	5	AAE23282	Aae23282 Mouse nec
10	1520	100.0	549	6	ABJ20222	Abj20222 Human IG
11	1520	100.0	555	4	AAM39143	Aam39143 Human pol
12	1520	100.0	595	5	AAE23288	Aae23288 Human nec
13	1520	100.0	634	5	AAE23287	Aae23287 Human nec
14	1495	98.4	559	4	AAM40929	Aam40929 Human pol
15	1487	97.8	438	4	AAG63984	Aag63984 Amino aci
16	1487	97.8	438	5	AAE23293	Aae23293 Mouse nec
17	1487	97.8	510	4	AAG63983	Aag63983 Amino aci
18	1487	97.8	510	5	AAE23292	Aae23292 Mouse nec
19	1487	97.8	549	4	AAG63982	Aag63982 Amino aci
20	1487	97.8	549	4	AAG63985	Aag63985 Amino aci
21	1487	97.8	549	5	AAE23291	Aae23291 Mouse nec
22	1181	77.7	267	4	AAM93536	Aam93536 Human pol
23	524.5	34.5	458	5	AAE23295	Aae23295 Human nec
24	524.5	34.5	514	6	ABJ20237	Abj20237 Human IG
25	524.5	34.5	517	3	AAAY32390	Aay32390 Herpesvir

26	524.5	34.5	517	5	AAE23294	Aae23294 Human nec
27	502	33.0	518	5	ABG77170	Abg77170 Prostate
28	459.5	30.2	497	5	AAE23303	Aae23303 Human nec
29	459.5	30.2	498	5	AAE23305	Aae23305 Human nec
30	459.5	30.2	510	4	AAB93365	Aab93365 Human pro
31	459.5	30.2	510	4	AAU00471	Aau00471 Human TAN
32	459.5	30.2	510	5	ABJ05562	Abj05562 Breast ca
33	459.5	30.2	510	6	ABJ20232	Abj20232 Human IG
34	459.5	30.2	510	6	ABR48229	Abr48229 Human bla
35	459.5	30.2	510	6	ABU56613	Abu56613 Lung canc
36	459.5	30.2	510	6	ABP97212	Abp97212 Tumour-as
37	459.5	30.2	510	7	ADB80512	Adb80512 Ovarian c
38	459.5	30.2	511	5	AAE23301	Aae23301 Human nec
39	459.5	30.2	580	5	AAE23302	Aae23302 Human nec
40	457.5	30.1	510	5	AAE23300	Aae23300 Human nec
41	457.5	30.1	510	6	ABJ20231	Abj20231 Human IG
42	374	24.6	412	6	ABJ20240	Abj20240 Human IG
43	374	24.6	412	7	ADE57027	Ade57027 Rat Prote
44	374	24.6	412	7	ADD45426	Add45426 Rat Prote
45	372	24.5	479	3	AAAY32389	Aay32389 Herpesvir

ALIGNMENTS

RESULT 1
AAE23290
ID AAE23290 standard; protein; 387 AA.
XX

AC AAE23290;
XX

DT 27-AUG-2002 (first entry)
XX

DE Human nectin-3beta-FLAGpolyHis fusion protein.
XX

KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX

OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX

PH Key Location/Qualifiers
FT Region 1..365
FT /note= "Human nectin-3alpha protein"
FT Region 366..381
FT /note= "FLAG peptide"
FT Region 382..387
FT /note= "PolyHis tag"

PN WO200228902-A2.
XX

PD 11-APR-2002.
XX

PF 05-OCT-2001; 2001WO-US031392.
XX

PR 05-OCT-2000; 2000US-0238557P.
XX

PA (IMMV) IMMUNEX CORP.
XX

PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX

DR WPI; 2002-426103/45.
XX

PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, edema,
PT sepsis, stroke.
XX

PS Claim 9; Page 105-107; 141pp; English.

XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta-
CC FLAGpolyHis fusion protein
XX
SQ

Sequence 387 AA;

Query Match 100.0%; Score 1520; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.7e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVQGEYQGRVLFK 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
65 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVQGEYQGRVLFK 124
QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSIDG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSIDG 184
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTFRFARGRRI 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTFRFARGRRI 244
QY 181 TCWKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPFKSVW 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
245 TCWKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPFKSVW 304
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSD 285
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSD 349

RESULT 2
AAE23289
ID AAE23289 standard; protein; 426 AA.
XX
AC AAE23289;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-FLAGpolyHis fusion protein.

XX Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
FH Key
FT Region
FT Location/Qualifiers
FT 1. .404
FT /note= "Human nectin-3alpha protein"
FT 405. .420
FT /note= "FLAG peptide"

FT Region 421. .426
FT /note= "PolyHis tag"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 104-105; 141pp; English.

The invention relates to a substantially purified nectin3alpha, beta,
gamma and nectin-4 polypeptides and their corresponding polynucleotides.
Nectin DNA and protein are useful for treating a disease associated with
cell adhesion activity, adherens junction formation activity, epithelial
or endothelial barrier function activity, endothelial proliferation or
migration activity, viral polypeptide binding activity. The epithelial or
endothelial barrier function disorder which is treated by the above
mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
asthma, allergy, allograft rejection, metastasis of cancer cells,
paracellular transport disorders such as magnesium transport defects in
the kidney or inflammatory bowel disease. Nectin DNA is also useful for
inhibiting angiogenesis in a mammal and treating endothelial migration,
proliferation or angiogenic condition of a tissue or a subject, such as
ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
stroke, restenosis, tumour growth and treating herpesvirus infection.
Nectin is also useful for modulating proliferation or migration of an
endothelial cell, an epithelial cell or a smooth muscle cell (vascular
smooth muscle cell). The present sequence is human nectin-3alpha-
FLAGpolyHis fusion protein

Sequence 426 AA;

Query Match 100.0%; Score 1520; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.9e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVQGEYQGRVLFK 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
65 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVQGEYQGRVLFK 124
QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSIDG 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSIDG 184
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTFRFARGRRI 180
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPFNETATIIISQYKLFPTFRFARGRRI 244
QY 181 TCWKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPFKSVW 240
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
245 TCWKHPALEKDIRYSPILDIQYAPEVSVTGYDGNWVFVGRKGNLKNADANPPPFKSVW 304
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSD 285
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSD 349

RESULT 3
AAE23299

ID AAE23299 standard; protein; 437 AA.
XX
AC AAE23299;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3gamma protein.
XX
KW Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
XX 05-OCT-2000; 2000US-0238557P.
PR (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37450.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 125-126; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3gamma protein.
CC Human nectin-3gamma gene is located on chromosome 3
XX
SQ Sequence 437 AA;
Query Match 100.0%; Score 1520; DB 5; Length 437;
Best Local Similarity 100.0%; Pred. No. 2e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVTAVGKQVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFK 60
DB 65 HVTAVGKQVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFK 124
QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG 120
DB 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG 184
QY 121 GNETVAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRI 180

Db 1.85 GNETVAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRI 244
QY 1.81 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPFKSVW 240
Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPFKSVW 304
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349
RESULT 4
AAE23284
ID AAE23284 standard; protein; 504 AA.
XX
AC AAE23284;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3beta protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI WPI; 2002-426103/45.
DR N-PSDB; AAD37443.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, allergy, edema,
PT sepsis, stroke.
PS Claim 1; Page 89-91; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX

FT Domain 74. .152 /note= "Extracellular Ig domain"
FT Modified-site 83 /note= "N-glycosylated"
FT Modified-site 125 /note= "N-glycosylated"
FT Modified-site 186 /note= "N-glycosylated"
FT Modified-site 189. .250 /note= "N-glycosylated"
FT Domain /note= "Extracellular Ig domain"
FT Modified-site 222 /note= "N-glycosylated"
FT Domain 287. .342 /note= "Extracellular Ig domain"
FT Modified-site 331 /note= "N-glycosylated"
FT Domain 386. .510 /note= "Intracellular C-terminal domain"
XX WO200228902-A2.
PN 11-APR-2002.
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37445.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX Claim 1; Page 98-99; 141pp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein.
XX Human nectin-3beta gene is located on chromosome 3
SQ Sequence 510 AA;

Query Match 100.0%; Score 1520; DB 5; Length 510;
Best Local Similarity 100.0%; Pred. NO. 2.5e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHPHQYGFSGVEYQGRVLFK 60
DB 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHPHQYGFSGVEYQGRVLFK 124
QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
|||||

Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSFPNETATIIISQYKLFPTTRFARGRI 180
|||||
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTTSFPNETATIIISQYKLFPTTRFARGRI 244
|||||
QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLKCNADANPPPFKSVW 240
|||||
Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLKCNADANPPPFKSVW 304
|||||
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
|||||
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349
|||||
RESULT 7
AAE23281
ID AAE23231 standard; protein; 542 AA.
XX AC AAE23231;
XX DT 27-AUG-2002 (first entry)
XX DE Human deleted nectin-3alpha protein.
XX KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; chromosome 3; asthma.
XX OS Homo sapiens.
XX PN WO200228902-A2.
XX PD 11-APR-2002.
XX PF 05-OCT-2001; 2001WO-US031392.
XX PR 05-OCT-2000; 2000US-0238557P.
XX PA (IMMV) IMMUNEX CORP.
XX PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37440.
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX Claim 1; Page 76-78; 141pp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha protein

CC containing 7 amino acids deleted from the N-terminal end. Human nectin-3
CC 3alpha gene is located on chromosome 3
XX
SQ Sequence 542 AA;

Query Match 100.0%; Score 1520; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFK 60
Db |||||
QY 58 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFK 117
Db |||||
QY 61 NYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db |||||
QY 118 NYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 177
Db |||||
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRI 180
Db |||||
QY 178 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRI 237
Db |||||
QY 181 TCVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPFKSVW 240
Db |||||
QY 238 TCVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPFKSVW 297
Db |||||
QY 241 SRLDGQWPDGGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGQRSD 285
Db |||||
QY 298 SRLDGQWPDGGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGQRSD 342
Db |||||

RESULT 8
AAE23283
ID AAE23283 standard; protein; 549 AA.
XX
AC AAE23283;
DT
XX 27-AUG-2002 (first entry)
XX Human nectin-3alpha protein.
DE
XX Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Modified-site 73 /note= "N-glycosylated"
FT Domain 74..152 /note= "Extracellular Ig domain"
FT Modified-site 83 /note= "N-glycosylated"
FT Modified-site 125 /note= "N-glycosylated"
FT Modified-site 186 /note= "N-glycosylated"
FT Domain 189..250 /note= "Extracellular Ig domain"
FT Modified-site 222 /note= "N-glycosylated"
FT Domain 287..342 /note= "Extracellular Ig domain"
FT Modified-site 331 /note= "N-glycosylated"
FT Domain 405..424 /note= "Transmembrane domain"
FT Domain 425..549 /note= "C-terminal domain"
XX
PN WO200228902-A2.

XX 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37442.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 89-91; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha DNA.
CC Human nectin-3alpha gene is located on chromosome 3
XX
SQ Sequence 549 AA;

Query Match 100.0%; Score 1520; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFK 60
Db |||||
QY 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEYQGRVLFK 124
Db |||||
QY 61 NYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db |||||
QY 125 NYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184
Db |||||
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRI 180
Db |||||
QY 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTFRFARGRRI 244
Db |||||
QY 181 TCVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPFKSVW 240
Db |||||
QY 245 TCVKHHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLCNADANPPPFKSVW 304
Db |||||
QY 241 SRLDGQWPDGGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGQRSD 285
Db |||||
QY 305 SRLDGQWPDGGLASDNTLHFVHPLTFNYSVGVYICKVTNSLGQRSD 349
Db |||||

RESULT 9
AAE23282
ID AAE23282 standard; protein; 549 AA.
XX
AC AAE23282;

XX 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin 3alpha fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
KW chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1. .7
FT /note= "Mouse nectin-3 protein"
FT Region 8. .549
FT /note= "Human nectin-3alpha protein"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37441.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 80-82; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
CC alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 549 AA;

Query Match 100.0%; Score 1520; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLEK 60
Db 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFVSQGEYQGRVLEK 124
QY 61 NYSLNDAITITLHNIGFSDSGKYICKAVTFFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDG 120
Db 125 NYSLNDAITITLHNIGFSDSGKYICKAVTFFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDG 184
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRI 244
QY 181 TCVVKHPALEKDRIYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVW 240
Db 245 TCVVKHPALEKDRIYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANPPPFKSVW 304
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349
RESULT 10
ABJ20222
ID ABJ20222 standard; protein; 549 AA.
XX
AC ABJ20222;
XX
DT 13-AUG-2003 (first entry)
XX
DE Human IG gene related protein SEQ ID No 45.
XX
KW Breast cancer; p53 pathway modulating agent; IG; colon cancer;
KW kidney cancer; lung cancer; ovary cancer; human.
XX
OS Homo sapiens.
XX
PN WO200299040-A2.
XX
PD 12-DEC-2002.
XX
PF 03-JUN-2002; 2002WO-US017313.
XX
PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 22-OCT-2001; 2001US-0338733P.
PR 15-FEB-2002; 2002US-0357253P.
PR 15-FEB-2002; 2002US-0357600P.
XX
PA (EXEL-) EXELIXIS INC.
XX
PI Friedman L, Florman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Lioubin MN;
XX
DR WPI; 2003-148660/14.
XX
PT Identifying a candidate p53 pathway modulators that are useful as targets
PT for therapeutics or for diagnosing cancers associated with defective p53
PT function, by providing an assay system having a purified IG polypeptide
PT or nucleic acid.
XX
PS Claim 13; Page 206-209; 248pp; English.
XX
CC The invention relates to a novel method for identifying a candidate p53
CC pathway modulating agent. The method comprises providing an assay system
CC having a purified IG polypeptide or nucleic acid, or their functionally
CC active fragment or derivative. The method is useful for identifying
CC modulators of the p53 pathway, particularly for identifying agents for
CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
CC cancer or cancer of the ovary) associated with defective p53 function.
CC The identified modulators are useful as targets for novel therapeutics.
CC The method is also useful for diagnosing disorders associated with
CC defective p53 function. The IG proteins or nucleic acids are useful as
CC modifiers of the p53 pathway, and as therapeutic targets for disorders

CC associated with defective p53 function. This sequence represents a human
CC protein relating to the human IG genes used in the assay for identifying
CC modulators of the p53 pathway of the invention
XX
SQ Sequence 549 AA;

Query Match 100.0%; Score 1520; DB 6; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.7e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFK 60
Db 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFK 124

QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSDLIDG 120
Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSDLIDG 184

QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI 244

QY 181 TCYVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVW 240
Db 245 TCYVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVW 304

QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349

RESULT 11
AAM39143
ID AAM39143 standard; protein; 555 AA.
XX
AC AAM39143;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2288.
XX
KW Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.

DR N-PSDE; AAI58299.
XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
PT
XX
PS Example 4; SEQ ID NO 2288; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with neurotropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 555 AA;

Query Match 100.0%; Score 1520; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 2.8e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFK 60
Db 71 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFSGVQGEYQGRVLFK 130

QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSDLIDG 120
Db 131 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSDLIDG 190

QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI 180
Db 191 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI 250

QY 181 TCYVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVW 240
Db 251 TCYVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFKSVW 310

QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 311 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 355

RESULT 12
AAE23288
ID AAE23288 standard; protein; 595 AA.
XX
AC AAE23288;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta-IgG1Fc region fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX

PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
XX
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 102-104; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3beta protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 595 AA;

Query Match 100.0%; Score 1520; DB 5; Length 595;
Best Local Similarity 100.0%; Pred. No. 3e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVEYQGRVLFK 60
Db 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVEYQGRVLFK 124

QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184

QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI 244

QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPKSVW 240
Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPKSVW 304

QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSYGVYICKVTNSLGQRSD 349

RESULT 13
AAE23287
ID AAE23287 standard; protein; 634 AA.
XX
AC AAE23287;
XX
DT 27-AUG-2002 (first entry)

XX Human nectin-3alpha-IgG1Fc region fusion protein.
DE
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
XX 05-OCT-2001; 2001WO-US031392.
PF
XX 05-OCT-2000; 2000US-0238557P.
PR (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
DR
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 9; Page 100-102; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region
XX
SQ Sequence 634 AA;

Query Match 100.0%; Score 1520; DB 5; Length 634;
Best Local Similarity 100.0%; Pred. No. 3.3e-125;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVEYQGRVLFK 60
Db 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFSGVEYQGRVLFK 124

QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184

QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARGRRI 244

QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPEKSVW 240
Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPEKSVW 304
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349
RESULT 14
AAM40929
ID AAM40929 standard; protein; 559 AA.
XX
AC AAM40929;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5860.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
PR 21-JAN-2000; 2000US-00488725.
PR 25-APR-2000; 2000US-00552317.
PR 20-JUN-2000; 2000US-00598042.
PR 19-JUL-2000; 2000US-00620312.
PR 03-AUG-2000; 2000US-00653450.
PR 14-SEP-2000; 2000US-00662191.
PR 19-OCT-2000; 2000US-00693036.
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI60085.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 5860; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX
SQ Sequence 559 AA;
Query Match 98.4%; Score 1495; DB 4; Length 559;
Best Local Similarity 98.9%; Pred. No. 4.5e-123;
Matches 280; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 HVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVQGEYQGRVLFK 60
Db 64 HVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVQGEYQGRVLFK 123
QY 61 NYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG 120
Db 124 NYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSLIDG 183
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRI 180
Db 184 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTFRFARRRI 243
QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPEKSVW 240
Db 244 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPEKSVW 303
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQR 283
Db 304 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSPGSK 346

RESULT 15
AAG63984
ID AAG63984 standard; protein; 438 AA.
XX
AC AAG63984;
XX

DT 26-NOV-2001 (first entry)

DE Amino acid sequence of murine nectin-3.

XX Nectin-3; cell adhesion; cell infiltration; cancer metastasis; cancer.

OS Mus sp.

XX WO200166736-A1.

XX 13-SEP-2001.

XX 09-MAR-2001; 2001WO-JP001871.

XX 09-MAR-2000; 2000JP-00065595.

XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX (TAKA/) TAKAHASHI K.

XX Takahashi K, Takai Y, Nakanishi H, Sato K;

XX WPI; 2001-570771/64.

XX N-PSDB; AAH78181.

XX New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and
PT corresponding antibodies.

XX Claim 3; Page 53-55; 64pp; Japanese.

XX The present sequence represents a murine nectin-3 polypeptide. Nectin-3
CC is an immunoglobulin-like cell adhesion molecule that shows homophilic
CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
CC polynucleotides are useful for investigating the mechanisms of cell
CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
CC malignancies of various cancers, and the development of methods for the
CC treatment and prevention of cancer

XX Sequence 438 AA;
SQ

Query Match 97.8%; Score 1487; DB 4; Length 438;
Best Local Similarity 96.5%; Pred. No. 1.6e-122;
Matches 275; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

Qy	1	HVTAVWGKNVSLKCLIEVN	1	QISWEKIHGKSSQT	VAVHHPOYGF	SVQGEYQGRVLFK	60
Db	65	HVTAVWGKNVSLKCLIEVN	1	QISWEKIHGKSSQT	VAVHHPOYGF	SVQGEYQGRVLFK	124
Qy	61	NYSLNDAITLHNIGFSD	SGKYICKAVTFPLGNAQS	STTVTLVEPTV	SLIKGPD	SLIDG	120
Db	125	NYSLNDAITLHNIGFSD	SGKYICKAVTFPLGNAQS	STTVTLVEPTV	SLIKGPD	SLIDG	184
Qy	121	GNETVAAICIAATGKPV	AHIDWEGDLGEMEST	TTSPNETAT	II	SOYKLFPTRFARGRI	180
Db	185	GNETVAAVCVAATGKPV	AQIDWEGDLGEMEST	TTSPNETAT	IV	SOYKLFPTRFARGRI	244
Qy	181	TCVVXHPALEKDIRY	SFILDIOYAPEVSV	TGYDGNWFVGRKGV	NLKNADAN	PPPFKSVW	240
Db	245	TCVVXHPALEKDIRY	SFILDIOYAPEVSV	TGYDGNWFVGRKGV	NLKNADAN	PPPFKSVW	304
Qy	241	SRLDGQWPDGLLASD	NTLHFVHPLTFNYS	GVYICKVTNSL	QGRSD		285
Db	305	SRLDGQWPDGLLASD	NTLHFVHPLTFNYS	GVYICKVTNSL	QGRSD		349

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Job time : 36.421 secs

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 23.8184 Seconds
(without alignments)
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Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
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5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
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12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1520	100.0	387	10	US-09-972-268-16
2	1520	100.0	426	10	US-09-972-268-15
3	1520	100.0	437	10	US-09-972-268-31
4	1520	100.0	504	10	US-09-972-268-8
5	1520	100.0	510	10	US-09-972-268-10
6	1520	100.0	510	10	US-09-972-268-12
7	1520	100.0	542	10	US-09-972-268-2
8	1520	100.0	549	10	US-09-972-268-4
9	1520	100.0	549	10	US-09-972-268-6
10	1520	100.0	549	14	US-10-161-572-45
11	1520	100.0	595	10	US-09-972-268-14
12	1520	100.0	634	10	US-09-972-268-13
13	1487	97.8	438	10	US-09-959-845-6
14	1487	97.8	438	10	US-09-972-268-19
15	1487	97.8	510	10	US-09-959-845-4

16	1487	97.8	510	10	US-09-972-268-18	Sequence 18, Appl
17	1487	97.8	549	10	US-09-959-845-2	Sequence 2, Appl
18	1487	97.8	549	10	US-09-972-268-17	Sequence 17, Appl
19	524.5	34.5	458	10	US-09-972-268-21	Sequence 21, Appl
20	524.5	34.5	514	14	US-10-161-572-60	Sequence 60, Appl
21	524.5	34.5	517	10	US-09-972-268-20	Sequence 20, Appl
22	502	33.0	518	9	US-09-919-172-20	Sequence 20, Appl
23	459.5	30.2	314	10	US-09-766-511B-36	Sequence 36, Appl
24	459.5	30.2	479	10	US-09-766-511B-35	Sequence 35, Appl
25	459.5	30.2	497	10	US-09-972-268-37	Sequence 37, Appl
26	459.5	30.2	498	10	US-09-972-268-39	Sequence 39, Appl
27	459.5	30.2	510	10	US-09-766-511B-33	Sequence 33, Appl
28	459.5	30.2	510	12	US-10-058-270A-54	Sequence 54, Appl
29	459.5	30.2	510	14	US-10-161-572-55	Sequence 55, Appl
30	459.5	30.2	510	14	US-10-241-220-94	Sequence 94, Appl
31	459.5	30.2	510	15	US-10-295-027-66	Sequence 66, Appl
32	459.5	30.2	510	15	US-10-173-999-76	Sequence 76, Appl
33	459.5	30.2	511	10	US-09-972-268-34	Sequence 34, Appl
34	459.5	30.2	580	10	US-09-972-268-36	Sequence 36, Appl
35	457.5	30.1	510	10	US-09-972-268-24	Sequence 24, Appl
36	457.5	30.1	510	14	US-10-161-572-54	Sequence 54, Appl
37	374	24.6	412	14	US-10-161-572-63	Sequence 63, Appl
38	372	24.5	479	10	US-09-972-268-22	Sequence 22, Appl
39	372	24.5	479	14	US-10-161-572-62	Sequence 62, Appl
40	372	24.5	538	10	US-09-972-268-23	Sequence 23, Appl
41	372	24.5	538	10	US-09-984-130-138	Sequence 138, App
42	372	24.5	538	10	US-09-836-353A-138	Sequence 138, App
43	372	24.5	538	14	US-10-161-572-61	Sequence 61, Appl
44	372	24.5	538	15	US-10-411-010-17	Sequence 17, Appl
45	370	24.3	522	15	US-10-264-049-2969	Sequence 2969, Ap

ALIGNMENTS

RESULT 1
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-16

Query Match 100.0%; Score 1520; DB 10; Length 387;
Best Local Similarity 100.0%; Pred. No. 4.4e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK	60
Db	65	HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK	124
QY	61	NYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDG	120
Db	125	NYSINDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDG	184

QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTRFARGRRI 244
QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVW 240
Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVW 304
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349
RESULT 2
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE T
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

Query Match 100.0%; Score 1520; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 5e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
Db 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 124
QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDLSLIDG 120
Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDLSLIDG 184
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTRFARGRRI 244
QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVW 240
Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVW 304
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349
RESULT 3
US-09-972-268-31
; Sequence 31, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 437
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-31
Query Match 100.0%; Score 1520; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 5.2e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
Db 65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 124
QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDLSLIDG 120
Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDLSLIDG 184
QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTRFARGRRI 244
QY 181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVW 240
Db 245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPFKSVW 304
QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349

RESULT 4
US-09-972-268-8
; Sequence 8, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 504
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-8
Query Match 100.0%; Score 1520; DB 10; Length 504;
Best Local Similarity 100.0%; Pred. No. 6.3e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
Db 59 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 118
QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDLSLIDG 120


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Db      119 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 178
QY      121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTRFARGRRI 180
Db      179 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTRFARGRRI 238
QY      181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 240
Db      239 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 298
QY      241 SRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db      299 SRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 343

RESULT 5
US-09-972-268-10
; Sequence 10, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest are
; OTHER INFORMATION: from human Nectin-3 beta
US-09-972-268-10

Query Match      100.0%; Score 1520; DB 10; Length 510;
Best Local Similarity 100.0%; Pred. No. 6.4e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFK 60
Db      65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFK 124
QY      61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db      125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184
QY      121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTRFARGRRI 180
Db      185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTRFARGRRI 244
QY      181 TCWKHPALEKDIRYSPILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 240
Db      245 TCWKHPALEKDIRYSPILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 304

RESULT 6
US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 510
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: homo sapiens
US-09-972-268-12

Query Match      100.0%; Score 1520; DB 10; Length 542;
Best Local Similarity 100.0%; Pred. No. 7e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFK 60
Db      65 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFK 124
QY      61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db      125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184
QY      121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTRFARGRRI 180
Db      185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTRFARGRRI 244
QY      181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 240
Db      245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 304

RESULT 7
US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match      100.0%; Score 1520; DB 10; Length 542;
Best Local Similarity 100.0%; Pred. No. 7e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFK 60
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Db      58 HVTAVWGKNSVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 117
QY      61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db      118 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 177
QY      121 GNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRI 180
Db      178 GNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRI 237
QY      181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPKSVW 240
Db      238 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPKSVW 297
QY      241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db      298 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 342

RESULT 8
US-09-972-268-4
; Sequence 4, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are from
; OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match      100.0%; Score 1520; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 7.le-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HVTAVWGKNSVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
Db      65 HVTAVWGKNSVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 124
QY      61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db      125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184
QY      121 GNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRI 180
Db      185 GNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRI 244
QY      181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPKSVW 240
Db      245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPKSVW 304
QY      241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db      305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349

RESULT 9
```

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US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 549
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-6

Query Match      100.0%; Score 1520; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 7.le-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 HVTAVWGKNSVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
Db      65 HVTAVWGKNSVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 124
QY      61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db      125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184
QY      121 GNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRI 180
Db      185 GNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRRI 244
QY      181 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPKSVW 240
Db      245 TCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANPPPKSVW 304
QY      241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db      305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349

RESULT 10
US-10-161-572-45
; Sequence 45, Application US/10161572
; Publication No. US20030087266A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS, INC.
; TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
; FILE REFERENCE: EX02-097C-PC
; CURRENT APPLICATION NUMBER: US/10/161,572
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 60/296,076
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: US 60/328,605
; PRIOR FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 60/338,733
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/357,253
; PRIOR FILING DATE: 2002-02-15
; PRIOR APPLICATION NUMBER: US 60/357,600
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 45
; LENGTH: 549
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 100.0%; Score 1520; DB 14; Length 549;
Best local Similarity 100.0%; Pred. No. 7.1e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
Db 65 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 124

QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184

QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRI 244

QY 181 TCVKVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 240
Db 245 TCVKVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 304

QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349

RESULT 11
US-09-972-268-14
; Sequence 14, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-Fc
US-09-972-268-14

Query Match 100.0%; Score 1520; DB 10; Length 595;
Best local Similarity 100.0%; Pred. No. 7.9e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
Db 65 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 124

QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184

QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRI 244

QY 181 TCVKVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 240
Db 245 TCVKVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 304

QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349

RESULT 12
US-09-972-268-13
; Sequence 13, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 634
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match 100.0%; Score 1520; DB 10; Length 634;
Best local Similarity 100.0%; Pred. No. 8.7e-137;
Matches 285; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 60
Db 65 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFK 124

QY 61 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 120
Db 125 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 184

QY 121 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRI 180
Db 185 GNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTRFARGRRI 244

QY 181 TCVKVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 240
Db 245 TCVKVHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLKCNADANPPPFKSVW 304

QY 241 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 285
Db 305 SRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSD 349

RESULT 13
US-09-959-845-6
; Sequence 6, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshimi TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595

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; PRIOR FILING DATE: 2000-03-09
;
; NUMBER OF SEQ ID NOS: 14
;
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 6
;   LENGTH: 438
;   TYPE: PRT
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; ORGANISM: Mouse
;
US-09-959-845-6

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RESULT 15
US-09-959-845-4
; Sequence 4, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshimi TAKAI
; APPLICANT: Hiroyuki NAKANISHI
; APPLICANT: Keiko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 510
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-4

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	Query Match	97.8%;	Score 1487;	DB 10;	Length 510;	
	Best Local Similarity	96.5%;	Pred. No. 9.4e-134;			
	Matches 275; Conservative	8;	Mismatches 2;	Indels 0;	Gaps 0	
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Dd	65	HVTAVWGKNVSLKCLIEVN	ETITQISWEKIHGKSTQTV	AHHHPQYGF	SVQGDYQG	RVLFX 1244
Qy	61	NYSLNDAITLHNIGFSDS	GKYICKAVTFPLGNAQS	TTVT	LVEPTVS	LIKGPDSLIDG 1200
Dd	125	NYSLNDAITLHNIGFSDS	GKYICKAVTFPLGNAQS	TTVT	LVEPTVS	LIKGPDSLIDG 18
Qy	121	GNETVAAICIAATGKP	VAHIDWEGDLGEMES	TTTSFP	NETATIISQY	KLFPTRFARGRRI 18
Dd	185	GNETVAAVCVAATGKP	VAQIDWEGDLGEMES	TTTSFP	NETATIVSQY	KLFPTRFARGRRI 24
Qy	181	TCVVKHPALEKDRIYS	FILDIQYAPEVSVTGYD	GNWFVG	RKGVNLKC	NADANPPPFKSVM 24
Dd	245	TCVVKHPALEKDRIYS	FILDIQYAPEVSVTGYD	GNWFVG	RKGVNLKC	NADANPPPFKSVM 30
Qy	241	SRLDGQPDPGLLASDN	TLHFVHPLTFENYS	GVYICK	VTNSLGQRSD	285
Dd	305	SRLDGQPDPGLLASDN	TLHFVHPLTFVNYSG	VYCVCK	VSNLSLGRSD	349

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Search completed: April 12, 2004, 10:25:23
Job time : 23.8184 secs
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 9.40791 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-2_COPY_58_342
Perfect score: 1520
Sequence: 1 HVTAVGKNVSLKCLIEVNE.....FNYSGVYICKVTNSLQGRSD 285

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	524.5	34.5	517	4	US-09-723-368-4
2	521.5	34.3	458	4	US-09-435-956A-1
3	502	33.0	518	4	US-09-919-172-20
4	372	24.5	479	4	US-09-723-368-2
5	361	23.8	408	4	US-09-724-864-62
6	247.5	16.3	440	4	US-09-866-028-61
7	247.5	16.3	442	4	US-09-778-510-20
8	247.5	16.3	442	4	US-09-930-803-1
9	244.5	16.1	423	4	US-09-778-510-22
10	217.5	14.3	398	4	US-09-778-510-4
11	207.5	13.7	398	4	US-09-778-510-6
12	207.5	13.7	398	4	US-09-907-794A-84
13	207.5	13.7	398	4	US-09-905-125A-84
14	207.5	13.7	398	4	US-09-902-775A-84
15	207.5	13.7	432	4	US-09-778-510-2
16	200	13.2	421	2	US-08-659-984A-1
17	200	13.2	421	3	US-08-660-531-1
18	200	13.2	444	2	US-08-659-984A-5
19	200	13.2	444	3	US-08-660-531-5
20	187.5	12.3	227	4	US-09-205-258-947
21	187.5	12.3	274	4	US-09-570-367C-19
22	187.5	12.3	274	4	US-09-915-524-19
23	162.5	10.7	278	4	US-09-570-367C-2
24	162.5	10.7	278	4	US-09-915-524-2
25	159.5	10.5	278	4	US-09-570-367C-21
26	159.5	10.5	278	4	US-09-915-524-21
27	154	10.1	477	2	US-08-432-016-3

28	154	10.1	477	2	US-08-684-594-3	Sequence 3, Appli
29	154	10.1	642	1	US-08-217-299-1	Sequence 1, Appli
30	154	10.1	698	2	US-08-602-725-36	Sequence 36, Appl
31	154	10.1	734	2	US-08-389-459A-17	Sequence 17, Appl
32	154	10.1	734	3	US-08-987-867A-17	Sequence 17, Appl
33	149.5	9.8	467	3	US-09-046-736-2	Sequence 2, Appli
34	149.5	9.8	1101	3	US-08-986-485-2	Sequence 2, Appli
35	144	9.5	313	4	US-09-700-397-4	Sequence 4, Appli
36	144	9.5	344	4	US-09-700-397-3	Sequence 3, Appli
37	141.5	9.3	387	4	US-09-175-928-2	Sequence 2, Appli
38	140	9.2	583	2	US-08-432-016-2	Sequence 2, Appli
39	140	9.2	583	2	US-08-684-594-2	Sequence 2, Appli
40	139.5	9.2	298	4	US-09-152-060-76	Sequence 76, Appl
41	137.5	9.0	312	4	US-09-254-465A-9	Sequence 9, Appli
42	137.5	9.0	312	4	US-09-907-794A-64	Sequence 64, Appl
43	137.5	9.0	312	4	US-09-905-125A-64	Sequence 64, Appl
44	137.5	9.0	312	4	US-09-902-775A-64	Sequence 64, Appl
45	137	9.0	582	4	US-09-702-705-334	Sequence 334, App

ALIGNMENTS

RESULT 1
US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match	34.5%	Score	524.5;	DB	4;	Length	517;
Best Local Similarity	38.1%	Pred. No.	1.3e-44;				
Matches	109;	Conservative	53;	Mismatches	113;	Indels	11;
						Gaps	5;
Qy	7	GKNVSLKCLIE---	VNETITQISWEKIHGKSSQTVAVHHPPQYGFSGVQGEYQGRVLFKNYS	63			
Db	44	GTDVVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAINPMSGMVSLAPYRVERVEFLRPS	103				
Qy	64	INDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSLIDG---	120				
Db	104	FTDGTIRLSRLEDEGVYICEFATFPTGNRESQLNLTVMNAKPT-NWIEGTQAVLRKKG	162				
Qy	121	-GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTSPNETATIIISQYKLFPTFFARGR	178				
Db	163	QDDKVLVATCTSANGKPPSVSVSWETRLKGEAYQEIRNPNGTIVTISRVLVPSREAHQQ	222				
Qy	179	RITCVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWVGRKGVNLKCNADANPPPFKS	238				

Db 223 SLACIVNYHM--DRFKESLTINLVQYEPVETIEGFGDNWYLQRMVDVLTCKADANPPATEY 280
QY 239 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS 284
Db 281 HWTTLNGLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRS 326

RESULT 2
US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: Higr and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 34.3%; Score 521.5; DB 4; Length 458;
Best Local Similarity 38.1%; Pred. No. 2.3e-44;
Matches 109; Conservative 52; Mismatches 114; Indels 11; Gaps 5;
QY 7 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 63
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSLAPYRERVEFLRPS 103
QY 64 LNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDLSIDG--- 120
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQNLNLTVMKPT-NWIEGTQAVLRAKKG 162
QY 121 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTPFARGR 178
Db 163 QDDKVLVATCTSANGKPPSVSVSWETRLKGEAEYQEIERNPNGTVTVISRYLVPSEAHQQ 222
QY 179 RITCVVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGKGVNLCNADANPPPFKS 238
Db 223 SLACIVNYHM--DRFKESLTINLVQYEPVETIEGFGDNWYLQRMVDVLTCKADANPPATEY 280
QY 239 VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS 284
Db 281 HWTTLNGLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRS 326

RESULT 3
US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CDI
US-09-919-172-20
Query Match 33.0%; Score 502; DB 4; Length 518;
Best Local Similarity 35.9%; Pred. No. 2.6e-42;
Matches 106; Conservative 53; Mismatches 108; Indels 28; Gaps 6;
QY 7 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 63
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSLAPYRERVEFLRPS 103
QY 64 LNDATITLHNIGFSDGKYICKAVTFPLGNAQSSTTVTLVVEPTVSLIKGPDLSIDG--- 120
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQNLNLTVMKPT-NWIEGTQAVLRAKKG 162
QY 121 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATIIISQYKLFPTPFARGR 169
Db 163 QDDKVLVATCTSANGKPPSVSVSWETRLKGEARVPGDSGT-----PMAPVTVISRYRL 214
QY 170 FPTRFARGRITCVVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGKGVNLCNKA 229
Db 215 VPSREAHQQSLACIVNYHM--DRFKESLTINLVQYEPVETIEGFGDNWYLQRMVDVLTCKA 272
QY 230 DANPPPFKS VMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRS 284
Db 273 DANPPATEYHWTTLNGLSLPKGVEAQNRTLFFKGPINYSLAGTYICEATNPIGTRS 327

RESULT 4
US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match 24.5%; Score 372; DB 4; Length 479;
Best Local Similarity 29.7%; Pred. No. 3.6e-29;
Matches 85; Conservative 51; Mismatches 110; Indels 40; Gaps 8;
QY 22 ITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEYQG--RVLF-----KNYSLNDAT 68

Db 65 ISLVWQRPDAPANHONVAAPHKMGPSFPSPKPGSERLSFVSAKQSTGQDTEAELQDAT 124
QY 69 ITHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPE-----TVSLIKGPDSDLIDGG 121
Db 125 LALHGLTVEDEGNYTCEFAFEPKGSVRGMTLWLVIAKPKNAEAKVTFSDP----- 177
QY 122 NETVAAICIAATGKPVABI-----DWEGDLGEMESTTTSPNETATIIISQYKLFPTTFA 175
Db 178 --TTVALCISKEGRPPPARISWLSLDWEAKETQVSGTLAG-----TVTTSRFTLVPSGRA 231
QY 176 RGRRTTCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANPPP 235
Db 232 DGVTVTKVHEHESFEEPALIPVTLVRYPPPEVSIISGYDDNWLGRDTATLSCDVRNPEP 291
QY 236 FKSWSRLDQGWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 292 TGYDWSSTTSPTPTSAVAQGSQ-L-VIHAVDSLFTTFVCTVTINAVG 336

RESULT 5
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050UL
; CURRENT APPLICATION NUMBER: US/09/724,864
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62

Query Match 23.8%; Score 361; DB 4; Length 408;
Best Local Similarity 33.4%; Pred. No. 3.7e-28;
Matches 98; Conservative 48; Mismatches 125; Indels 22; Gaps 10;
QY 3 TAVWGNVSLKCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLF 59
Db 39 TGVLGSTTLHCSLTSNENVTITQITWMKKDSGGSHALVAVFHPKKGPNKEPERVKFLA 98
QY 60 KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPE--TVSLIKGPDSDL 117
Db 99 AQQDLRNASIAISNLSVEDEGIYECQIATFPRGSRSTNAWLKVQARPKNTAEALEPSPTL 158
QY 118 I--DGGNETVAAICIAATGKPVABIDW-----EGDLGEMESTTTSPNETATIIISQYKLF 171
Db 159 ILQD-----VAKCISANGHPGGRISWPSNVNGSHREMKE-PSQPG-TTIVTSYLSMVP 210
QY 172 TRFARGRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTGYDGNWVFGVGRKGVNLKCNAD 230
Db 211 SRQADGKNITCTVEHESLQELDQLLVLSQPYPPENVSISGYDGNWVGLTNLTLTCEAH 270
QY 231 ANPPPFKS--VMSRLDQGWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 271 SKPAPDMAGYNWSTNTGDFPNSVKRQGNMLISTVEDGLNNTVIVCEVTNALG 323

RESULT 6
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin

; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 16.3%; Score 247.5; DB 4; Length 440;
Best Local Similarity 26.6%; Pred. No. 1.4e-16;
Matches 77; Conservative 58; Mismatches 126; Indels 29; Gaps 11;
QY 2 VTAVWGNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKN 61
Db 50 VTVIEGEVATISC--QVNSKSDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLLN 99
QY 62 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVPEPTVSLIK-GPDSLIDG 120
Db 100 FSSSELKVSILTNSISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMDIQKDTAVEG 157
QY 121 GNETVAAICIAATGKPVABIDW-EGDL-----GEMESTTTSPNETATIIISQYKLFPTTRF 174
Db 158 --EEIEVNCNTAMASKPATIRWFKGNTELKKGSEVEWSDMY-----TVTSQMLKLVHKE 210
QY 175 ARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKG--VNLKCNADAN 232
Db 211 DGVVPVICQVEHPAVTGNLQTRYLEVQYKQPQVHIQMTYPLQGLTREGDALELTCEAIGK 270
QY 233 PPPFKSVWSRLDQGWPDGGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQ 282
Db 271 PQPVMVTWVRVDEMPQHAVLSGPNL-FINNLNKNTDNGTYRCEASNIVGK 319

RESULT 7
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 442
; TYPE: PRT
; ORGANISM: Homo sapien

Db39TVVAGGTVVLKQVQKDHED-SSLQWS---NPAQOTL-----YFGEKRALRDNRIQLVSS88

QY63SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSDLIDGNN122

Db89TPHELISISNVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSSL-REK145

QY123ETVAAICIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLPFTRFARGR178

Db146ETATLNCQSSGSKPAAQLTWRKGDQDLHGDQTRIQEDPNKGKTFVSSSVSFQVTTREDDGA205

QY179RITCVVKHPALE-KDIRYSFILDIQYAPEVSVTYDGNWVFVGRKGVNLKCNADANPPPFK237

Db206NIVCSVNHESLKGADRSTSORIEVLTYPTAMIRPEPAHPREGQK-LLLHCEGRGNPVPOQ264

QY238SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG281

Db265YVWVK-EGSEPLKMTQESALIFPF-LNKSDSGTYGCTATSNMG306

RESULT 11

US-09-778-510-6

Sequence 6, Application US/09778510

Patent No. 6512095

GENERAL INFORMATION:

APPLICANT: Baum, Peter

TITLE OF INVENTION: Molecules Designated B7L1

FILE REFERENCE: 2844-US

CURRENT APPLICATION NUMBER: US/09/778,510

CURRENT FILING DATE: 2001-02-07

PRIOR APPLICATION NUMBER: PCT/US99/17906

PRIOR FILING DATE: 1999-08-05

PRIOR APPLICATION NUMBER: 60/095,663

PRIOR FILING DATE: 1998-08-07

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 6

LENGTH: 398

TYPE: PRT

ORGANISM: Homo sapien

US-09-778-510-6

Query Match13.7%; Score 207.5; DB 4; Length 398;

Best Local Similarity26.4%; Pred. No. 1.3e-12;

Matches75; Conservative49; Mismatches139; Indels21; Gaps11;

QY3TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNY62

Db39TVVAGGTVVLKQVQKDHED-SSLQWS---NPAQOTL-----YFGEKRALRDNRIQLVTS88

QY63SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITVTVLVEPTVSLIKGPDSDLIDGNN122

Db89TPHELISISNVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSSL-REK145

QY123ETVAAICIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLPFTRFARGR178

Db146DTATLNCQSSGSKPAAQLTWRKGDQDLHGDQTRIQEDPNKGKTFVSSSVTFQVTTREDDGA205

QY179RITCVVKHPALE-KDIRYSFILDIQYAPEVSVTYDGNWVFVGRKGVNLKCNADANPPPFK237

Db206SIVCSVNHESLKGADRSTSORIEVLTYPTAMIRPPHPREGQK-LLLHCEGRGNPVPOQ264

QY238SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG281

Db265YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMG306

RESULT 12

US-09-907-794A-84

Sequence 84, Application US/09907794A

Patent No. 6635468

GENERAL INFORMATION:

APPLICANT: Genentech, Inc.

US-09-907-794A-84

Query Match13.7%; Score 207.5; DB 4; Length 398;

Best Local Similarity26.4%; Pred. No. 1.3e-12;

Matches75; Conservative49; Mismatches139; Indels21; Gaps11;

APPLICANT: Ashkenazi, Avi

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerlitsen, Mary E.

APPLICANT: Goddard, A.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, Christopher J.

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth, J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William, I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: 10466-14

CURRENT APPLICATION NUMBER: US/09/907,794A

CURRENT FILING DATE: 2001-07-17

PRIOR APPLICATION NUMBER: PCT/US00/04414

PRIOR FILING DATE: 2000-02-22

PRIOR APPLICATION NUMBER: US 60/143,048

PRIOR FILING DATE: 1999-07-07

PRIOR APPLICATION NUMBER: US 60/145,698

PRIOR FILING DATE: 1999-07-26

PRIOR APPLICATION NUMBER: US 60/146,222

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: PCT/US99/20594

PRIOR FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: PCT/US99/20944

PRIOR FILING DATE: 1999-09-13

PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/21547

PRIOR FILING DATE: 1999-09-15

PRIOR APPLICATION NUMBER: PCT/US99/23089

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: PCT/US99/28214

PRIOR FILING DATE: 1999-11-29

PRIOR APPLICATION NUMBER: PCT/US99/28313

PRIOR FILING DATE: 1999-11-30

PRIOR APPLICATION NUMBER: PCT/US99/28564

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/28565

PRIOR FILING DATE: 1999-12-02

PRIOR APPLICATION NUMBER: PCT/US99/30095

PRIOR FILING DATE: 1999-12-16

PRIOR APPLICATION NUMBER: PCT/US99/30911

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US99/30999

PRIOR FILING DATE: 1999-12-20

PRIOR APPLICATION NUMBER: PCT/US00/00219

PRIOR FILING DATE: 2000-01-05

NUMBER OF SEQ ID NOS: 423

SEQ ID NO 84

LENGTH: 398

TYPE: PRT

ORGANISM: Homo sapiens

US-09-907-794A-84

Query Match13.7%; Score 207.5; DB 4; Length 398;

Best Local Similarity26.4%; Pred. No. 1.3e-12;

Matches75; Conservative49; Mismatches139; Indels21; Gaps11;

QY 3 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNY 62
Db 39 TVVAGGTVVLKQVKDHED-SSLQWS---NPAQQTLL-----YFGEKRALRDNRIQLVTS 88
QY 63 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGNN 122
Db 89 TPHELISISNVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145
QY 123 ETVAACIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTTFEARGR 178
Db 146 DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTTREDDGA 205
QY 179 RITCVVKHPALE-KDIRYSFILDIIQYAPEVSVTYGDNWFWVGRKGVNLCNADANPPPFK 237
Db 206 SIVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHPREGQK-LLLHCEGRGNPVPQQ 264
QY 238 SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 265 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMG 306

RESULT 13
US-09-905-125A-84
; Sequence 84, Application US/09905125A
; Patent No. 6664376
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William, I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: 10466-14
; CURRENT APPLICATION NUMBER: US/09/905,125A
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: 2000-02-22
; PRIOR APPLICATION NUMBER: US 60/143,048
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: US 60/145,698
; PRIOR FILING DATE: 1999-07-26
; PRIOR APPLICATION NUMBER: US 60/146,222
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/20944
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547
; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: PCT/US99/23089
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: PCT/US99/28214
; PRIOR FILING DATE: 1999-11-29
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: PCT/US99/28564
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/28565
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: 1999-12-16
; PRIOR APPLICATION NUMBER: PCT/US99/30911
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US99/30999
; PRIOR FILING DATE: 1999-12-20
; PRIOR APPLICATION NUMBER: PCT/US00/00219
; PRIOR FILING DATE: 2000-01-05
; NUMBER OF SEQ ID NOS: 423
; SEQ ID NO 84
; LENGTH: 398
; TYPE: PRM
; ORGANISM: Homo sapiens
US-09-905-125A-84
Query Match 13.7%; Score 207.5; DB 4; Length 398;
Best Local Similarity 26.4%; Pred. No. 1.3e-12;
Matches 75; Conservative 49; Mismatches 139; Indels 21; Gaps 11;
QY 3 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPPQYGFVSQGEYQGRVLFKNY 62
Db 39 TVVAGGTVVLKQVKDHED-SSLQWS---NPAQQTLL-----YFGEKRALRDNRIQLVTS 88
QY 63 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGNN 122
Db 89 TPHELISISNVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145
QY 123 ETVAACIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIIISQYKLFPTTFEARGR 178
Db 146 DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTTREDDGA 205
QY 179 RITCVVKHPALE-KDIRYSFILDIIQYAPEVSVTYGDNWFWVGRKGVNLCNADANPPPFK 237
Db 206 SIVCSVNHESLKGADRSQRIEVLVYPTAMIRPDPPHPREGQK-LLLHCEGRGNPVPQQ 264
QY 238 SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 265 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMG 306

RESULT 14
US-09-902-775A-84
; Sequence 84, Application US/09902775A
; Patent No. 6686451
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, A.
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth, J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Mather, Jennie P.

APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William, I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: 10466-14
CURRENT APPLICATION NUMBER: US/09/902,775A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 60/143,048
PRIOR FILING DATE: 1999-07-07
PRIOR APPLICATION NUMBER: US 60/145,698
PRIOR FILING DATE: 1999-07-26
PRIOR APPLICATION NUMBER: US 60/146,222
PRIOR FILING DATE: 1999-07-28
PRIOR APPLICATION NUMBER: PCT/US99/20594
PRIOR FILING DATE: 1999-09-08
PRIOR APPLICATION NUMBER: PCT/US99/20944
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/21547
PRIOR FILING DATE: 1999-09-15
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: 1999-11-30
PRIOR APPLICATION NUMBER: PCT/US99/28564
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/28565
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: PCT/US99/30911
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US99/30999
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: PCT/US00/00219
PRIOR FILING DATE: 2000-01-05
NUMBER OF SEQ ID NOS: 423
SEQ ID NO 84
LENGTH: 398
TYPE: PRT
ORGANISM: Homo sapiens
US-09-902-775A-84

Query Match 13.7%; Score 207.5; DB 4; Length 398;
Best Local Similarity 26.4%; Pred. No. 1.3e-12;
Matches 75; Conservative 49; Mismatches 139; Indels 21; Gaps 11;

QY 3 TAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFKNY 62
Db 39 TVVAGGTIVLKQVKDHED-SSLQWS---NPAQQTL-----YFGEKRALRDNRIQLVTS 88
QY 63 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGN 122
Db 89 TPHELISISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145
QY 123 ETVAACIAATGKPVAHIDWEGDLGEMESTTSF---PN-ETATIIISQYKLFPTTRFARGR 178
Db 146 DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGA 205
QY 179 RITCVVKHPALE-KDIRYSFILDIQYAPEVSVTYDGNWFGVGRKGVNLKCNADANPPPFK 237
Db 206 SIVCSVNHESLKGADRSTQRIEVLVYPTAMIRPDPPHPREGQK-LLHCEGRGNPVPQQ 264

QY 238 SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 265 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMG 306

RESULT 15
US-09-778-510-2
Sequence 2, Application US/09778510
Patent No. 6512095
GENERAL INFORMATION:
APPLICANT: Baum, Peter
TITLE OF INVENTION: Molecules Designated B7L1
FILE REFERENCE: 2844-US
CURRENT APPLICATION NUMBER: US/09/778,510
CURRENT FILING DATE: 2001-02-07 PCT/US99/17906
PRIOR APPLICATION NUMBER: 60/095,663
PRIOR FILING DATE: 1998-08-07
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 432
TYPE: PRT
ORGANISM: Homo sapien
US-09-778-510-2

Query Match 13.7%; Score 207.5; DB 4; Length 432;
Best Local Similarity 26.4%; Pred. No. 1.5e-12;
Matches 75; Conservative 49; Mismatches 139; Indels 21; Gaps 11;

QY 3 TAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEYQGRVLFKNY 62
Db 73 TVVAGGTIVLKQVKDHED-SSLQWS---NPAQQTL-----YFGEKRALRDNRIQLVTS 122
QY 63 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGN 122
Db 123 TPHELISISNVALADEGEYTCISFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 179
QY 123 ETVAACIAATGKPVAHIDWEGDLGEMESTTSF---PN-ETATIIISQYKLFPTTRFARGR 178
Db 180 DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGKTFVSSSVTFQVTRDDGA 239
QY 179 RITCVVKHPALE-KDIRYSFILDIQYAPEVSVTYDGNWFGVGRKGVNLKCNADANPPPFK 237
Db 240 SIVCSVNHESLKGADRSTQRIEVLVYPTAMIRPDPPHPREGQK-LLHCEGRGNPVPQQ 298
QY 238 SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 281
Db 299 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMG 340

Search completed: April 12, 2004, 09:49:20
Job time : 10.4079 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:40 ; Search time 9.18182 Seconds
(without alignments)
3635.278 Million cell updates/sec

Title: US-09-972-268-4_COPY_58_404
Perfect score: 1844
Sequence: 1 GPIIIEPHVTAVGKNVSLK.....KKLPFLSTLATIKDDTIAT 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1391	75.4	407	2	T08732	hypothetical prote
2	516	28.0	518	2	JC4024	poliovirus recepto
3	420	22.8	530	2	A53437	poliovirus recepto
4	419	22.7	467	1	HLMSP3	poliovirus recepto
5	401.5	21.8	538	2	I68093	PRR2 delta - human
6	396.5	21.5	392	2	B44194	poliovirus recepto
7	396.5	21.5	417	2	A44194	poliovirus recepto
8	396.5	21.5	478	2	I53960	PRR2 alpha - human
9	383.5	20.8	392	1	RWHUPD	poliovirus recepto
10	383.5	20.8	417	1	RWHUPA	poliovirus recepto
11	320	17.4	416	2	A54017	colon carcinoma-as
12	227.5	12.3	764	2	A49448	irregular chiasm C
13	200.5	10.9	5175	2	T20992	hypothetical prote
14	200.5	10.9	5198	2	T43290	hemimentin precurs
15	198	10.7	4391	2	A38096	perlecan precursor
16	189	10.2	853	1	IJBONC	neural cell adhesi
17	187.5	10.2	274	2	A47639	OX-2 membrane gly
18	181.5	9.8	1896	2	T08851	Down syndrome cell
19	174	9.4	858	1	IJRTNC	neural cell adhesi
20	174	9.4	7962	2	I38346	elastic titin - hu
21	173.5	9.4	761	1	IJHUNG	neural cell adhesi
22	172	9.3	588	2	JH0506	adhesion molecule
23	172	9.3	588	2	A45254	surface glycoprote
24	170	9.2	847	2	JH0371	B-cell adhesion pr
25	169.5	9.2	1091	1	IJCHNL	neural cell adhesi
26	168.5	9.1	637	2	B33785	myelin-associated
27	167	9.1	765	2	C42632	cell adhesion mole
28	167	9.1	812	2	B42632	cell adhesion mole
29	167	9.1	932	2	A42632	cell adhesion mole

30	166.5	9.0	582	1	BNRT3S	myelin-associated
31	166.5	9.0	626	1	A61084	myelin-associated
32	166.5	9.0	626	1	BNRT3	myelin-associated
33	165	8.9	725	1	IJMSNG	neural cell adhesi
34	165	8.9	1115	1	IJMSNL	neural cell adhesi
35	164.5	8.9	569	2	A46462	T cell activation
36	164.5	8.9	3707	2	S18252	heparan sulfate pr
37	162.5	8.8	278	1	TDRTOX	OX-2 membrane gly
38	162	8.8	739	2	JN0581	vascular cell adhe
39	160	8.7	587	2	JH0464	DM-GRASP precursor
40	158	8.6	702	2	A36319	carcinoembryonic a
41	156	8.5	458	2	S23969	cell-adhesion mole
42	154.5	8.4	1018	2	A54744	contactin 1 precu
43	153.5	8.3	1018	2	JC4211	neural adhesion pr
44	152	8.2	725	2	JE0099	neural cell adhesi
45	152	8.2	1088	1	IJXLNL	neural cell adhesi

ALIGNMENTS

RESULT 1

T08732

hypothetical protein DKFZp566B0846.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 13-Aug-1999

C;Accession: T08732

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

submitted to the Protein Sequence Database, May 1999

A;Reference number: Z16474

A;Accession: T08732

A;Molecule type: mRNA

A;Residues: 1-407 <OTT>

A;Cross-references: EMBL:AL050071

A;Experimental source: fetal kidney; clone DKFZp566B0846

C;Genetics:

A;Note: DKFZp566B0846.1

Query Match 75.4%; Score 1391; DB 2; Length 407;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	86	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAICIAATGK	145
DB	1	SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSLIDGGNETVAAICIAATGK	60
QY	146	HIDWEGDLGEMESTTSPNETATIIISQYKLFPTFARRRITCVVKKHPALEKDIRYSFI	205
DB	61	HIDWEGDLGEMESTTSPNETATIIISQYKLFPTFARRRITCVVKKHPALEKDIRYSFI	120
QY	206	LDIQYAPEVSVTGYDGNWFWGRKGNLKNADANPPPKSVWSRLDGQWPDGLASDNTL	265
DB	121	LDIQYAPEVSVTGYDGNWFWGRKGNLKNADANPPPKSVWSRLDGQWPDGLASDNTL	180
QY	266	HFVHPLTFNYSGVYICKVNSLQORSDDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT	325
DB	181	HFVHPLTFNYSGVYICKVNSLQORSDDQKVIYISDPPTTTTLQPTIQWHPSTADIEDLAT	240
QY	326	EPKKLPPLSTLATIKDDTIAT	347
DB	241	EPKKLPPLSTLATIKDDTIAT	262

RESULT 2

JC4024

poliovirus receptor-related protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 13-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 05-Nov-1999

C;Accession: JC4024

R;Lopez, M.; Eberle, F.; Mattei, M.G.; Gabert, J.; Birg, F.; Maroc, C.; Dubr

Gene 155, 261-265, 1995

A;Title: Complementary DNA characterization and chromosomal localization of a human gene

A;Reference number: JC4024; MUID:95237621; PMID:7721102

A;Accession: JC4024
A;Molecule type: mRNA
A;Residues: 1-518 <LOP>
A;Cross-references: EMBL:X76400; NID:g732795; PIDN:CAA53980.1; PID:g732796
C;Genetics:
A;Gene: GDB:PVRR1
A;Cross-references: GDB:583951
A;Map position: 11q23-11q24
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: glycoprotein; transmembrane protein
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-518/Product: poliovirus receptor-related protein #status predicted <MAT>
F;356-379/Domain: transmembrane #status predicted <TMM>
F;36,72,82,139,287,308,333/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 28.0%; Score 516; DB 2; Length 518;
Best Local Similarity 35.7%; Pred. No. 5.8e-31;
Matches 110; Conservative 56; Mismatches 114; Indels 28; Gaps 6;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKONVAIYNPSMGVSLAPYRERVEFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVVLVEPTVSLIKGPDSLIDG--- 127
Db 104 FTDGTIRLSRLELEDEGVYICEFATFPTGNRESQLNLTVMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWE-----GDLGMESTTTSPFNETATISQYKL 176
Db 163 QDDKVLVATCTSANGKPPSVVSWETRLKGEARVPGDSGT-----PMAPVTVISRYRL 214
QY 177 FPTREARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNA 236
Db 215 VPSREAHQQSACIVNYHM--DRPKESLTINVQYEPEVTIEGFDGNWYQLQRMVDVKLTCKA 272
QY 237 DANPPFPKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNSLGORSQDKVI 296
Db 273 DANPATEYHWTTLNGSLPKGVEAQNRLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332
QY 297 YISDPPTT 304
Db 333 NITEFPYT 340

RESULT 3
A53437
poliovirus receptor mPVR - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Oct-1994 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A53437
R;Aoki, J.; Koike, S.; Ise, I.; Sato-Yoshida, Y.; Nomoto, A.
J. Biol. Chem. 269, 8431-8438, 1994
A;Title: Amino acid residues on human poliovirus receptor involved in interaction with P
A;Reference number: A53437; MUID:94179228; PMID:8132569
A;Accession: A53437
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-530 <AOK>
A;Cross-references: GB:D26107; NID:g475017; PIDN:BAA05103.1; PID:g825507
A;Experimental source: C57/BL6, brain
A;Note: sequence extracted from NCBI backbone (NCBIN:146664, NCBIP:146667)
C;Superfamily: poliovirus receptor; immunoglobulin homology
F;47-133/Domain: immunoglobulin homology <IMM>

Query Match 22.8%; Score 420; DB 2; Length 530;
Best Local Similarity 31.8%; Pred. No. 9.1e-24;
Matches 101; Conservative 50; Mismatches 137; Indels 30; Gaps 9;

QY 5 VEPHVTAVWGKNVSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY-- 60
Db 38 VLPEVRGRLGTVLPCVLPVGRADGVKVTCTVEHESFEELPVTLSVRYPPVEVSISSYDDNWYLG 94
QY 61 QGRVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP- 113
Db 95 KDRLSFVRARPETNADLRDATLAFRGLRVEDEGNYTCEFATFNGTRRGVTWLRVIAQPE 154
QY 114 ----TVSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGLGEMESTTTSPFN---E 166
Db 155 NHAEAEVTVIGPQSV-----AVARCVSTGGRPPARITWISSLG-EAKDTQEPGIQAG 206
QY 167 TATIISQYKLPPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWG 226
Db 207 TVTIISRYSLVPVGRADGVKVTCTVEHESFEELPVTLSVRYPPVEVSISSYDDNWYLG 266
QY 227 RKGVNLKCNADANPPFPKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNS 286
Db 267 RSEAILTCDVRSNPEPTDYDWSVTSSTGVPFASAVAQGSQQL-LVHSVDRMVNTTICTATNA 325
QY 287 LGORSQDKVIYISDPPTT 304

Db 95 KDRLSFVRARPETNADLRDATLAFRGLRVEDEGNYTCEFATFNGTRRGVTWLRVIAQPE 154
QY 114 ----TVSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGLGEMESTTTSPFN---E 166
Db 155 NHAEAEVTVIGPQSV-----AVARCVSTGGRPPARITWISSLG-EAKDTQEPGIQAG 206
QY 167 TATIISQYKLPPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWG 226
Db 207 TVTIISRYSLVPVGRADGVKVTCTVEHESFEELPVTLSVRYPPVEVSISSYDDNWYLG 266
QY 227 RKGVNLKCNADANPPFPKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNS 286
Db 267 RSEAILTCDVRSNPEPTDYDWSVTSSTGVPFASAVAQGSQQL-LVHSVDRMVNTTICTATNA 325
QY 287 LGORSQDKVIYISDPPTT 304
Db 326 VGTGRAEQVILVRESPT 343

RESULT 4
HLMSP3
poliovirus receptor homolog precursor - mouse
C;Species: Mus musculus domesticus (western European house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
C;Accession: A38211
R;Morrison, M.E.; Racaniello, V.R.
J. Virol. 66, 2807-2813, 1992
A;Title: Molecular cloning and expression of a murine homolog of the human poliovirus r
A;Reference number: A38211; MUID:92219365; PMID:1560525
A;Accession: A38211
A;Molecule type: DNA
A;Residues: 1-467 <MOR>
A;Cross-references: GB:M80206; NID:g199785; PIDN:AAA39734.1; PID:g199786
C;Superfamily: poliovirus receptor; immunoglobulin homology
C;Keywords: duplication; glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-467/Product: poliovirus receptor homolog #status predicted <MAT>
F;26-354/Domain: extracellular #status predicted <EXT>
F;47-133/Domain: immunoglobulin homology <IMM1>
F;167-231/Domain: immunoglobulin homology <IMM2>
F;267-322/Domain: immunoglobulin homology <IMM3>
F;355-374/Domain: transmembrane #status predicted <TMN>
F;375-467/Domain: intracellular #status predicted <INT>
F;54-131,174-229,274-320/Disulfide bonds: #status predicted
F;128,138,315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.7%; Score 419; DB 1; Length 467;
Best Local Similarity 31.2%; Pred. No. 9.2e-24;
Matches 102; Conservative 50; Mismatches 145; Indels 30; Gaps 9;

QY 5 VEPHVTAVWGKNVSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY-- 60
Db 38 VLPEVRGRLGTVLPCVLPVGRADGVKVTCTVEHESFEELPVTLSVRYPPVEVSISSYDDNWYLG 94
QY 61 QGRVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP- 113
Db 95 KDRLSFVRARPETNADLRDATLAFRGLRVEDEGNYTCEFATFNGTRRGVTWLRVIAQPE 154
QY 114 ----TVSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGLGEMESTTTSPFN---E 166
Db 155 NHAEAEVTVIGPQSV-----AVARCVSTGGRPPARITWISSLG-EAKDTQEPGIQAG 206
QY 167 TATIISQYKLPPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWG 226
Db 207 TVTIISRYSLVPVGRADGVKVTCTVEHESFEELPVTLSVRYPPVEVSISSYDDNWYLG 266
QY 227 RKGVNLKCNADANPPFPKSVWSRLDGQWPDGLASDNTLHFVHPLTFNYSGVYICKVTNS 286
Db 267 RSEAILTCDVRSNPEPTDYDWSVTSSTGVPFASAVAQGSQQL-LVHSVDRMVNTTICTATNA 325
QY 287 LGORSQDKVIYISDPPTT 304

Db 326 VGTGRABQVILLVRDTPQASRDVGPLVW 352

RESULT 5

I68093

PRR2 delta - human

C:Species: Homo sapiens (man)

C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000

C:Accession: I68093

R:Eberle, F.; Dubreuil, P.; Mattei, M.G.; Devilard, E.; Lopez, M.

Gene 159, 267-272, 1995

A:Title: The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is th

A:Reference number: I53960; MUID:95347610; PMID:7622062

A:Accession: I68093

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-538 <RES>

A:Cross-references: GB:S79172; NID:g1042204; PID:g1042205

C:Genetics:

A:Gene: PRR2delta

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:276-331/Domain: immunoglobulin homology <IMM>

Query Match 21.8%; Score 401.5; DB 2; Length 538;

Best Local Similarity 29.2%; Pred. No. 2.2e-22;

Matches 96; Conservative 57; Mismatches 133; Indels 43; Gaps 9;

QY 5 VEPHTAVWGKNSVLSKCLIEV---EVNETITQISWEKIHGKSS-QTVAVHHPPQYGFSGVQGEY 60

Db 38 VLPEVRGQLGGTVLPCVGLYISLVWQRPDAPANHQNVAAFHPKMGPSFFSPK 97

QY 61 QG--RVLF-----KNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108

Db 98 PGSESLSFSAKQSTGQDTEAELQDATALHGLTVEDEGNYTCEFAFPKGSVRGMTWLR 157

QY 109 VLVEP-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVVHI-----DWEGDLGE 155

Db 158 VIAKPKNQAEAKVTFPSQDP-----TTVALCISKEGRPPARISLWSSLDWEAKETQ 208

QY 156 MESTTTSFPNETATISQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVS 215

Db 209 VSGTLG----TIVTSTRFTLVPSGRADGVTVTCCKVEHESFEFEPALIPVTLVSRYPPEVS 264

QY 216 VTGYDGNWFVGRKGVNLKCNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNY 275

Db 265 ISGYDDNWYLGRDATALSCDVRNPEPTGYDWTSTSGTFTSAVAQGSQQL-VIHAVDSL 323

QY 276 SGVYICKVTNSLQSRSDQKVIYISDPPPT 304

Db 324 NTTFTVCTVITNAVGMGRABEQVIFVRETPNT 352

RESULT 6

B44194

poliovirus receptor (clone AGM-delta-1) - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: B44194

R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A:Title: A second gene for the African green monkey poliovirus receptor that has no puta

A:Reference number: A44194; MUID:93059651; PMID:1331508

A:Accession: B44194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-392 <KOI>

A:Cross-references: GB:S48817

C:Superfamily: poliovirus receptor; immunoglobulin homology

F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 21.5%; Score 396.5; DB 2; Length 392;

Best Local Similarity 31.4%; Pred. No. 3.5e-22;

Matches 99; Conservative 55; Mismatches 140; Indels 21; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNSVLSKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51

Db 27 GDIIVQAPTQVPGFLGDSVTLPCLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGN 85

QY 52 YGFSVQGEYQGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 111

Db 36 YSEPKRLEFVAARL--GTELRDASLRMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143

QY 112 EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVVHIWEGDLGEMESTTTS--FPNET 167

Db 144 KPQNTAEVQKVQLT----GKPVVVARCVSTGGRPPAHITWHSDLGGMPTNSQAPGFLSGT 199

QY 158 ATIIISQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227

Db 200 VTTSLWILVPSSQVDGKSVTCCKVEHESFEKPKQLLTVNLTVIYYPPEVSIISGYDNNWYLSQ 259

QY 228 KGVNLKCNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287

Db 260 NEATLTCDARSNPEPTGYNNWSTTMGPLPPFAVAQAQL-LIRPVDKPINTTFCICNTNAL 318

QY 288 GQRSDQKVIYISDPP 302

Db 319 GARQALTVQVKEGP 333

RESULT 7

A44194

poliovirus receptor (clone AGM-alpha-1) - green monkey

C:Species: Cercopithecus aethiops (green monkey, grivet)

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000

C:Accession: A44194

R:Koike, S.; Ise, I.; Sato, Y.; Yonekawa, H.; Gotoh, O.; Nomoto, A.

J. Virol. 66, 7059-7066, 1992

A:Title: A second gene for the African green monkey poliovirus receptor that has no puta

A:Reference number: A44194; MUID:93059651; PMID:1331508

A:Accession: A44194

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-417 <KOI>

A:Cross-references: GB:S48777

C:Superfamily: poliovirus receptor; immunoglobulin homology

C:Keywords: transmembrane protein

F:259-314/Domain: immunoglobulin homology <IMM>

Query Match 21.5%; Score 396.5; DB 2; Length 417;

Best Local Similarity 31.4%; Pred. No. 3.8e-22;

Matches 99; Conservative 55; Mismatches 140; Indels 21; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNSVLSKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51

Db 27 GDIIVQAPTQVPGFLGDSVTLPCLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGN 85

QY 52 YGFSVQGEYQGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLV 111

Db 86 YSEPKRLEFVAARL--GTELRDASLRMFGLRVEDEGNYTCLFVTFPQGSRSVDIWLRLVA 143

QY 112 EP--TVSLIKGPDSLIDGGNETVAAICIAATGKPVVHIWEGDLGEMESTTTS--FPNET 167

Db 144 KPQNTAEVQKVQLT----GKPVVVARCVSTGGRPPAHITWHSDLGGMPTNSQAPGFLSGT 199

QY 168 ATIIISQYKLFPTRFARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR 227

Db 200 VTTSLWILVPSSQVDGKSVTCCKVEHESFEKPKQLLTVNLTVIYYPPEVSIISGYDNNWYLSQ 259

QY 228 KGVNLKCNADANPPFPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287

Db 260 NEATLTCDARSNPEPTGYNNWSTTMGPLPPFAVAQAQL-LIRPVDKPINTTFCICNTNAL 318

QY 288 GQRSDQKVIYISDPP 302

Db 319 GARQALTVQVKEGP 333

Db 194 TAKSVLRLLTPKKEHHNTNFSCQAQNTA-DRTYRSAKIRVEVKYAPKVKVNMVMSLPGGAG 252
QY 221 GNVFVGRKG-----VNLKCNADANPPFPKSVWSRLDQWPDGLLASDN 263
Db 253 GS--VGGAGGGSVHMSTGSRIVEHSQVRLCERADANPSDVRVRFIND-----EPIIGGQK 306
QY 264 TLHFVHPLTFENYGVYI-CKVTNSLQSRDQKVIYISDPT----- 303
Db 307 TEMVIRNVTWKFDIAIVKCEVQNSVGKSEDSSETLDSIYAPSRQRPOSMEADVGSVSLT 366
QY 304 ---TTTLQPTIQW--HPS 316
Db 367 CEVDNPNQPEIWIQHPS 384

RESULT 13

T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C;Accession: T20992; T24733
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20992
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WIL>
A;Cross-references: EMBL:Z47068; PIDN:CAA87335.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone F15G9
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24733
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5175 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87344.1; GSPDB:GN00028; CESP:F15G9.4a
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: CESP:F15G9.4a
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077/1

Query Match 10.9%; Score 200.5; DB 2; Length 5175;
Best Local Similarity 25.9%; Pred. No. 4.3e-06;
Matches 96; Conservative 48; Mismatches 153; Indels 73; Gaps 21;
QY 2 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOQYGSVQGE 59
Db 793 PTIIESPHTVRVNIERQVTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG- 847
QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSL 117
Db 848 -----NULLITDAQI-----EDQGQFTCIARN-TYGOQSQSTTLMVTGLVSPVLGH 891
QY 118 IKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLF 177
Db 892 VPPEQLIEGQDLTSL--CVVVLGTPKPSIVWIKDKPVEE-----GPTIKIEGGGSL 943
QY 178 PTRFARGR---RITCVVKHPALEKDIRYSFIL---DIQYAPE-----VSVTGYDGNW- 223
Db 944 RLRGNPKDEGKYTCIAVSPAGNSTLHINVLKPKPEFVYKPEGGIVFKPTISGMDEKHV 1003
QY 224 -----FVGRKGVNLKCNADANPPFPKSVWSRLDQWP-----DGLLASDNTLHFVH 269
Db 1004 AVNSTHDVLDGEGFAIPCVCVSGTTPPI-ITW-YLDGR-PITPNSRDFVTADNTL-IVR 1059
QY 270 PLTFNYSGVYICKVTNSLQSRDQKVIYISDPPTTTTLOPTIQWHPSTADIEDLATEPKK 329
Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTPMISPGQSSF-----NMVVDDLFTIPCD 1114

QY 330 L---PFPLST 336
Db 1115 VYGDPKPVIT 1124
RESULT 14
T43290
hemacentin precursor - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 18-Feb-2000
C;Accession: T43290; T20993; T24734
R;Vogel, B.E.; Hedgecock, E.M.
submitted to the EMBL Data Library, June 1998
A;Description: Hemacentin is required for hemidesmosome mediated cell adhesion and germ
A;Reference number: Z22396
A;Accession: T43290
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
A;Cross-references: EMBL:AF074901; PIDN:AAAC26792.1
R;Sulston, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19355
A;Accession: T20993
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-5198 <WIL>
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A;Experimental source: clone F15G9
R;Kershaw, J.
submitted to the EMBL Data Library, December 1994
A;Reference number: Z19929
A;Accession: T24734
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A;Molecule type: DNA
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A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone T09B9
C;Genetics:
A;Gene: him-4; F15G9.4b
A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/1
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 5100/1

Query Match 10.9%; Score 200.5; DB 2; Length 5198;
Best Local Similarity 25.9%; Pred. No. 4.4e-06;
Matches 96; Conservative 48; Mismatches 153; Indels 73; Gaps 21;
QY 2 PIIVE-PHVTAV-WGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOQYGSVQGE 59
Db 793 PTIIESPHTVRVNIERQVTLQCL-AVGIPPEIEWQK---GNVLLATLNNPRYTQLADG- 847
QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTT--VTVLVEPTVSL 117
Db 848 -----NULLITDAQI-----EDQGQFTCIARN-TYGOQSQSTTLMVTGLVSPVLGH 891
QY 118 IKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLF 177
Db 892 VPPEQLIEGQDLTSL--CVVVLGTPKPSIVWIKDKPVEE-----GPTIKIEGGGSL 943
QY 178 PTRFARGR---RITCVVKHPALEKDIRYSFIL---DIQYAPE-----VSVTGYDGNW- 223
Db 944 RLRGNPKDEGKYTCIAVSPAGNSTLHINVLKPKPEFVYKPEGGIVFKPTISGMDEKHV 1003
QY 224 -----FVGRKGVNLKCNADANPPFPKSVWSRLDQWP-----DGLLASDNTLHFVH 269
Db 1004 AVNSTHDVLDGEGFAIPCVCVSGTTPPI-ITW-YLDGR-PITPNSRDFVTADNTL-IVR 1059
QY 270 PLTFNYSGVYICKVTNSLQSRDQKVIYISDPPTTTTLOPTIQWHPSTADIEDLATEPKK 329
Db 1060 KADKSYSGVYTCQATNSAGDNEQKTTIRIMNTPMISPGQSSF-----NMVVDDLFTIPCD 1114

QY 330 L---PFPLST 336
Db 1115 VYGDPKPVIT 1124

RESULT 15

A38096

perlecan precursor - human
N;Alternate names: basement membrane heparan sulfate proteoglycan; heparan sulfate prote

C;Species: Homo sapiens (man)
C;Date: 07-Apr-1994 #sequence revision 07-Apr-1994 #text change 05-Nov-1999
C;Accession: A38096; S19256; S77946; A41059; A40306; B33625; A33625; A41736
R;Murdoch, A.D.; Dodge, G.R.; Cohen, I.; Tuan, R.S.; Iozzo, R.V.

J. Biol. Chem. 267, 8544-8557, 1992
A;Title: Primary structure of the human heparan sulfate proteoglycan from basement membr

tor, laminin, neural cell adhesion molecules, and epidermal growth factor.

A;Reference number: A38096; MUID:92235084; PMID:1569102

A;Accession: A38096

A;Molecule type: mRNA

A;Residues: 1-4391 <MUR>

A;Cross-references: GB:M85289; NID:g184426; PIDN:AAA52700.1; PID:g184427

R;Kallunki, P.; Tryggvason, K.

J. Cell Biol. 116, 559-571, 1992

A;Title: Human basement membrane heparan sulfate proteoglycan core protein: a 467-kD pro

cell adhesion molecules, and epidermal growth factor.

A;Reference number: A41736; MUID:92112994; PMID:1730768

A;Accession: S19256

A;Molecule type: mRNA

A;Residues: 1-57, 'D', '59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R',

71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-3

A;Cross-references: EMBL:X62515

R;Tryggvason, K.

submitted to the EMBL Data Library, October 1991

A;Reference number: S77946

A;Accession: S77946

A;Molecule type: mRNA

A;Residues: 1-57, 'D', '59-434, 'A', 436, 'FL', 438-449, 'Q', 451-502, 'A', 503-792, 'K', 794-908, 'R',

71-2979, 'H', 2981-2994, 'G', 2996-3167, 'T', 3169-3240, 'R', 3242-3426, 'R', 3428-3631, 'Q', 3633-4

A;Cross-references: EMBL:X62515; NID:g29469; PIDN:CAA44373.1; PID:g29470

R;Kallunki, P.; Eddy, R.L.; Byers, M.G.; Kestilae, M.; Shows, T.B.; Tryggvason, K.

Genomics 11, 389-396, 1991

A;Title: Cloning of human heparan sulfate proteoglycan core protein, assignment of the g

A;Reference number: A41059; MUID:92120650; PMID:1685141

A;Accession: A41059

A;Molecule type: mRNA

A;Residues: 'RT', 892-908, 'R', 910-1101, 'L', 1103-1132, 'L', 1134-1221, 'L', 1223-1397 <KA2>

A;Cross-references: GB:S76436; NID:g243370; PIDN:AAB21121.1; PID:g243371

R;Dodge, G.R.; Kovalszky, I.; Chu, M.L.; Hassell, J.R.; McBride, O.W.; Yi, H.F.; Iozzo,

Genomics 10, 673-680, 1991

A;Title: Heparan sulfate proteoglycan of human colon: partial molecular cloning, cellula

A;Reference number: A40306; MUID:91365376; PMID:1679749

A;Accession: A40306

A;Molecule type: mRNA

A;Residues: 1018-1405, 'G', 1407-1409, 'G', 1411-1465 <DOD>

A;Cross-references: GB:M64283; NID:g184424; PIDN:AAA52699.1; PID:g184425

R;Heremans, A.; van der Schueren, B.; De Cock, B.; Paulsson, M.; Cassiman, J.J.; van den

J. Cell Biol. 109, 3199-3211, 1989

A;Title: Matrix-associated heparan sulfate proteoglycan: core protein-specific monoclonal

anes.

A;Reference number: A33625; MUID:90078352; PMID:2687294

A;Accession: B33625

A;Molecule type: protein

A;Residues: 1379-1384, 'X', 1386-1388, 'X', 1390-1398 <HE2>

A;Accession: A33625

A;Molecule type: protein

A;Residues: 2166-2171, 'X', 2173-2175, 'X', 2177-2185 <HE3>

A;Note: peptide potentially matches four different regions of sequence shown

C;Genetics:

A;Gene: GDB:HSPG2

A;Cross-references: GDB:126372; OMIM:142461

A;Map position: lp36.1-lp36.1

C;Superfamily: LDL receptor ligand-binding repeat homology; EGF homology; laminin G repe

C;Keywords: chondroitin sulfate proteoglycan; glycoprotein; heparan sulfate; transmembr
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-4391/Product: perlecan #status predicted <MAT>
F;22-193/Domain: I <DOM1>
F;194-530/Domain: II <DOM2>
F;199-234/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;285-319/Domain: LDL receptor ligand-binding repeat homology <LDL2>
F;325-359/Domain: LDL receptor ligand-binding repeat homology <LDL3>
F;368-403/Domain: LDL receptor ligand-binding repeat homology <LDL4>
F;531-1676/Domain: III <DOM3>
F;1159-1206/Domain: laminin-type EGF-like homology <LEG>
F;1563-1610/Domain: laminin-type EGF-like homology <EG7>
F;1613-1668/Domain: laminin-type EGF-like homology <LEG8>
F;1677-3686/Domain: IV <DOM4>
F;2007-2034/Domain: transmembrane #status predicted <TRM>
F;3687-4391/Domain: V <DOM5>
F;3845-3880/Domain: EGF homology <EGF1>
F;3888-3921/Domain: EGF homology <EGF>
F;3953-4106/Domain: laminin G repeat homology <LG2>
F;4147-4175/Domain: EGF homology <EGF2>
F;4149-4151/Region: motor neuron attachment (L-R-E) motif
F;4299-4301/Region: motor neuron attachment (L-R-E) motif
F;65,71,76/Binding site: heparan sulfate (Ser) (covalent) #status predicted
F;89,554,1755,2121,3072,3105,3279,3780,3836,4068/Binding site: carbohydrate (Asn) (cova
F;2995,3933,4179/Binding site: chondroitin sulfate (Ser) (covalent) #status predicted

Query Match 10.7%; Score 198; DB 2; Length 4391;
Best Local Similarity 22.8%; Pred. No. 5.4e-06;
Matches 89; Conservative 55; Mismatches 147; Indels 100; Gaps 18;

QY 2 PIIVE---PHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVQG 58

Db 2926 PIYIEASSSHVTE--GQTLDLNCVVP-GQAHAQVTWYKRGG-----SLPARHQTHG----- 2973

QY 59 EYQGRVLFKNYSLNDATITLHNTGFSDSGKYICKAVTFPLGNAQSSTTVTV----- 109

Db 2974 -----SQLRLHLVSPADSGEYVCRAASGPGPEQASFTVTPPSEGSSYR 3018

QY 110 LVEPTVSLIKGPDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETAT 169

Db 3019 LRSPVIS-IDPPSSTVQQGD-ASFKCLIHDAAPISLEWKNRQLELDNVHISPN--GS 3074

QY 170 IISQYKLFPTTRFARGRRITCVVKHPALEKDIRYSFI-LDIOYAPEVSVTGYDGNWVGRK 228

Db 3075 IIT---IVGTRPSNHGTYRCVASN---AYGVAQSVVNLNVHGPTVSVLPEGPVVVKVGK 3128

QY 229 GYNLKNADANPPFKSVMSRLDG-----QWPDGLLASDNLHVFHPLTFNYSGVYICK 282

Db 3129 AVTLEC-VSAGEPRSSARWTRISSTPAKLEQRTYGLMDSHAVLQ-ISSAKPSDAGTYVCL 3186

QY 283 VTNSLGQRSDQKVIYIS-----DPPPTTTLQ-----PTIQWH 314

Db 3187 AQNALGTAQKQVEVIVDTGAMAPGAPOVQAEAEELTVEAGHTATLRCSATGSPAPTIHW- 3245

QY 315 PSTADIEDLATEPKKLPFPLSTLTIKDDTI 345

Db 3246 -----SKLRSPLQWHRLEGDTL 3263

Search completed: April 12, 2004, 09:47:02
Job time : 10.1818 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 12, 2004, 09:26:00 ; Search time 5.54545 Seconds
(without alignments)
3258.226 Million cell updates/sec

Title: US-09-972-268-4_COPY_58_404
Perfect score: 1844
Sequence: 1 GPIIIEPHVTAVWGKNSLK.....KKLPFLSLTIKDDTIAT 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	550.5	29.9	515	1 PVR1_MOUSE	Q9jfk6 mus musculus
2	538.5	29.2	517	1 PVR1_HUMAN	Q15223 homo sapien
3	534.5	29.0	515	1 PVR1_PIG	Q9gl76 sus scrofa
4	420	22.8	530	1 PVR2_MOUSE	P32507 mus musculus
5	401.5	21.8	538	1 PVR2_HUMAN	Q92692 homo sapien
6	396.5	21.5	417	1 PVR_CERAE	P32506 cercopithec
7	383.5	20.8	417	1 PVR_HUMAN	P15151 homo sapien
8	227.5	12.3	764	1 ICCR_DROME	Q08180 drosophila
9	211.5	11.5	837	1 NCM2_MOUSE	O35136 mus musculus
10	198	10.7	4391	1 PGBM_HUMAN	P98160 homo sapien
11	189	10.2	853	1 NCA1_BOVIN	P31836 bos taurus
12	187.5	10.2	278	1 OX2G_HUMAN	P41217 homo sapien
13	181.5	9.8	2012	1 DSCA_HUMAN	O60469 homo sapien
14	176	9.5	837	1 NCM2_HUMAN	O15394 homo sapien
15	174	9.4	858	1 NCA1_RAT	P13596 rattus norv
16	173.5	9.4	353	1 CEPU_CHICK	Q90773 gallus gall
17	173.5	9.4	761	1 NCA2_HUMAN	P13592 homo sapien
18	173.5	9.4	848	1 NCA1_HUMAN	P13591 homo sapien
19	172	9.3	588	1 C166_CHICK	P42292 gallus gall
20	170	9.2	847	1 CD22_HUMAN	P20273 homo sapien
21	169.5	9.2	1091	1 NCA1_CHICK	P13590 gallus gall
22	168.5	9.1	626	1 MAG_MOUSE	P20917 mus musculus
23	166.5	9.0	626	1 MAG_HUMAN	P20916 homo sapien
24	166.5	9.0	626	1 MAG_RAT	P07722 rattus norv
25	165	8.9	725	1 NCA2_MOUSE	P13594 mus musculus
26	165	8.9	1115	1 NCA1_MOUSE	P13595 mus musculus
27	164.5	8.9	569	1 TACT_HUMAN	P40200 homo sapien
28	164.5	8.9	3707	1 PGBM_MOUSE	Q05793 mus musculus
29	162.5	8.8	278	1 OX2G_MOUSE	O54901 mus musculus
30	162.5	8.8	278	1 OX2G_RAT	P04218 rattus norv
31	162	8.8	739	1 VCA1_MOUSE	P29533 mus musculus
32	159.5	8.6	509	1 SHS1_RAT	P97710 r protein-t
33	158	8.6	702	1 CEAS_HUMAN	P06731 homo sapien

34	156	8.5	519	1 ECTO_RAT	P16573 rattus norv
35	154.5	8.4	1018	1 CONT_HUMAN	Q12860 homo sapien
36	152.5	8.3	1709	1 SN_HUMAN	Q9bzz2 homo sapien
37	152	8.2	337	1 OPCM_CHICK	Q98892 gallus gall
38	152	8.2	1088	1 NCA1_XENLA	P16170 xenopus lae
39	150.5	8.2	1694	1 SN_MOUSE	Q62230 mus musculus
40	149.5	8.1	1092	1 NCA2_XENLA	P36335 xenopus lae
41	148	8.0	344	1 NTRI_MOUSE	Q99pj0 mus musculus
42	148	8.0	344	1 NTRI_RAT	Q62718 rattus norv
43	147	8.0	344	1 NTRI_HUMAN	Q9p121 homo sapien
44	146.5	7.9	345	1 OPCM_BOVIN	P11834 bos taurus
45	146	7.9	1234	1 NPHN_RAT	Q9r044 rattus norv

ALIGNMENTS

RESULT 1
PVR1_MOUSE STANDARD; PRT: 515 AA.
AC Q9JKF6; Q9ERL5; Q9J117;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 1 precursor (Herpes virus entry mediator C) (Hvec) (Nectin 1).
GN PVR1 OR PRR1 OR HVEC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20243787; PubMed=10781093;
RA Menotti L., Lopez M., Avitabile E., Stefan A., Cocchi F., Adelaide J., Lecocq E., Dubreuil P., Campadelli-Piume G.;
RT "The murine homolog of human nectin1 delta serves as a species nonspecific mediator for entry of human and animal alpha herpesviruses in a pathway independent of detectable binding to gD.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:4867-4872(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20541977; PubMed=11090177;
RA Shukla D., Dal Canto M.C., Rowe C.L., Spear P.G.;
RT "Striking similarity of murine nectin-lalpha to human nectin-lalpha (Hvec) in sequence and activity as a glycoprotein D receptor for alphaherpesvirus entry.";
RL J. Virol. 74:11773-11781(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster;
RA Zhan J., Wimmer E.;
RT "Mouse nectin-1 (mPRR1), a herpesvirus receptor, is expressed in the floor plate during embryogenesis, suggesting a role in neural development.";
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PROBABLY INVOLVED IN CELL ADHESION. RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC -!- SUBUNIT: Interacts with HSV glycoprotein D (gD).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF239762; AAF60333.1; -.


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FT DOMAIN 377 515 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 141 IG-LIKE V-TYPE.
FT DOMAIN 145 243 IG-LIKE C2-TYPE 1.
FT DOMAIN 247 334 IG-LIKE C2-TYPE 2.
FT DOMAIN 437 443 POLY-GLY.
FT DOMAIN 444 447 POLY-GLY.
FT DISULFID 51 124 BY SIMILARITY.
FT DISULFID 172 226 BY SIMILARITY.
FT DISULFID 269 316 BY SIMILARITY.
FT CARBOHYD 36 36 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 297 297 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 332 332 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 515 AA; 57047 MW; BFAB00320DDE3785 CRC64;

Query Match 29.0%; Score 534.5; DB 1; Length 515;
Best Local Similarity 37.8%; Pred. No. 6.8e-35;
Matches 113; Conservative 54; Mismatches 121; Indels 11; Gaps 5;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHHPQYGFSPVQGEYQGRVLFKNYS 70
Db 44 GTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPAMGVSVLAPYRVERFLRPS 103

QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG--- 127
Db 104 FTDGTTIRLSRLEDEGVYICEFATFPAGNRESQNLITVMKFT-NWIEGTQAVLRAKKG 162

QY 128 -GNETVAALCIAATGKPVAHIDWEGDL-GEMESTTTSFPNETATILISQYKLFPTRFARGR 185
Db 163 KODKVLVATCTTSANGKPPSVSVSWETHLKGEAEYQEIIRNPNGIVTVISRYRLVPSREDHRQ 222

QY 186 RITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGVGRKGVNLCNADANPPPFKS 245
Db 223 SLACIVNVHM--DRFRESLTNLVQYEPEVTIEGFDGNWYLQRMVVKLTCKADANPPATEY 280

QY 246 VMSRLDQWPDGILLASDNTLHFVHPLTFENYSGVYICKVTNSLQGRSDQKVIYISDPPTT 304
Db 281 HWTTLNGSLPKGVBAQNRTLFFRGPIYNSAGTYICEATNPIGTRSGQVEWNITEFPYT 339
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RESULT 4
PVR2_MOUSE
ID PVR2_MOUSE STANDARD; PRT; 530 AA.
AC P32507; Q62096;
DT 01-OCT-1993 (Rel. 27, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Poliovirus receptor related protein 2 precursor (Murine herpesvirus
DE entry protein B) (mHvEB) (Nectin 2) (Poliovirus receptor homolog).
DE PVR2 OR PVS OR PVR OR MPH.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM ALPHA).
RX MEDLINE=92219365; PubMed=1560525;
RA Morrison M.E., Racaniello V.R.;
RT "Molecular cloning and expression of a murine homolog of the human
RT poliovirus receptor gene."
RL J. Virol. 66:2807-2813(1992).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=94179228; PubMed=8132569;
RA Aoki J., Koike S., Ise I., Sato-Yoshida Y., Nomoto A.;
RT "Amino acid residues on human poliovirus receptor involved in
RT interaction with poliovirus."
RL J. Biol. Chem. 269:8431-8438(1994).
```

```
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM BETA).
RC STRAIN=FVB/N; TISSUE=Colon;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=99214397; PubMed=10196354;
RA Shukla D., Rowe C.L., Dong Y., Racaniello V.R., Spear P.G.;
RT "The murine homolog (Mph) of human herpesvirus entry protein B (HvEB)
RT mediates entry of pseudorabies virus but not herpes simplex virus
RT types 1 and 2."
RL J. Virol. 73:4493-4497(1999).
CC -!- FUNCTION: RECEPTOR FOR ALPHAPERPEVIRUS (SUCH AS MURINE HSV) ENTRY
CC INTO CELLS.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Beta;
CC IsoId=P32507-1; Sequence=Displayed;
CC Name=Alpha;
CC IsoId=P32507-2; Sequence=VSP_002630, VSP_002631;
CC -!- TISSUE SPECIFICITY: Brain, spinal cord, spleen, kidney, heart and
CC liver.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -----
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CC use by non-profit institutions as long as its content is in no way
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CC -----
CC EMBL; M80206; AAA39734.1; -.
CC EMBL; D26107; BAA05103.1; -.
CC EMBL; BC059941; AAH59941.1; -.
CC PIR; A38211; HLMSP3.
CC PIR; A53437; A53437.
CC MGD; MGI:97822; Pvr12.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG LIKE; 3.
CC Immunoglobulin domain; Receptor; Transmembrane; Glycoprotein; Signal;
KW Repeat; Alternative splicing.
KW SIGNAL 1 31 POTENTIAL.
FT CHAIN 32 530 POLIOVIRUS RECEPTOR RELATED PROTEIN 2.
FT DOMAIN 32 351 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 352 372 POTENTIAL.
FT DOMAIN 373 530 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 32 147 IG-LIKE V-TYPE.
```


FT	DOMAIN	153	247	IG-LIKE C2-TYPE 1.
FT	DOMAIN	252	337	IG-LIKE C2-TYPE 2.
FT	DISULFID	54	131	BY SIMILARITY.
FT	DISULFID	174	229	BY SIMILARITY.
FT	DISULFID	274	320	BY SIMILARITY.
FT	CARBOHYD	128	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	315	315	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	VARSPLIC	339	467	ESPSTAGAGATGGIIGGIAAIIATAVAGTGILICRQORKE
FT				ORLQAADDEEELEGGPSYKPPTPPKAKLEEPEMPSQLFTLGA
FT				SEHSPVKTPYFDAGVSCADQEMPRYHELPTLEERSGPLLGG
FT				ATGLGP -> DTPQASRDVGPLVWGAAGTLLVLLLAGGFL
FT				ALILLRGRRRRKSPGGGNDGRGSDYDPKTOVFGNGGPFVFW
FT				RSASPEPMRPDGRDEEEEMKAEGLMLPPHESPKDDM
FT				ESHLDGSLISRRAYV (in isoform Alpha).
FT				/FTid=VSP 002630.
FT	VARSPLIC	468	530	Missing (in isoform Alpha).
FT				/FTid=VSP 002631.
FT	SEQUENCE	530 AA;	57317 MW;	0ED71BF2B231BBE CRC64;
SQ				
Query Match 22.8%; Score 420; DB 1; Length 530;				
Best Local Similarity 31.8%; Pred. No. 8.4e-26;				
Matches 101; Conservative 50; Mismatches 137; Indels 30; Gaps 9;				
QY	5	VEPHVTAVWGNVSLKC--LIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY--	60	
Db	38	VLPEVGRGLGTVELPCHLLPPTERVSVQVWQLDQ---TVVAAFHPSFGVDFPNQFS	94	
QY	61	QGRVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTPPLGNAQSSTTIVLVEP-	113	
Db	95	KDRLSFVRARPETNADLRDATLAFRLRVEDEGNYTCEFAFPNGTRRGVTWLRVIAQPE	154	
QY	114	-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPN---	166	
Db	155	NHAAEQEVTIGQSV-----AVARCVSTGGRPPARITWISSLGG-EAKDTQEPGQAG	206	
QY	167	TATISQYKLFPTTRFARGRRITCVVKHPALEKDRIYSFILDIQYAPEVSVTGYDGNWFG	226	
Db	207	TVTIISRYSLVPVGRADGVKTCRVEHESFEEPIILLPVTLSVRYPPPEVSIISGYDDNWYLG	266	
QY	227	RKGVNLKCNADANPPPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNS	286	
Db	267	RSEAILTCVRSNPEPTDYDWTSTSGVFPASAVAQGSOL-LVHSVDRMVNTTICTATNA	325	
QY	287	LGQRSDQKVIYISDPPTT	304	
Db	326	VGTGRAEQVILVRESPT	343	
RESULT 5				
PVR2_HUMAN	STANDARD;	PRT;	538 AA.	
AC	Q92692; O75455; Q96J29;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	10-OCT-2003 (Rel. 42, Last annotation update)			
DE	Poliovirus receptor related protein 2 precursor (Herpes virus entry mediator B) (HvEB) (Nectin 2) (CD112 antigen).			
DE	PVRL2 OR PRR2 OR HVEB.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RN	SEQUENCE FROM N.A. (ISOFORM DELTA).			
RX	MEDLINE=95347610; PubMed=7622062;			
RA	Eberle F., Dubreuil P., Mattei M.-G., Devilard E., Lopez M.;			
RT	"The human PRR2 gene, related to the human poliovirus receptor gene (PVR), is the true homolog of the murine MPH gene.";			
RL	Gene 159:267-272(1995).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).			
RX	MEDLINE=98321161; PubMed=9657005;			

RA	Warner M.S., Geraghty R.J., Martinez W.M., Montgomery R.I.,
RA	Whitbeck J.C., Xu R., Eisenberg R.J., Cohen G.H., Spear P.G.;
RT	"A cell surface protein with herpesvirus entry activity (HvEB) confers
RT	susceptibility to infection by mutants of herpes simplex virus type
RT	1, herpes simplex virus type 2, and pseudorabies virus.";
RL	Virology 246:179-189(1998).
RN	[3]
RP	SEQUENCE FROM N.A. (ISOFORM ALPHA).
RC	TISSUE=Brain;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA	Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length
RT	human and mouse cDNA sequences.";
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN	[4]
RP	SEQUENCE OF 31-538 FROM N.A.
RA	Yoshiura K., Murray J.C.;
RT	"A transcriptional map in the region of 19ql3 derived using direct
RT	sequencing and exon trapping.";
RL	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN	[5]
RP	SEQUENCE OF 449-538 FROM N.A.
RX	MEDLINE=99449047; PubMed=10520737;
RA	Freitas E.M., Zhang W.J., Lalonde J.P., Tay G.K., Gaudieri S.,
RA	Ashworth L.K., Van Bockxmeer F.M., Dawkins R.L.;
RT	"Sequencing of 42kb of the APO E-C2 gene cluster reveals a new gene:
RT	PEREC1.";
RL	DNA Seq. 9:89-101(1998).
CC	-!- FUNCTION: RECEPTOR FOR ALPHAHERPESVIRUS (HSV-1, HSV-2 AND
CC	PSEUDORABIES VIRUS) ENTRY INTO CELLS.
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-!- ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=2;
CC	Name=Delta;
CC	isoId=Q92692-1; Sequence=Displayed;
CC	Name=Alpha;
CC	isoId=Q92692-2; Sequence=VSP_002628, VSP_002629;
CC	-!- TISSUE SPECIFICITY: Ubiquitous.
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC	-!- DATABASE: NAME=PROW; NOTE=PROW 1:74-77(2000);
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/guide/204270028_g.htm".
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; X80038; CAA56342.1; --
DR	EMBL; AF058448; AAC23797.1; --
DR	EMBL; BC003091; AAH03091.1; --
DR	EMBL; AF044968; AAC82348.1; --
DR	EMBL; AF044962; AAC82348.1; JOINED.
DR	EMBL; AF044963; AAC82348.1; JOINED.


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FT CARBOHYD 313 313 N-LINKED (GLCNAC... ) (POTENTIAL).
FT VARSPLIC 386 392 EHASASA -> HHQSCHN (in isoform Delta).
FT /FTid=VSP 002622.
FT VARSPLIC 393 417 Missing (in isoform Delta).
FT /FTid=VSP 002623.
SQ SEQUENCE 417 AA; 45464 MW; DA4AD0FE4D2F6E1F CRC64;

Query Match 21.5%; Score 396.5; DB 1; Length 417;
Best Local Similarity 31.4%; Pred. No. 4.5e-24;
Matches 99; Conservative 55; Mismatches 140; Indels 21; Gaps 10;

QY 1 GPIIVE--PHVTAVWGKNSVSLKCLIEV---NET-ITQISWEKIHGKSSQTVAVHH---PQ 51
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 27 GDIIVQAPTQVPGFLGDSVTLPCYLQVPGMEETHVSQLTWSR-HGESGSMVAFHQTQGP 85
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 52 YGFSVQGEYQGRVLFKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLV 111
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 86 YSEPKRLEFVAARL--GTELRDASLRMFGLRVEDEGNTCLFVTFPQGRSVDIWLRLVA 143
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 112 EP--TVSLIKGPDLSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTS--FPNET 167
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 144 KPQNTAEVQKVQLT---GKPVVAVRCVSTGGRPPAH'TWHSDLGMENTSQAPEFLSGT 199
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 168 ATIIISQYKLFPTFRFARGRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGR 227
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 200 VVTSLMWILVPSQVDGKSVTCCKVEHSEFEKPPQLLTVNLTVYYPPEVSISGYDNNWYLSQ 259
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 228 KGVNLKCNADANPPFKSVNSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 260 NEATLTCDARSNPEPTGYNWSSTMGLPLPPFAVAQAQL-LIRPVDKPIINTTFCNVTNAL 318
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
QY 288 GQRSDQKVIYISDPP 302
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 319 GARQAELTVQVKEGP 333
| | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :

RESULT 7
PVR_HUMAN STANDARD; PRT; 417 AA.
AC P15151; P15152; Q15267; Q15268;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Poliovirus receptor precursor (CD155 antigen).
GN PVR OR PVS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89168426; PubMed=2538245;
RA Mendelsohn C.L., Wimmer E., Racaniello V.R.;
RT "Cellular receptor for poliovirus: molecular cloning, nucleotide
sequence, and expression of a new member of the immunoglobulin
superfamily.";
RL Cell 56:855-865 (1989).
RN [2]
RP REVISIONS.
RA Racaniello V.R.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=91006015; PubMed=2170108;
RA Koike S., Horie H., Ise I., Okitsu A., Yoshida M., Iizuka N.,
RA Takeuchi K., Takegami T., Nomoto A.;
RT "The poliovirus receptor protein is produced both as membrane-bound
and secreted forms.";
RL EMBO J. 9:3217-3224 (1990).
RN [4]
RP SEQUENCE FROM N.A.
RA Kodoyianni V., Severin J., Ge Y., Grable L., Kvistad E., Gordon L.,
RA Shannon M., Brower A., Olsen A.S., Smith L.M.;
```

```
RT "Sequence analysis of a 1Mb region in 19ql3.2 containing a zinc finger
gene cluster.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP DOMAINS.
RX MEDLINE=91239515; PubMed=18511992;
RA Koike S., Ise I., Nomoto A.;
RT "Functional domains of the poliovirus receptor.";
RL Proc. Natl. Acad. Sci. U.S.A. 88:4104-4108 (1991).
RN [6]
RP MUTAGENESIS OF CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=93059689; PubMed=1331527;
RA Zibert A., Wimmer E.;
RT "N glycosylation of the virus binding domain is not essential for
function of the human poliovirus receptor.";
RL J. Virol. 66:7368-7373 (1992).
CC -!- FUNCTION: Not known. Used by poliovirus to bind and enter the
cell.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (isoforms alpha and
delta). Secreted (isoforms beta and gamma).
CC -!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=4;
Name=Alpha;
IsoId=P15151-1; Sequence=Displayed;
Name=Beta;
IsoId=P15151-2; Sequence=VSP_002617;
Name=Gamma;
IsoId=P15151-3; Sequence=VSP_002618, VSP_002619;
Name=Delta;
IsoId=P15151-4; Sequence=VSP_002620, VSP_002621;
CC -!- MISCCELLANEOUS: THE V-TYPE DOMAIN IS NECESSARY AND SUFFICIENT FOR
VIRUS BINDING AND UPTAKE.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC -!- DATABASE: NAME=PROV; NOTE=CD guide CD155 entry;
WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd155.htm".
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EMBL; M24407; AAA36461.1; -
EMBL; M24406; AAA36462.1; -
EMBL; X64116; CAA45478.1; -
EMBL; X64117; CAA45478.1; JOINED.
EMBL; X64118; CAA45478.1; JOINED.
EMBL; X64119; CAA45478.1; JOINED.
EMBL; X64120; CAA45478.1; JOINED.
EMBL; X64121; CAA45478.1; JOINED.
EMBL; X64122; CAA45478.1; JOINED.
EMBL; X64123; CAA45478.1; JOINED.
EMBL; X64116; CAA45479.1; -
EMBL; X64117; CAA45479.1; JOINED.
EMBL; X64118; CAA45479.1; JOINED.
EMBL; X64119; CAA45479.1; JOINED.
EMBL; X64120; CAA45479.1; JOINED.
EMBL; X64121; CAA45479.1; JOINED.
EMBL; X64122; CAA45479.1; JOINED.
EMBL; X64123; CAA45479.1; JOINED.
EMBL; X64116; CAA45480.1; -
EMBL; X64117; CAA45480.1; JOINED.
EMBL; X64118; CAA45480.1; JOINED.
EMBL; X64119; CAA45480.1; JOINED.
EMBL; X64120; CAA45480.1; JOINED.
EMBL; X64122; CAA45480.1; JOINED.
EMBL; X64123; CAA45480.1; JOINED.
EMBL; AC068948; AAF69803.1; -
PIR; A43024; RWHUPD.
PIR; S12048; RWHUPA.
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DR	Genew;	HGNC:9705;	PVR.
DR	MIM;	173850;	-.
DR	GO;	GO:0005737;	C:cytoplasm; TAS.
DR	GO;	GO:0005615;	C:extracellular space; TAS.
DR	GO;	GO:0016021;	C:integral to membrane; TAS.
DR	GO;	GO:0004872;	F:receptor activity; TAS.
DR	GO;	GO:0007125;	P:invasive growth; TAS.
DR	InterPro;	IPR007110;	Ig-like.
DR	InterPro;	IPR003596;	Ig_v.
DR	Pfam;	PF00047;	ig; 3.
DR	SMART;	SM00406;	IGv; 1.
DR	PROSITE;	PS50835;	IG_LIKE; 3.
DR	Immunoglobulin domain;	Receptor;	Transmembrane; Glycoprotein; Signal;
KW	Repeat;	Antigen;	Alternative splicing; Polymorphism.
KW	SIGNAL	1	20
FT	CHAIN	21	417
FT	DOMAIN	21	343
FT	DOMAIN	344	367
FT	TRANSMEM	368	417
FT	DOMAIN	24	139
FT	DOMAIN	145	237
FT	DOMAIN	244	328
FT	DISULFID	49	123
FT	DISULFID	166	221
FT	DISULFID	266	312
FT	CARBOHYD	105	105
FT	CARBOHYD	120	120
FT	CARBOHYD	188	188
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FT	CARBOHYD	237	237
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FT	CARBOHYD	313	313
FT	VARSPIC	340	384
FT	VARSPIC	331	331
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FT	VARSPIC	385	392
FT	VARSPIC	393	417
FT	VARIANT	67	67
FT	VARIANT	340	340
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SQ	Query Match	20.8%;	Score 383.5; DB 1; Length 417;
	Best Local Similarity	30.2%;	Pred. No. 4.8e-23;
	Matches	95;	Conservative 56; Mismatches 143; Indels 21; Gaps 9;
QY	1	GPIIVE--PHVTAVWGKVNLSKCLIEVNET----	ITQISWEKIHGKSSQTVAVH---PQ 51
Db	27	GDVVVQAPTQVPGFLGDSVTLPCYLQVPMNEVTHVSQLTWAR-HGESGSMVAFHQTQGPS	85
QY	52	YGFSVQGEYQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLV	111
Db	86	YSESKRLEFVAARL--GAELRNASLRMFLGRVEDEGNYTCLFTTFPGSRSDIWLRLVA	143
QY	112	EP--TVSLIKGPDLSIDGGNETVAAICIAATCKPVAHIDWEGDLGEMESTT--TSFPNET	167
Db	144	KPONTAEVQKVQLT----GEPVPMARCVSTGCRPPAQITWHSDDLGMPTNSQVPGFLSGT	199
QY	168	ATIISQYKLFPTFARGRRITCVVXKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGR	227
Db	200	VTVTSWLILVPSSQVDGKNVTCVHESEFEKPOLLTVNLTVYPPPEVSISSGYNWYLGQ	259
QY	228	KGVNLCNADANPPPKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL	287
Db	260	NEATLTCDARSNPEPIGYNWSTTMGFLPPFAVAGQAQL-LIRPVDKPIINTTLCNVTNAL	318

QY	288	QQRSDQKVIYISDPP	302
Db	319	GARQAELTVQVKEGP	333
RESULT 8			
ID	ICCR_DROME	STANDARD;	PRT; 764 AA.
AC	Q08180;		
DT	01-FEB-1995	(Rel. 31, Created)	
DT	01-FEB-1995	(Rel. 31, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	Irregular chiasm C-roughest protein precursor (IRREC protein).		
GN	RST.		
OS	Drosophila melanogaster (Fruit fly).		
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;		
OC	Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;		
OC	Ephydroidea; Drosophilidae; Drosophila.		
OX	NCBI_TaxID=7227;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=94102535; Pubmed=7503814;		
RA	Ramos R.G., Igloi G.L., Lichte B., Baumann U., Maier D.,		
RA	Schneider T., Brandstaetter J.H., Froehlich A., Fischbach K.-F.;		
RT	"The irregular chiasm C-roughest locus of Drosophila, which affects axonal projections and programmed cell death, encodes a novel immunoglobulin-like protein."		
RT	Genes Dev. 7:2533-2547(1993).		
CC	-!- FUNCTION: REQUIRED FOR CORRECT AXONAL PATHWAY FORMATION IN THE OPTIC LOBE AND FOR PROGRAMMED CELL DEATH IN THE DEVELOPING RETINA.		
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.		
CC	-!- TISSUE SPECIFICITY: POSTEMBRYONIC EXPRESSION IS STRONG IN THE DEVELOPING OPTIC LOBE AND IN THE EYE IMAGINAL DISC.		
CC	-!- DEVELOPMENTAL STAGE: STRONGLY EXPRESSED IN EMBRYOS. ALSO FOUND IN LATE LARVAL AND PUPAL STAGES.		
CC	-!- SIMILARITY: Contains 5 immunoglobulin-like C2-type domains.		
CC	-----		
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CC	EMBL; Z21641; CAA79756.1; -.		
DR	EMBL; L11040; AAA16632.1; -.		
DR	PIR; A49448; A49448.		
DR	FlyBase; FBgn003285; rst.		
DR	GO; GO:0016202; P:regulation of myogenesis; IMP.		
DR	InterPro; IPR007110; Ig-like.		
DR	InterPro; IPR003598; Ig_c2.		
DR	Pfam; PF00047; ig; 4.		
DR	SMART; SM00408; IGC2; 1.		
DR	PROSITE; PS50835; IG_LIKE; 5.		
KW	Transmembrane; Immunoglobulin domain; Glycoprotein; Signal; Repeat; Cell adhesion.		
KW	SIGNAL	1	19
FT	CHAIN	20	764
FT	DOMAIN	20	533
FT	TRANSMEM	534	556
FT	DOMAIN	557	764
FT	DOMAIN	21	123
FT	DOMAIN	117	230
FT	DOMAIN	245	261
FT	DOMAIN	237	343
FT	DOMAIN	346	419
FT	DOMAIN	430	530
FT	DOMAIN	637	660
FT	CAREOHYD	211	211
FT	CAREOHYD	313	313
FT	CAREOHYD	393	393
FT	POTENTIAL.		
FT	IRREGULAR CHIASM C-ROUGHES		
FT	EXTRACELLULAR (POTENTIAL).		
FT	POTENTIAL.		
FT	CYTOPLASMIC (POTENTIAL).		
FT	IG-LIKE C2-TYPE 1.		
FT	IG-LIKE C2-TYPE 2.		
FT	GLY-RICH.		
FT	IG-LIKE C2-TYPE 3.		
FT	IG-LIKE C2-TYPE 4.		
FT	IG-LIKE C2-TYPE 5.		
FT	GLN-RICH (OPA-REPEAT).		
FT	N-LINKED (GLCNAC. . .)		
FT	N-LINKED (GLCNAC. . .)		
FT	N-LINKED (GLCNAC. . .)		

Db 209 PAIMPMQKSFNATARGEMTLTKASGSPDPT-ISWFR----- 246

QY 58 GEYQGRVLFKN--YSL--NDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVLEP 113

Db 247 ---NGKLIENEKYLKGSNTLTVRNIIKNDGGSYVCKA-TNKAGEDQKQAFLOQVFVQP 302

QY 114 TVSLIKGPDSLIDGNET-----VAAICIAATGKPVAHIDWEGDL-GEMESTTTSFPNE 166

Db 303 HILQLK-----NETTSENGHVTLVC-EAEGEPVPEITWKRAIDGVNMFSEGDKSPDG 352

QY 167 TATIISQYKLFPTFRFARRITCVWKHPALEKDIRY-----SPILDIQYAP- 212

Db 353 RIEVKQGH-----GRSSLHIRDVKLSDSGRYDCEAASRIGGHQHSWHLDIEYAPK 402

QY 213 ----EVSVTGYDGNWFVGRKGVNLKCNADANPPPKSV-WSRLDGQWPDGLLASDNTLHF 267

Db 403 FVSNQTMYSWEGN-----PINISCDVTANPP--ASIHWR-----EKLLEPAKNTTHL 449

QY 268 -----VHPLTENYSGVYICKVTNSLQSRDQKVIYISDPPTTTTLQPTIQWHP 315

Db 450 KTHSVGRKMILEIAPTSDNDGFRYCNCTATNRIGTRFQYILELADVPSPPHGVKLIELSQ 509

QY 316 STA-----DIEDLATEPKKL 330

Db 510 TTAKISFNKPESHGGVPIHHYQVDVKEVASETWKI 544

RESULT 10

PGBM_HUMAN

ID PGBM_HUMAN STANDARD; PRT; 4391 AA.

AC P98160; Q16287; Q9H3V5;

DT 01-OCT-1996 (Rel. 34, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Basement membrane-specific heparan sulfate proteoglycan core

DE protein precursor (HSPG) (Perlecan) (PLC).

GN HSPG2.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92112994; PubMed=1730768;

RA Kallunki P., tryggvason K.;

RT "Human basement membrane heparan sulfate proteoglycan core protein: a

RT 467-kD protein containing multiple domains resembling elements of the

RT low density lipoprotein receptor, laminin, neural cell adhesion

RT molecules, and epidermal growth factor.";

RL J. Cell Biol. 116:559-571(1992).

RN [2]

RP SEQUENCE FROM N.A.

RT TISSUE=Colon, and Skin;

RX MEDLINE=92235084; PubMed=1569102;

RA Murdoch A.D., Dodge G.R., Cohen I., Tuan R.S., Iozzo R.V.;

RT "Primary structure of the human heparan sulfate proteoglycan from

RT basement membrane (HSPG2/perlecan). A chimeric molecule with multiple

RT domains homologous to the low density lipoprotein receptor, laminin,

RT neural cell adhesion molecules, and epidermal growth factor.";

RL J. Biol. Chem. 267:8544-8557(1992).

RN [3]

RP SEQUENCE OF 22-4391 FROM N.A., AND VARIANT SJS1 TYR-1532.

RX MEDLINE=20553141; PubMed=1101850;

RA Nicole S., Davoine C.-S., Topaloglu H., Cattolico L., Barral D.,

RA Beighton P., Ben-Hamida C., Hammouda H., Cruaud C., White P.S.,

RA Samson D., Urtizberea J.A., Lehmann-Horn F., Weissenbach J.,

RA Hentati F., Fontaine B.;

RT "Perlecan, the major proteoglycan of basement membranes, is altered in

RT patients with Schwartz-Jampel syndrome (chondrodystrophic myotonia).";

RL Nat. Genet. 26:480-483(2000).

RN [4]

RP SEQUENCE OF 1016-1470 FROM N.A.

RC TISSUE=Colon;

RX MEDLINE=91365376; PubMed=1679749;

RA Dodge G.R., Kovalszky I., Chu M.L., Hassell J.R., McBride O.W.,

RA Yi H.F., Iozzo R.V.;

RT "Heparan sulfate proteoglycan of human colon: partial molecular

RT cloning, cellular expression, and mapping of the gene (HSPG2) to the

RT short arm of human chromosome 1.";

RL Genomics 10:673-680(1991).

RN [5]

RP SEQUENCE OF 890-1396 FROM N.A.

RC TISSUE=Fibrosarcoma;

RX MEDLINE=92120660; PubMed=1685141;

RA Kallunki P., Eddy R.L., Byers M.G., Kestila M., Shows T.B.,

RA Tryggvason K.;

RT "Cloning of human heparan sulfate proteoglycan core protein,

RT assignment of the gene (HSPG2) to 1p36.1-->p35 and identification of

RT a BamHI restriction fragment length polymorphism.";

RL Genomics 11:389-396(1991).

RN [6]

RP SEQUENCE OF 1-21 FROM N.A.

RX MEDLINE=94052171; PubMed=8234307;

RA Cohen I.R., Graessel S., Murdoch A.D., Iozzo R.V.;

RT "Structural characterization of the complete human perlecan gene and

RT its promoter.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:10404-10408(1993).

RN [7]

RP CARBOHYDRATE-LINKAGE SITE ASN-2121.

RX MEDLINE=22660472; PubMed=12754519;

RA Zhang H., Li X.-J., Martin D.B., Aebersold R.;

RT "Identification and quantification of N-linked glycoproteins using

RT hydrazide chemistry, stable isotope labeling and mass spectrometry.";

RL Nat. Biotechnol. 21:660-666(2003).

CC -!- FUNCTION: This protein is an integral component of basement

CC membranes. It is responsible for the fixed negative electrostatic

CC charge and is involved in the charge-selective ultrafiltration

CC properties. It serves as an attachment substrate for cells.

CC -!- SUBUNIT: Purified perlecan has a strong tendency to aggregate in

CC dimers or stellate structures. It interacts with other basement

CC membrane components such as laminin, prolargin and collagen type

CC IV.

CC -!- SUBCELLULAR LOCATION: Extracellular.

CC -!- TISSUE SPECIFICITY: Found in the basement membranes.

CC -!- PTM: CONTAINS THREE HEPARAN SULFATE CHAINS AS WELL AS N-LINKED

CC AND O-LINKED OLIGOSACCHARIDES.

CC -!- DISEASE: Defects in HSPG2 are the cause of Schwartz-Jampel

CC syndrome (SJS1) [MIM:255800]; a rare autosomal recessive disorder

CC characterized by permanent myotonia (prolonged failure of muscle

CC relaxation) and skeletal dysplasia, resulting in reduced stature,

CC kyphoscoliosis, bowing of the diaphyses and irregular epiphyses.

CC -!- SIMILARITY: Contains 4 LDL-receptor class A domains.

CC -!- SIMILARITY: Contains 11 laminin EGF-like domains.

CC -!- SIMILARITY: Contains 3 laminin IV domains.

CC -!- SIMILARITY: Contains 22 immunoglobulin-like C2-type domains.

CC -!- SIMILARITY: Contains 3 laminin G-like domains.

CC -!- SIMILARITY: Contains 4 EGF-like domains.

CC -!- SIMILARITY: Contains 1 SEA domain.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL; X62515; CAA44373.1; -.

CC EMBL; M85289; AAA52700.1; -.

CC EMBL; AL445795; CAC18534.1; -.

CC EMBL; M64283; AAA52699.1; -.

CC EMBL; S76436; AAB21121.2; -.

CC EMBL; L22078; -; NOT ANNOTATED_CDS.

CC PIR; A38096; A38096.

CC HSSP; P00740; 1EDM.

CC Siena-2DPAGE; P98160; -.

CC IsoId=O60469-1; Sequence=Displayed;
CC Name=Short; Synonyms=CHD2-42;
CC IsoId=O60469-2; Sequence=VSP_002502, VSP_002503;
CC TISSUE SPECIFICITY: Primarily expressed in brain.
CC -!- SIMILARITY: Contains 10 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 6 fibronectin type III domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF023450; AAC17967.1; -
CC EMBL; AF023449; AAC17966.1; -
CC EMBL; AF217525; AAF27525.1; -
CC EMBL; AL163283; CAB90464.1; -
CC EMBL; AL163282; CAB90436.1; -
CC EMBL; AL163281; CAB90444.1; -
CC Genew; HGNC:3039; DSCAM.
CC MIM; 602523; -
CC GO; GO:0005887; C:integral to plasma membrane; TAS.
CC GO; GO:0005624; C:membrane fraction; TAS.
CC GO; GO:0007155; P:cell adhesion; TAS.
CC GO; GO:0007399; P:neurogenesis; TAS.
CC InterPro; IPR008957; FN_III-like.
CC InterPro; IPR003961; FN_III.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003598; Ig_c2.
CC Pfam; PF00041; fn3; 6.
CC Pfam; PF00047; ig; 9.
CC SMART; SM00060; FN3; 6.
CC SMART; SM00408; IGC2; 7.
CC PROSITE; PS50835; IG_LIKE; 9.
KW Immunoglobulin domain; Signal; Glycoprotein; Signal; Cell adhesion; Repeat;
KW Transmembrane; Alternative splicing.
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 2012 DOWN SYNDROME CELL ADHESION MOLECULE.
FT DOMAIN 18 1595 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1596 1616 POTENTIAL.
FT DOMAIN 1617 2012 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 39 129 IG-LIKE C2-TYPE 1.
FT DOMAIN 125 216 IG-LIKE C2-TYPE 2.
FT DOMAIN 225 305 IG-LIKE C2-TYPE 3.
FT DOMAIN 313 401 IG-LIKE C2-TYPE 4.
FT DOMAIN 407 500 IG-LIKE C2-TYPE 5.
FT DOMAIN 504 592 IG-LIKE C2-TYPE 6.
FT DOMAIN 596 685 IG-LIKE C2-TYPE 7.
FT DOMAIN 690 783 IG-LIKE C2-TYPE 8.
FT DOMAIN 787 883 IG-LIKE C2-TYPE 9.
FT DOMAIN 885 972 FIBRONECTIN TYPE-III 1.
FT DOMAIN 984 1076 FIBRONECTIN TYPE-III 2.
FT DOMAIN 1088 1177 FIBRONECTIN TYPE-III 3.
FT DOMAIN 1189 1273 FIBRONECTIN TYPE-III 4.
FT DOMAIN 1285 1377 IG-LIKE C2-TYPE 10.
FT DOMAIN 1380 1463 FIBRONECTIN TYPE-III 5.
FT DOMAIN 1477 1562 FIBRONECTIN TYPE-III 6.
FT DISULFID 46 102 BY SIMILARITY.
FT DISULFID 145 197 BY SIMILARITY.
FT DISULFID 246 293 BY SIMILARITY.
FT DISULFID 335 385 BY SIMILARITY.
FT DISULFID 428 484 BY SIMILARITY.
FT DISULFID 525 575 BY SIMILARITY.
FT DISULFID 617 669 BY SIMILARITY.
FT DISULFID 711 766 BY SIMILARITY.
FT DISULFID 809 865 BY SIMILARITY.
FT DISULFID 1307 1359 BY SIMILARITY.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 78 78 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 470 470 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 487 487 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT	CARBOHYD	512	512	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	556	556	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	658	658	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	666	666	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	710	710	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	748	748	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	795	795	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	924	924	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1142	1142	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1160	1160	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1250	1250	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1271	1271	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1341	1341	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	CARBOHYD	1488	1488	N-LINKED (GLCNAC. . .)	(POTENTIAL).
FT	VARSPLIC	1562	1571	NFATLNYDGS -> KEAARCKEFS (in isoform Short).	
FT				/FTId=VSP_002502.	
FT	VARSPLIC	1572	2012	Missing (in isoform Short).	
FT				/FTId=VSP_002503.	
FT	CONFELICT	1893	2012	HRPGDLIHLPPYLMDFLNRRGGPGTSRDLSLGQACLEPQK	
FT				SRTLKPTVLEPIPMEEAASSASSTREGSQWPGAVATLPQR	
FT				EGAEELGQAAMSSQESLLDSRGLKGNPNYAKSYTLV ->	
FT				IGQVTSYICLHLEWTEFC (IN REF. 1).	
SQ	SEQUENCE	2012 AA; 222259 MW; 0E33CFB781A08334 CRC64;			

Query Match 9.8%; Score 181.5; DB 1; Length 2012;
Best Local Similarity 23.7%; Pred. No. 3.7e-06;
Matches 82; Conservative 55; Mismatches 148; Indels 61; Gaps 17;

QY	1	GPIIIVP--HVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQV 58
Db	503	GPASIRPMKNITAIAGRDYIHCRV-IGYPYSIKWY----KNSNLLPFNHRQVAPE--- 554
QY	59	EYQGRVLFKNYSINDATITLHNIGFS-DSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSL 117
Db	555	-----NNGTLKLSDVQKEVDEBYTCNVLVQPQLSTQSQSVHVTVKVPPFIQP 601
QY	118	IKGPDSLIDGGNETVAACIAATGKPVAHIDWEGD---LGEMESTTSPNETATIISQ 173
Db	602	FEFPRFSI---GQVFIPCVVVGDLPTITWQKDRPIGPSLGVTIDNIDFTSSLRISN 658
QY	174	YKLFPTFRFARGRRITCVVKHPALEKDIRYSFILDIIQYAPEVSVTGYDGNWFWGRKGWNLK 233
Db	659	LSLM-----HNGNYTCIARNEAAA--VEHOSQLIVRPPKFFVQPRDQDGIYG-KAVILN 710
QY	234	CNADANPPPFKSVWSRLDQ-----WPDGL-----LASDNTLHFVHPLTFNYSGVYICKV 283
Db	711	CSAEGYPVP-TIVWFKSGAGVPQFQPIALNGRIQVLSNGSLLIKHVVEED-SGYVLCVKV 768
QY	284	TNSLGQRSDQKVIYISDPPTTTTLOPTIQHHPSTADIEDLATEPKK 329
Db	769	SNDVG-ADVSKSMYL-----TVKIPAMITSYPNTT-----LATQGQK 804

RESULT 14
NCM2_HUMAN
ID NCM2_HUMAN STANDARD; PRT; 837 AA.
AC O15394;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Neural cell adhesion molecule 2 precursor (N-CAM 2).
GN NCM2 OR NCM21.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97369930; PubMed=9226371;
RA Paoloni-Giacobino A., Chen H., Antonarakis S.E.;
RT "Cloning of a novel human neural cell adhesion molecule gene (NCAM2)

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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X06564; CAA29809.1; -.
DR EMBL; M32611; AAA41679.1; -.
DR PIR; S00846; IJRTNC.
DR PDB; 1EPF; 27-OCT-00.
DR InterPro; IPR008957; FN III-like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; ig; 5.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00408; IGC2; 5.
DR PROSITE; PS50835; IG_LIKE; 5.
KW Cell adhesion; Glycoprotein; Transmembrane; Repeat;
KW Immunoglobulin domain; Alternative splicing; Signal; Heparin-binding;
KW 3D-structure.
FT SIGNAL 1 19
FT CHAIN 20 858
FT FT
FT FT
FT DOMAIN 20 721
FT TRANSMEM 722 739
FT DOMAIN 740 858
FT DOMAIN 20 111
FT DOMAIN 116 205
FT DOMAIN 212 302
FT DOMAIN 309 414
FT DOMAIN 417 502
FT DOMAIN 514 615
FT DOMAIN 616 712
FT DOMAIN 152 156
FT DOMAIN 161 165
FT DISULFID 41 96
FT DISULFID 139 189
FT DISULFID 235 288
FT DISULFID 330 396
FT DISULFID 437 490
FT CARBOHYD 222 222
FT CARBOHYD 316 316
FT CARBOHYD 348 348
FT CARBOHYD 434 434
FT CARBOHYD 460 460
FT CARBOHYD 489 489
SQ SEQUENCE 858 AA; 94658 MW; EALA06A4EA0550F6 CRC64;
NEURAL CELL ADHESION MOLECULE 1, 140 kDa
ISOFORM.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE 1.
IG-LIKE C2-TYPE 2.
IG-LIKE C2-TYPE 3.
IG-LIKE C2-TYPE 4.
IG-LIKE C2-TYPE 5.
FIBRONECTIN TYPE-III 1.
FIBRONECTIN TYPE-III 2.
HEPARIN-BINDING (POTENTIAL).
HEPARIN-BINDING (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).

Query Match 9.4%; Score 174; DB 1; Length 858;
Best Local Similarity 22.5%; Pred. No. 4.9e-06;
Matches 78; Conservative 67; Mismatches 131; Indels 70; Gaps 18;
QY 8 HVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQG--RVL 65
Db 222 NATANLGQSVTLVCDADGFPPEPT-MSWTK-----DGEPIENEEDDEKHI 265
QY 66 FKNYSLNDAITTLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDLSI 125
Db 266 FSD---DSSELTIRNVDKNDEAEYVCIAEN-KAGEQDASIHLKVFAPKITYVENQTAM- 320
QY 126 DGGNETVAAICIAATGKPVAHIDWE---GDIGEMESTTTSFPNETATI-----I 171
Db 321 -ELEEQVTLTC-EASGDPIPSITWRTSTRTNISSEKASWTRPEKQETLDGHMVVRSHARV 378
QY 172 SQYKLPFTRFARGRRITCVVKHPALEKDIRYSPILDIQYAPE----VSVTGYDGNWFVGR 227
Db 379 SSLTLKSIQYTDAGEYICTASN-TIGQDSQ-SMYLEVQYAPKLQGPVAVYTWEGN----- 431
QY 228 KGVNLKCNADANPPFPKSVWSRLDGQWPDGLLASDNTLHF-----VHPLTFNY 275
Db 432 -QVNITCEVFAYPSATIS-WFR-DGQ-----LLPSSNYSNIKIYNTPSASYLEVTPDSEND 484

QY 276 SGVYICKVTNSLQGRSDQKVYIISDPPTTTTLQPTIQWHPSTADIE 321
Db 485 FGNYNCTAVNRIGQESLEFILVQADTPSSPSID-RVEPYSSAQVQ 529

Search completed: April 12, 2004, 09:39:46
Job time : 7.54545 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:29:15 ; Search time 28.1818 Seconds
(without alignments)
3884.945 Million cell updates/sec

Title: US-09-972-268-4_COPY_58_404
Perfect score: 1844
Sequence: 1 GPIIVEPHVTAVGKNVSLK.....KKLPFLSTLTIKDDTIAT 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL_25.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phage.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_rvirus.*
 - 16: sp_bacteriap.*
 - 17: sp_archheap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1844	100.0	549	4 Q9NQS3	Q9nqs3 homo sapien
2	1767	95.8	549	11 Q9JLB9	Q9jlb9 mus musculu
3	1723	93.4	549	11 Q9D006	Q9d006 mus musculu
4	1567	85.0	438	11 Q9JLB7	Q9jlb7 mus musculu
5	1567	85.0	510	11 Q9JLB8	Q9jlb8 mus musculu
6	1391	75.4	407	4 Q9Y412	Q9y412 homo sapien
7	1218	66.1	267	4 Q8NC05	Q8nc05 homo sapien
8	862	46.7	304	4 Q9BVA9	Q9bva9 homo sapien
9	534.5	29.0	295	11 Q9ERF5	Q9erf5 mesocricetu
10	528	28.6	298	6 Q9GL74	Q9gl74 cercopithe
11	526.5	28.6	295	6 Q9GL75	Q9gl75 bos taurus
12	476.5	25.8	510	4 Q96NY8	Q96ny8 homo sapien
13	476.5	25.8	510	4 Q96K15	Q96k15 homo sapien
14	457.5	24.8	483	11 Q9DBP8	Q9dbp8 mus musculu
15	457.5	24.8	508	11 Q8R007	Q8r007 mus musculu
16	457.5	24.8	508	11 Q8CED8	Q8ced8 mus musculu

17	420	22.8	530	11 Q80XJ5	Q80xj5 mus musculu
18	419	22.7	467	11 Q91VT9	Q91vt9 mus musculu
19	419	22.7	467	11 Q8C6F2	Q8c6f2 mus musculu
20	396.5	21.5	449	4 Q9UEI6	Q9uei6 homo sapien
21	394.5	21.4	412	11 Q9RIE1	Q9riel rattus norv
22	389.5	21.1	412	11 Q63611	Q63611 rattus norv
23	386.5	21.0	400	6 Q8HY16	Q8hy16 cebus apell
24	383.5	20.8	417	4 Q96BJ1	Q96bj1 homo sapien
25	381.5	20.7	403	6 Q8HY15	Q8hy15 lemur catta
26	378	20.5	408	11 Q91WP1	Q91wp1 mus musculu
27	376	20.4	408	11 Q8K094	Q8k094 mus musculu
28	375	20.3	408	11 Q8BVF6	Q8bvf6 mus musculu
29	371.5	20.1	401	6 Q08835	Q08835 cercopithec
30	337	18.3	412	6 Q8HY14	Q8hy14 oryctolagus
31	334	18.1	415	11 Q60977	Q60977 mus musculu
32	295	16.0	456	11 Q8R5M8	Q8r5m8 mus musculu
33	286	15.5	442	4 Q9BY67	Q9by67 homo sapien
34	284	15.4	445	11 Q8R4L1	Q8r4l1 mus musculu
35	282.5	15.3	445	11 Q8K3T6	Q8k3t6 mus musculu
36	281.5	15.3	443	4 Q8N2F4	Q8n2f4 homo sapien
37	264.5	14.3	394	13 Q7ZXX1	Q7zxx1 xenopus lae
38	263.5	14.3	801	5 Q86LF8	Q86lf8 drosophila
39	257.5	14.0	417	11 Q7TNL1	Q7tnl1 mus musculu
40	257.5	14.0	800	5 Q86LF9	Q86lf9 drosophila
41	256.5	13.9	333	4 Q86WB8	Q86wb8 homo sapien
42	253.5	13.7	336	11 Q9D6E7	Q9d6e7 mus musculu
43	253.5	13.7	336	11 Q80VG4	Q80vg4 mus musculu
44	234	12.7	435	4 Q8N3J6	Q8n3j6 homo sapien
45	234	12.7	437	4 Q8IZP8	Q8izp8 homo sapien

ALIGNMENTS

RESULT 1

Q9NQS3
ID Q9NQS3 PRELIMINARY; PRT; 549 AA.
AC Q9NQS3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Nectin 3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Borg J.-P., Lecocq E., Adelaide J., Campadelli-Fiume G.,
RA Dubreuil P., Lopez M.,
RT "Human nectin 3/PRR3: A novel member of the PVR/PRR/nectin family that
RT interacts with afadin.";
RL Gene 0:0-0(2000).
DR EMBL; AF282874; AAF97597.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
SQ SEQUENCE 549 AA; 61002 MW; 6D1104CCB4A9D731 CRC64;

Query Match 100.0%; Score 1844; DB 4; Length 549;
Best Local Similarity 100.0%; Pred. No. 4.1e-150;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOQFSVQGEY	60
Db	58	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPOQFSVQGEY	117
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYCKAVTFPLGNAQSSTTVTLVEPTVSLIKG	177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTNFNSGVVICKVTNSLQORSQDKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTNFNSGVVICKVTNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 404
RESULT 2
Q9JLB9 PRELIMINARY; PRT; 549 AA.
AC Q9JLB9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Cell adhesion molecule nectin-3 alpha.
GN PVRL3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
MEDLINE=20209403; PubMed=10744716;
SatoH-Horikawa K., Nakanishi H., Takahashi K., Miyahara M.,
Tachibana K., Mizoguchi A., Takai Y.;
"Nectin-3: a new member of immunoglobulin-like cell adhesion molecules
that shows homophilic and heterophilic cell-cell adhesion
activities.";
J. Biol. Chem. 275:10291-10299 (2000).
RL EMBL; AF195833; AAF63685.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60583 MW; 5492C9ABB472F185 CRC64;
Query Match 95.8%; Score 1767; DB 11; Length 549;
Best Local Similarity 94.2%; Pred. No. 1.7e-143;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
QY 1 GPIIIVPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GSIIIVPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWFWGKGVNLCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTNFNSGVVICKVTNSLQORSQDKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTNFNSGVVCKVNSLQORSQDKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 404
RESULT 3
Q9D006 PRELIMINARY; PRT; 549 AA.
AC Q9D006;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE 2610301B19Rik protein.
GN PVRL3 OR 2610301B19RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
Kueh P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
Schraml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Hayashizaki Y.;
"Functional annotation of a full-length mouse cDNA collection.";
Nature 409:685-690 (2001).
RT EMBL; AK011949; BAB27933.1; -.
DR MGD; MGI:1930171; Pvrl3.
DR GO; GO:0005913; C:cell-cell adherens junction; IDA.
DR GO; GO:0005194; F:cell adhesion molecule activity; IDA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0007155; P:cell adhesion; IDA.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 3.
SQ SEQUENCE 549 AA; 60703 MW; 32775CBEC7319B32 CRC64;
Query Match 93.4%; Score 1723; DB 11; Length 549;
Best Local Similarity 91.9%; Pred. No. 1.1e-139;
Matches 319; Conservative 16; Mismatches 12; Indels 0; Gaps 0;
QY 1 GPIIIVPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
Db 58 GSIIIVPHVTAVMGKNVSLKCLIEVNETITQISWEKIHGKSTQTVAVHHPOYGFVSQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237

DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
GN DKFZP566B0846.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Ottenwaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL050071; CAB43256.1; -.
DR PIR; T08732; T08732.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 407 AA; 45718 MW; 4E6B6C05068D63AC CRC64;

Query Match 75.4%; Score 1391; DB 4; Length 407;
Best Local Similarity 100.0%; Pred. No. 2.7e-111;
Matches 262; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKPPVA 145
Db 1 SGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDGGNETVAAICIAATGKPPVA 60

QY 146 HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRITCVVKHPALEKDIRYSFI 205
Db 61 HIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTRFARGRITCVVKHPALEKDIRYSFI 120

QY 206 LDIQYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPKSVWSRLDGQWPDGLLASDNTL 265
Db 121 LDIQYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPKSVWSRLDGQWPDGLLASDNTL 180

QY 266 HFVHPLTFNYSVGVYICKVTNSLQSRSDQKVIYISDPPTTTTLOPTIQWHPSTADIEDLAT 325
Db 181 HFVHPLTFNYSVGVYICKVTNSLQSRSDQKVIYISDPPTTTTLOPTIQWHPSTADIEDLAT 240

QY 326 EPKCLPPLSTLTIATIKDDTIAT 347
Db 241 EPKCLPPLSTLTIATIKDDTIAT 262

RESULT 7
Q8NC05 PRELIMINARY; PRT; 267 AA.
ID Q8NC05
AC Q8NC05
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ90624.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahari K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK075105; BAC11404.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 1.

DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
KW Hypothetical protein.
SQ SEQUENCE 267 AA; 29253 MW; 4F464A8A1BA0C451 CRC64;

Query Match 66.1%; Score 1218; DB 4; Length 267;
Best Local Similarity 99.6%; Pred. No. 1.2e-96;
Matches 232; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 35 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 94

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 95 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 154

QY 221 PDSLIDGGNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 155 PDSLIDGGNETVAAICIAATGKPPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 214

QY 181 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLK 233
Db 215 FARRRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLK 267

RESULT 8
Q9BVA9 PRELIMINARY; PRT; 304 AA.
ID Q9BVA9
AC Q9BVA9;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to nectin 3, DKFZP566B0846 protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Cervix;
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001336; AAH01336.1; -.
DR InterPro; IPR007110; Ig-like.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
SQ SEQUENCE 304 AA; 34826 MW; 8BEAACF94A6BA745 CRC64;

Query Match 46.7%; Score 862; DB 4; Length 304;
Best Local Similarity 100.0%; Pred. No. 6.5e-66;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 189 CVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPKSVWS 248
Db 1 CVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWVGRKGVNLKCNADANPPPKSVWS 60

QY 249 RLDGQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQSRSDQKVIYISDPPTTTTLQ 308
Db 61 RLDGQWPDGLLASDNTLHFVHPLTFNYSVGVYICKVTNSLQSRSDQKVIYISDPPTTTTLQ 120

QY 309 PTIQWHPSTADIEDLATEPKLPPLSTLTIATIKDDTIAT 347
Db 121 PTIQWHPSTADIEDLATEPKLPPLSTLTIATIKDDTIAT 159

RESULT 9
Q9ERF5 PRELIMINARY; PRT; 295 AA.
ID Q9ERF5
AC Q9ERF5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Mesocricetus auratus (Golden hamster).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
OC Mesocricetus.
OX NCBI_TaxID=10036;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
DR EMBL; AF308634; AAG30283.1; --
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 295
SQ SEQUENCE 295 AA; 33112 MW; 03E5C4DCB5032E7F CRC64;

Query Match 29.0%; Score 534.5; DB 11; Length 295;
Best Local Similarity 38.3%; Pred. No. 9.9e-38;
Matches 113; Conservative 58; Mismatches 113; Indels 11; Gaps 6;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHKSSQTVAVHHPQYGFSGVQGRVLFKNYS 70
Db 3 GTDVVLHCSFANPLPSVKITQVTWQKATNGSKQNMAIYNPTMGVSVLPPEYKRVFELRPS 62

QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG--- 127
Db 63 FIDGTIRLSHLEDEGMVICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRAR 121

QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTSPNETATIISQYKLFPTRFARGR 185
Db 122 QDDKVVVATCTSANGKPPSVSWETRLKGEAEYQEIRNPNGTIVISRYRLVPSREAH 181

QY 186 RITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLCNADANPPPEKS 245
Db 182 SLACIVNY-HLDR-FRESLTINVQYEPEVTIEGFGDNWYLRQTDVKTCKADANPPATEY 239

QY 246 VMSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 300
Db 240 HWTTLNGSLPKGVEAQNRTLFFRGPINYSLAGTYICEATNPIGTRSGQVEVNITE 294

RESULT 10
Q9GL74 Q9GL74 PRELIMINARY; PRT; 298 AA.
AC Q9GL74;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Cercopithecus aethiops (Green monkey) (Grivet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
DR EMBL; AF308635; AAG30284.1; --

DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00409; IG; 2.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 298
SQ SEQUENCE 298 AA; 33309 MW; AEAD41842B8CA200 CRC64;

Query Match 28.6%; Score 528; DB 6; Length 298;
Best Local Similarity 37.6%; Pred. No. 3.7e-37;
Matches 112; Conservative 57; Mismatches 115; Indels 14; Gaps 6;

QY 14 GKNVSLKCLIE---VNETITQISWEKI---HGKSSQTVAVHHPQYGFSGVQGRVLFK 67
Db 3 GTDVVLHCSFANPLPSVKITQVTWQKITQATNGSKQNVAIYNPMSGVSVLAPYRERVEFL 62

QY 68 NYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSDLIDG 127
Db 63 RPSFTDGTIRLSRLEDEGVYICEFATFPTGNRESQNLNLTVMAKPT-NWIEGTQAVLRA 121

QY 128 ---GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTSPNETATIISQYKLFPTRFA 182
Db 122 KKGQDDKVLVATCTSANGKPPSVSWETRLKGEAEYQEIRNPNGTIVISRYRLVPSREA 181

QY 183 RGRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFWGRKGVNLCNADANPPP 242
Db 182 HQQSLACIVNYHM--DRFKESLTINVQYEPEVTIEGFGDNWYLRQMDVKTCKADANPPA 239

QY 243 FKSWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRSDQKVIYISD 300
Db 240 TEYHWTTLNGSLPKGVEAQNRTLFFKGPISYSLAGTYICEATNPIGTRSGQVEVNITE 297

RESULT 11
Q9GL75 Q9GL75 PRELIMINARY; PRT; 295 AA.
AC Q9GL75;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Herpesvirus entry mediator C (Fragment).
GN HVEC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21176378; PubMed=11277703;
RA Milne R.S.B., Connolly S.A., Krummenacher C., Eisenberg R.J.,
RA Cohen G.H.;
RT "Porcine HveC, a member of the highly conserved HveC/nectin 1 family,
RT is a functional alphaherpesvirus receptor."
RL Virology 281:315-328(2001).
DR EMBL; AF308633; AAG30282.1; --
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00406; igv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
FT NON_TER 1
FT NON_TER 295
SQ SEQUENCE 295 AA; 33082 MW; 7C35D64022146AFA CRC64;

Query Match 28.6%; Score 526.5; DB 6; Length 295;
Best Local Similarity 38.7%; Pred. No. 4.8e-37;
Matches 115; Conservative 54; Mismatches 113; Indels 15; Gaps 8;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHKSSQTVAVHHPQYGFSGVQGRVLFKNYS 70
Db 3 GTDVVLHCSFANPLPGVKITQVTWQKATNGSKQNVAIYNPAMGVSVLAPYRERVEFLRPS 62

QY 71 LNDATITLHNIGFSDSGYICKAVTFPLGNAQSTTVTLVVEPTVSLIKGPDLSLI---DG 127
Db 63 FTDGTLRLSRLEDEGVYICEFATFPAGNRSQLNLTVMAKPT-NWIEGTHAVLRARKG 121
QY 128 GNETV-AAICIAATGKPAHIDWEGDL-GEMESTTTSFPNETATIISQYKLFPTTRFARGR 185
Db 122 QDEKVLVATCTSANGKPPSVSWETRLKGEAEYQEIERNPNGITVVISRYRLVPSREARHQ 181
QY 186 RITCVVKHPALEKDIRY--SFILDIQYAPEVSVTGYDGNWFGVGRKGNLKNADANPPPF 243
Db 182 SLACIVNY---HMD-RFWEISLTNLVQVEPEVTIEGFDGNWYLQRMVDVCLTKCADANPPAT 237
QY 244 KSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 238 EYHWTTLNGLPKGVEAQNRTLFFRGPNYSLAGTYVCEATNPIGTRSQAQVEVNITE 294
RESULT 12
Q96NY8 PRELIMINARY; PRT; 510 AA.
AC Q96NY8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Nectin 4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Raymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RA "Nectin4/PRR4: A new afadin-associated member of the nectin family
RT that trans-interacts with nectin1/PRR1 through V domain interaction.";
RL J. Biol. Chem. 0:0-0(2001).
DR EMBL; AF426163; AAL23958.1; --
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 510 AA; 55454 MW; DCF5ELD794F27FA CRC64;
Query Match 25.8%; Score 476.5; DB 4; Length 510;
Best Local Similarity 35.3%; Pred. No. 2.1e-32;
Matches 106; Conservative 58; Mismatches 125; Indels 11; Gaps 8;
QY 9 VTAVWGKNVSLKCLI--EVNETITQISWEKIH-GKSSQTVAVHHPQYGFVSQGEYQGRVL 65
Db 40 VTVVLGQDAKLPFCFYRGDSGEVQGVAVARVDAGEGAQELALLHSHKYLHVS PAYEGRVE 99
QY 66 FKNYSLN--DATITLHNIGFSDSGYICKAVTFPLGNAQSTTVTLVVEPTVSLIKGPD 123
Db 100 QPPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQARLRLRVLPPLPSLNPGP-A 158
QY 124 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTRFAR 183
Db 159 LEEGQGLTLAASC-TAEGSPAPSVTWDTEVKGTTSSRSFKHSRSAAVTSEFHLVPSRSMN 217
QY 184 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGN--WFGVGRKGNLKNADANPP 241
Db 218 GQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPP 277
QY 242 PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDP 301
Db 278 PSYN-WTRLDGPLPSGVRVDGDTLGF-PPLTTEHSGIYVCHVSNEFFSSRDSQVTVVDLDP 335
RESULT 13
Q96K15 PRELIMINARY; PRT; 510 AA.
ID Q96K15

Q96K15;
01-DEC-2001 (TReMBLrel. 19, Created)
01-DEC-2001 (TReMBLrel. 19, Last sequence update)
01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ14847.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;
RT "NEDO human cDNA sequencing project."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027753; BAB55344.1; --
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Hypothetical protein; Immunoglobulin domain.
SQ SEQUENCE 510 AA; 55382 MW; 9B68CD50F086429E CRC64;
Query Match 25.8%; Score 476.5; DB 4; Length 510;
Best Local Similarity 35.3%; Pred. No. 2.1e-32;
Matches 106; Conservative 58; Mismatches 125; Indels 11; Gaps 8;
QY 9 VTAVWGKNVSLKCLI--EVNETITQISWEKIH-GKSSQTVAVHHPQYGFVSQGEYQGRVL 65
Db 40 VTVVLGQDAKLPFCFYRGDSGEVQGVAVARVDAGEGAQELALLHSHKYLHVS PAYEGRVE 99
QY 66 FKNYSLN--DATITLHNIGFSDSGYICKAVTFPLGNAQSTTVTLVVEPTVSLIKGPD 123
Db 100 QPPPPRNPLDGSVLLRNAVQADEGEYECRVSTFPAGSFQARLRLRVLPPLPSLNPGP-A 158
QY 124 LIDGNETVAAICIAATGKPAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTRFAR 183
Db 159 LEEGQGLTLAASC-TAEGSPAPSVTWDTEVKGTTSSRSFKHSRSAAVTSEFHLVPSRSMN 217
QY 184 GRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGN--WFGVGRKGNLKNADANPP 241
Db 218 GQPLTCVVSHPGLLQDQRITHILHVSFLAEASVRGLEDQNLWHIGREGAMLKCLSEGQPP 277
QY 242 PFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISDP 301
Db 278 PSYN-WTRLDGPLPSGVRVDGDTLGF-PPLTTEHSGIYVCHVSNEFFSSRDSQVTVVDLDP 335
RESULT 14
Q9DBP8 PRELIMINARY; PRT; 483 AA.
AC Q9DBP8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 1200017F15Rik protein.
GN PVRL4 OR 1200017F15RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itch M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sabaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.,
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK004821; BAB23592.1; -.
DR MGD; MGI:1918990; Pvr14.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain.
SQ SEQUENCE 483 AA; 53030 MW; F8F0466C000852E8 CRC64;

Query Match 24.8%; Score 457.5; DB 11; Length 483;
Best Local Similarity 34.5%; Pred. No. 8.5e-31;
Matches 106; Conservative 55; Mismatches 121; Indels 25; Gaps 9;

QY 9 VTAVGKNVSLKCLI--EVNETITQISWEKIH-GKSSQTVAVHHPQYGFSGVEYQGRV- 64
Db 39 VTVVLGQDAKLPCFYRGDPDEQVGQVAVARVDPNEGIRELALLHSHKYGLHVPAYEDRVE 98
QY 65 -----LFGKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVS 116
Db 99 QPPPPRDPL-----DGSVLLRNAVQADEGEYECRVSTFPAGSFQARMRLRLVLPPLPS 151
QY 117 LIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIISQYKL 176
Db 152 LNPGP-PLEEGQGLTLAASC-TAEGSPAPSVTWDTEVKGTQSSRSFTHPRSAAVTSEFHL 209
QY 177 PPTRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGN--WFGVGRKGVNLKC 234
Db 210 VPSRSMNGQPLTCVVSHPGLLQDRRITHTLQVAFLAESVRGLEQDNLWQVGREGATLKC 269
QY 235 NADANPPFPKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQK 294
Db 270 LSEGQPPP-KYNWTRLDGPLPSGVRVKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQV 327
QY 295 VIYISDP 301
Db 328 TVEVLDP 334

RESULT 15
Q8R007 PRELIMINARY; PRT; 508 AA.
AC Q8R007;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to poliovirus receptor-related 4 (Nectin 4).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.
RX MEDLINE=21560925; PubMed=11544254;
RA Raymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RT "Nectin4/PRR4, a new afadin-associated member of the nectin family
that trans-interacts with nectin1/PRR1 through V domain interaction.";
RL J. Biol. Chem. 276:43205-43215(2001).
RN [3]
RP SEQUENCE FROM N.A.
RA Raymond N., Fabre S., Lecocq E., Adelaide J., Dubreuil P., Lopez M.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC024948; AAH24948.1; -.
DR EMBL; AF472510; AAL79833.1; -.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00047; ig; 3.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS50835; IG_LIKE; 3.
KW Immunoglobulin domain; Receptor.
SQ SEQUENCE 508 AA; 55657 MW; 24DAEBD21F22E376 CRC64;

Query Match 24.8%; Score 457.5; DB 11; Length 508;
Best Local Similarity 34.5%; Pred. No. 9.1e-31;
Matches 106; Conservative 55; Mismatches 121; Indels 25; Gaps 9;

QY 9 VTAVGKNVSLKCLI--EVNETITQISWEKIH-GKSSQTVAVHHPQYGFSGVEYQGRV- 64
Db 39 VTVVLGQDAKLPCFYRGDPDEQVGQVAVARVDPNEGIRELALLHSHKYGLHVPAYEDRVE 98
QY 65 -----LFGKNSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVS 116
Db 99 QPPPPRDPL-----DGSVLLRNAVQADEGEYECRVSTFPAGSFQARMRLRLVLPPLPS 151
QY 117 LIKGPDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTFPNETATIISQYKL 176
Db 152 LNPGP-PLEEGQGLTLAASC-TAEGSPAPSVTWDTEVKGTQSSRSFTHPRSAAVTSEFHL 209
QY 177 PPTRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGN--WFGVGRKGVNLKC 234
Db 210 VPSRSMNGQPLTCVVSHPGLLQDRRITHTLQVAFLAESVRGLEQDNLWQVGREGATLKC 269
QY 235 NADANPPFPKSVWSRLDGQWPDGGLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQK 294
Db 270 LSEGQPPP-KYNWTRLDGPLPSGVRVKGDTLGF-PPLTTEHSGVYVCHVSNELSSRDSQV 327
QY 295 VIYISDP 301
Db 328 TVEVLDP 334

Search completed: April 12, 2004, 09:45:09
Job time : 29.1818 secs

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:25:25 ; Search time 41.9091 Seconds
(without alignments)
2339.444 Million cell updates/sec

Title: US-09-972-268-4_COPY_58_404
Perfect score: 1844
Sequence: 1 GPIIIEPHVTAVWGKNVSLK.....KKLPFPLSTLATIKDDTIAT 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match	Length	DB ID	Description
	Score	Match				
1	1844	100.0	426	5	AAE23289	Aae23289 Human nec
2	1844	100.0	542	5	AAE23281	Aae23281 Human del
3	1844	100.0	549	5	AAE23283	Aae23283 Human nec
4	1844	100.0	549	5	AAE23282	Aae23282 Mouse nec
5	1844	100.0	549	6	ABJ20222	Abj20222 Human IG
6	1844	100.0	555	4	AAM39143	Aam39143 Human pol
7	1844	100.0	634	5	AAE23287	Aae23287 Human nec
8	1767	95.8	549	4	AAG63982	Aag63982 Amino aci
9	1767	95.8	549	4	AAG63985	Aag63985 Amino aci
10	1767	95.8	549	5	AAE23291	Aae23291 Mouse nec
11	1613	87.5	559	4	AAM40929	Aam40929 Human pol
12	1602	86.9	387	5	AAE23290	Aae23290 Human nec
13	1602	86.9	437	5	AAE23299	Aae23299 Human nec
14	1602	86.9	504	5	AAE23284	Aae23284 Human del
15	1602	86.9	510	5	AAE23285	Aae23285 Mouse nec
16	1602	86.9	510	5	AAE23286	Aae23286 Human nec
17	1602	86.9	595	5	AAE23288	Aae23288 Human nec
18	1567	85.0	438	4	AAG63984	Aag63984 Amino aci
19	1567	85.0	438	5	AAE23293	Aae23293 Mouse nec
20	1567	85.0	510	4	AAG63983	Aag63983 Amino aci
21	1567	85.0	510	5	AAE23292	Aae23292 Mouse nec
22	1218	66.1	267	4	AAM93536	Aam93536 Human pol
23	594	32.2	258	5	ABB90250	Abb90250 Human pol
24	538.5	29.2	458	5	AAE23295	Aae23295 Human nec
25	538.5	29.2	514	6	ABJ20237	Abj20237 Human IG

26	538.5	29.2	517	3	AAV32390	Aay32390 Herpesvir
27	538.5	29.2	517	5	AAE23294	Aae23294 Human nec
28	516	28.0	518	5	ABG77170	Abg77170 Prostate
29	476.5	25.8	497	5	AAE23303	Aae23303 Human nec
30	476.5	25.8	510	4	AAE23365	Aab93365 Human pro
31	476.5	25.8	510	4	AAU00471	Aau00471 Human TAN
32	476.5	25.8	510	5	ABJ05562	Abj05562 Breast ca
33	476.5	25.8	510	6	ABJ20232	Abj20232 Human IG
34	476.5	25.8	510	6	ABR48229	Abr48229 Human bla
35	476.5	25.8	510	6	ABU56613	Abu56613 Lung canc
36	476.5	25.8	510	6	ABP97212	Abp97212 Tumour-as
37	476.5	25.8	510	7	ADB80512	Adb80512 Ovarian c
38	474.5	25.7	510	5	AAE23300	Aae23300 Human nec
39	474.5	25.7	510	6	ABJ20231	Abj20231 Human IG
40	470	25.5	498	5	AAE23305	Aae23305 Human nec
41	470	25.5	511	5	AAE23301	Aae23301 Human nec
42	470	25.5	580	5	AAE23302	Aae23302 Human nec
43	401.5	21.8	538	5	AAE23297	Aae23297 Human nec
44	401.5	21.8	538	6	ABJ20238	Abj20238 Human IG
45	401.5	21.8	538	8	ADE86687	Ade86687 Human pol

ALIGNMENTS

RESULT 1
AAE23289
ID AAE23289 standard; protein; 426 AA.
XX
AC AAE23289;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3alpha-FLAGpolyHis fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX

Key	Location/Qualifiers
FT Region	1..404
FT Region	/note= "Human nectin-3alpha protein"
FT Region	405..420
FT Region	/note= "FLAG peptide"
FT Region	421..426
FT Region	/note= "PolyHis tag"

WO200228902-A2.

11-APR-2002.

05-OCT-2001; 2001WO-US031392.

05-OCT-2000; 2000US-0238557P.

(IMMV) IMMUNEX CORP.

Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

WPI; 2002-426103/45.

Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1, useful for treating or preventing heart failure, malaria, glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema, sepsis, stroke.

Claim 9; Page 104-105; 141pp; English.


```
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC FLAGpolyHis fusion protein
XX
SQ Sequence 426 AA;
Query Match 100.0%; Score 1844; DB 5; Length 426;
Best Local Similarity 100.0%; Pred. No. 1.1e-147;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVQGEY 60
Db 58 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVQGEY 117
QY 61 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSPFILDIOYAPEVSVTGYDGNWVFGKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSPFILDIOYAPEVSVTGYDGNWVFGKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 347
Db 358 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 404
RESULT 2
AAE23281
ID AAE23281 standard; protein; 542 AA.
XX
AC AAE23281;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human deleted nectin-3alpha protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; chromosome 3; asthma.
XX
OS Homo sapiens.
XX
PN W0200228902-A2.
XX
PD 11-APR-2002.
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XX 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Baum ER, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
XX N-PSDB; AAD37440.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 76-78; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3alpha protein
CC containing 7 amino acids deleted from the N-terminal end. Human nectin-
CC 3alpha gene is located on chromosome 3
XX
SQ Sequence 542 AA;
Query Match 100.0%; Score 1844; DB 5; Length 542;
Best Local Similarity 100.0%; Pred. No. 1.5e-147;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVQGEY 60
Db 51 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVQGEY 110
QY 61 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 111 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 170
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 180
Db 171 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLPFTR 230
QY 181 FARGRRITCVVKHPALEKDIRYSPFILDIOYAPEVSVTGYDGNWVFGKGVNLKCNADANP 240
Db 231 FARGRRITCVVKHPALEKDIRYSPFILDIOYAPEVSVTGYDGNWVFGKGVNLKCNADANP 290
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 291 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 350
QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 347
Db 351 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 397
RESULT 3
AAE23283
```

AAE23283 standard; protein; 549 AA.
AAE23283;
27-AUG-2002 (first entry)
Human nectin-3alpha protein.
Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
paracellular transport disorder; kidney; diabetic retinopathy; allergy;
allograft rejection; metastasis; restenosis; inflammatory bowel disease;
oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
Homo sapiens.
Key Location/Qualifiers
Modified-site 73
Domain 74..152
/note= "N-glycosylated"
Modified-site 83
/note= "Extracellular Ig domain"
Modified-site 125
/note= "N-glycosylated"
Modified-site 186
/note= "N-glycosylated"
Domain 189..250
/note= "Extracellular Ig domain"
Modified-site 222
/note= "N-glycosylated"
Domain 287..342
/note= "Extracellular Ig domain"
Modified-site 331
/note= "N-glycosylated"
Domain 405..424
/note= "Transmembrane domain"
Domain 425..549
/note= "C-terminal domain"
WO200228902-A2.
11-APR-2002.
05-OCT-2001; 2001WO-US031392.
05-OCT-2000; 2000US-0238557P.
(IMMV) IMMUNEX CORP.
Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
WPI; 2002-426103/45.
N-PSDB; AAD37442.
Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
useful for treating or preventing heart failure, malaria,
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
sepsis, stroke.
Claim 1; Page 89-91; 141pp; English.
The invention relates to a substantially purified nectin3alpha, beta,
gamma and nectin-4 polypeptides and their corresponding polynucleotides.
Nectin DNA and protein are useful for treating a disease associated with
cell adhesion activity, adherens junction formation activity, epithelial
or endothelial barrier function activity, endothelial proliferation or
migration activity, viral polypeptide binding activity. The epithelial or
endothelial barrier function disorder which is treated by the above
mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
asthma, allergy, allograft rejection, metastasis of cancer cells,
paracellular transport disorders such as magnesium transport defects in
the kidney or inflammatory bowel disease. Nectin DNA is also useful for

inhibiting angiogenesis in a mammal and treating endothelial migration,
proliferation or angiogenic condition of a tissue or a subject, such as
ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
stroke, restenosis, tumour growth and treating herpesvirus infection.
Nectin is also useful for modulating proliferation or migration of an
endothelial cell, an epithelial cell or a smooth muscle cell (vascular
smooth muscle cell). The present sequence is human nectin-3alpha DNA.
Human nectin-3alpha gene is located on chromosome 3
Sequence 549 AA;
Query Match 100.0%; Score 1844; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.5e-147;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 60
DB 58 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFSVQGEY 117
QY 61 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
DB 118 QGRVLFKNYSLNDAITILHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 180
DB 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLPFTR 237
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGVDGNWFGVGRKGNLKCNDANP 240
DB 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGVDGNWFGVGRKGNLKCNDANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSYVICKVTNSLGQRSDQKVIYISD 300
DB 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSYVICKVTNSLGQRSDQKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSLATIKDDTIAT 347
DB 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSLATIKDDTIAT 404
RESULT 4
AAE23282
ID AAE23282 standard; protein; 549 AA.
XX
AC AAE23282;
XX
DT 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin 3alpha fusion protein.
XX
KW Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; mouse;
KW stroke; tumour; cancer; herpesvirus infection; asthma; fusion protein;
KW chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..7
FT /note= "Mouse nectin-3 protein"
FT Region 8..549
FT /note= "Human nectin-3alpha protein"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.

XX 05-OCT-2000; 2000US-0238557P.
PR (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI
XX
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37441.
DR
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
XX Claim 1; Page 80-82; 141pp; English.
XX
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein containing
CC mouse nectin-3 protein and human nectin-3alpha protein. Human nectin-3
CC alpha gene is located on chromosome 3. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
XX Sequence 549 AA;
SQ

Query Match 100.0%; Score 1844; DB 5; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.5e-147;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 297
QY 241 PPKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPKSVWSRLDGOWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 347
Db 358 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPPLSTLATIKDDTIAT 404

RESULT 5
ABJ20222
ID ABJ20222 standard; protein; 549 AA.

XX AC
XX
XX DT 13-AUG-2003 (first entry)
XX
XX DE Human IG gene related protein SEQ ID No 45.
XX
XX KW Breast cancer; p53 pathway modulating agent; IG; colon cancer;
KW kidney cancer; lung cancer; ovary cancer; human.
XX
XX OS Homo sapiens.
XX
XX PN WO200299040-A2.
XX
XX PD 12-DEC-2002.
XX
XX PF 03-JUN-2002; 2002WO-US017313.
XX
XX PR 05-JUN-2001; 2001US-0296076P.
PR 10-OCT-2001; 2001US-0328605P.
PR 22-OCT-2001; 2001US-0338733P.
PR 15-FEB-2002; 2002US-0357253P.
PR 15-FEB-2002; 2002US-0357600P.
XX
XX (EXEL-) EXELIXIS INC.
XX
XX PI Friedmann L, Plowman GD, Belvin M, Francis-Lang H, Li D, Funke RP;
PI Lioubin MN;
XX
XX DR WPI; 2003-148660/14.
XX
XX PT Identifying a candidate p53 pathway modulators that are useful as targets
PT for therapeutics or for diagnosing cancers associated with defective p53
PT function, by providing an assay system having a purified IG polypeptide
PT or nucleic acid.
XX
XX PS Claim 13; Page 206-209; 248pp; English.
XX
XX CC The invention relates to a novel method for identifying a candidate p53
CC pathway modulating agent. The method comprises providing an assay system
CC having a purified IG polypeptide or nucleic acid, or their functionally
CC active fragment or derivative. The method is useful for identifying
CC modulators of the p53 pathway, particularly for identifying agents for
CC treating disorders (e.g. breast cancer, colon cancer, kidney cancer, lung
CC cancer or cancer of the ovary) associated with defective p53 function.
CC The identified modulators are useful as targets for novel therapeutics.
CC The method is also useful for diagnosing disorders associated with
CC defective p53 function. The IG proteins or nucleic acids are useful as
CC modifiers of the p53 pathway, and as therapeutic targets for disorders
CC associated with defective p53 function. This sequence represents a human
CC protein relating to the human IG genes used in the assay for identifying
CC modulators of the p53 pathway of the invention
XX
SQ

Sequence 549 AA;

Query Match 100.0%; Score 1844; DB 6; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.5e-147;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLCNADANP 240

Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDQWPDGILLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGILLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 404

RESULT 6

AAM39143
ID AAM39143 standard; protein; 555 AA.

XX AC AAM39143;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2288.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

OS WO200153312-A1.

PN 26-JUL-2001.

PD 26-DEC-2000; 2000WO-US034263.

PF 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-0052317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

PA Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI58299.

XX Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.

XX Example 4; SEQ ID NO 2288; 10078pp; English.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activity, chemotactic/chemokinetic activity, haemostatic
CC Activin/inhibin activity, cancer diagnosis and therapy, drug screening,
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX SQ Sequence 555 AA;

Query Match 100.0%; Score 1844; DB 4; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.6e-147;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIIVPHVTAVWGKNSLKLIENVETITQISWEKIHGSSQTVAVHHPQYGFVSQGEY 60
Db 64 GPIIIVPHVTAVWGKNSLKLIENVETITQISWEKIHGSSQTVAVHHPQYGFVSQGEY 123

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 124 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 183

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180
Db 184 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 243

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 244 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 303

QY 241 PPFKSVWSRLDQWPDGILLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 300
Db 304 PPFKSVWSRLDQWPDGILLASDNTLHFVHPLTFNYSVGYICKVTNSLQSRSDQKVIYISD 363

QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 347

Db 364 PPTTTTLOPTIQWHPSTADIEDLATEPKKLPFPLSTLTIKDDTIAT 410

RESULT 7

AAE23287

ID AAE23287 standard; protein; 634 AA.

XX AAE23287;

DT 27-AUG-2002 (first entry)

XX Human nectin-3alpha-IgG1Fc region fusion protein.

DE Human; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
XX paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis; IgG1;
KW stroke; tumour; herpesvirus infection; fusion protein; immunoglobulin G1;
KW cancer; asthma.

XX Homo sapiens.

OS Unidentified.

OS Chimeric.

XX WO200228902-A2.

XX 11-APR-2002.

XX 05-OCT-2001; 2001WO-US0311392.

XX 05-OCT-2000; 2000US-0238557P.

XX (IMMV) IMMUNEX CORP.

XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;

XX WPI; 2002-426103/45.

XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.

Claim 9; Page 100-102; 141pp; English.

The invention relates to a substantially purified nectin3alpha, beta, gamma and nectin-4 polypeptides and their corresponding polynucleotides. Nectin DNA and protein are useful for treating a disease associated with cell adhesion activity, adherens junction formation activity, epithelial or endothelial barrier function activity, endothelial proliferation or migration activity, viral polypeptide binding activity. The epithelial or endothelial barrier function disorder which is treated by the above mentioned method is inflammation, sepsis, oedema, diabetic retinopathy, asthma, allergy, allograft rejection, metastasis of cancer cells, paracellular transport disorders such as magnesium transport defects in the kidney or inflammatory bowel disease. Nectin DNA is also useful for inhibiting angiogenesis in a mammal and treating endothelial migration, proliferation or angiogenic condition of a tissue or a subject, such as ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis, stroke, restenosis, tumour growth and treating herpesvirus infection. Nectin is also useful for modulating proliferation or migration of an endothelial cell, an epithelial cell or a smooth muscle cell (vascular smooth muscle cell). The present sequence is a fusion protein containing human nectin-3alpha protein fused to immunoglobulin IgG1 Fc region

Sequence 634 AA;

```

XX 09-MAR-2000; 2000JP-00065595.
XX PR
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
XX PA (TAKA/) TAKAHASHI K.
XX PI Takahashi K, Takai Y, Nakanishi H, Sato K;
XX WI; 2001-570771/64.
DR N-PSD3; AAH78179.
DR
XX
PT New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and
PT corresponding antibodies.
XX
PS Claim 1; Page 37-40; 64pp; Japanese.
XX
CC The present sequence represents a murine nectin-3 polypeptide. Nectin-3
CC is an immunoglobulin-like cell adhesion molecule that shows homophilic
CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
CC polynucleotides are useful for investigating the mechanisms of cell
CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
CC malignancies of various cancers, and the development of methods for the
CC treatment and prevention of cancer
XX
SQ Sequence 549 AA;
Query Match          95.8%; Score 1767; DB 4; Length 549;
Best Local Similarity 94.2%; Pred. No. 5.2e-141;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY      1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSSQTVAVHHPOYGFSVQGEY 60
Db      58 GSIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKHGKSTQTVAVHHPOYGFSVQGDY 117
QY     61 QGRVLFNKYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVS LIKG 120
Db    118 QGRVLFNKYSLNDATITLHNIGFSDSGKIYICKAVTFPLGNAQSSTTVTLVEPTVS LIKG 177
QY    121 PDSLIDGGNETVAACIAATGKPVAAHDWEGDLGEMESSTTSFPNETATIIISQYKLPFTR 180
Db    178 PDSLIDGGNETVAACVAAATGKPVAQIDWEGDLGEMESSTTSFPNETATIVS QYKLPFTR 237
QY    181 FARGRRITCVVKHPALEKDRIYSFILDIQYAPEVSVTGVDGNWFVGKGVNLKCNDANP 240
Db    238 FARGRRITCVVKHPALEKDRIYSFILDIQYAPEVSVTGVDGNWFVGKGVNLKCNDANP 297
QY    241 PPFKSVWSRLDGQWPDGLLASDNTILHFVHPLTFNYSGVYICKVTNSLQORS DQKV IYISD 300
Db    298 PPFKSVWSRLDGQWPDGLLASDNTILHFVHPLTVNYSGVYCKVSNLSLQORS DQKV IYISD 357
QY    301 PPTTTTLQPTIONHESTADIEDLATEPKKLPPFLSTLATIKDDTIAT 347
Db    358 PPTTTTLQPTVQHSSPADVQDIATEHKKLPFPLSTLATLKDDTIGT 404

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XX 09-MAR-2001; 2001WO-JP001871.
XX 09-MAR-2000; 2000JP-00065595.
XX (NISC-) JAPAN SCI & TECHNOLOGY CORP.
PA (TAKA/) TAKAHASHI K.
XX Takahashi K, Takai Y, Nakanishi H, Sato K;
PI WPI; 2001-570771/64.
XX N-PSDB; AAH78182.
DR
XX New protein family for diagnosing and treating tumor infiltration and
PT metastasis comprises the mouse nectin-3 protein families and
PT corresponding antibodies.
XX
PS Disclosure; Page 56-61; 64pp; Japanese.
XX
PS The present sequence represents a murine nectin-3 polypeptide. Nectin-3
XX is an immunoglobulin-like cell adhesion molecule that shows homophilic
CC and heterophilic cell-cell adhesion activities. Nectin-3 polypeptides and
CC polynucleotides are useful for investigating the mechanisms of cell
CC adhesion, infiltration and metastasis of cancer cells, the diagnosis of
CC malignancies of various cancers, and the development of methods for the
CC treatment and prevention of cancer
XX
SQ Sequence 549 AA;
Query Match 95.8%; Score 1767; DB 4; Length 549;
Best Local Similarity 94.2%; Pred. No. 5.2e-141;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQVGSVQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTAVVHHPQVGSVQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAVCVAATGKPVQAIDWEGDLGEMESTTSPNETATIVSQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357
QY 301 PPTTTTLQPTVQWHSSPADVQDIATBHKKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLQPTVQWHSSPADVQDIATBHKKLPFPLSTLATIKDDTIAT 404
RESULT 10
AAE23291
ID AAE23291 standard; protein; 549 AA.
XX
AC AAE23291;
XX
DT 27-AUG-2002 (first: entry)
DE Mouse nectin-3 alpha protein.
XX
KW Mouse; nectin-3alpha; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma.

XX Mus musculus.
OS
XX WO200228902-A2.
PN
XX 11-APR-2002.
PD
XX 05-OCT-2001; 2001WO-US031392.
XX 05-OCT-2000; 2000US-0238557P.
XX (IMMV) IMMUNEX CORP.
PA
XX Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
PI WPI; 2002-426103/45.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Disclosure; Page 107-109; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is mouse nectin-3alpha protein
XX
SQ Sequence 549 AA;
Query Match 95.8%; Score 1767; DB 5; Length 549;
Best Local Similarity 94.2%; Pred. No. 5.2e-141;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;
QY 1 GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQVGSVQGEY 60
Db 58 GSIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSTQTAVVHHPQVGSVQGDY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTSPNETATIISQYKLPFTR 180
Db 178 PDSLIDGGNETVAAVCVAATGKPVQAIDWEGDLGEMESTTSPNETATIVSQYKLPFTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD 357
QY 301 PPTTTTLQPTVQWHSSPADVQDIATBHKKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLQPTVQWHSSPADVQDIATBHKKLPFPLSTLATIKDDTIAT 404


```
RESULT 11
AAM40929
ID AAM40929 standard; protein; 559 AA.
XX
AC AAM40929;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 5860.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US034263.
XX
PR 23-DEC-1999; 99US-00471275.
XX
PR 21-JAN-2000; 2000US-00488725.
XX
PR 25-APR-2000; 2000US-00552317.
XX
PR 20-JUN-2000; 2000US-00598042.
XX
PR 19-JUL-2000; 2000US-00620312.
XX
PR 03-AUG-2000; 2000US-00653450.
XX
PR 14-SEP-2000; 2000US-00662191.
XX
PR 19-OCT-2000; 2000US-00693036.
XX
PR 29-NOV-2000; 2000US-00727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
PI Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI; 2001-442253/47.
DR N-PSDB; AAI60085.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders such
PT as central nervous system injuries.
XX
PS Example 2; SEQ ID NO 5860; 10078pp; English.
XX
CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification
XX
SQ Sequence 559 AA;
Query Match 87.5%; Score 1613; DB 4; Length 559;
Best Local Similarity 90.5%; Pred. No. 6.1e-128;
Matches 316; Conservative 3; Mismatches 22; Indels 8; Gaps 5;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
```

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Db 57 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 116
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVEPTVSLIKG 120
Db 117 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVEPTVSLIKG 176
QY 121 PDSLIDGNETVAALCIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 180
Db 177 PDSLIDGNETVAALCIAATGKPVAHIDWEGDLGEMESTTTFPNETATIIISQYKLPFTR 236
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 237 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 296
QY 241 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQGRS-DQKVIVIS 299
Db 297 PPFKSVMSRLDQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSPGSKEVTQKVHPTF 356
QY 300 DPPTTTTLQP---TIQW-HPSTADI-EDLATEPKKL-PFPLSTLATIK 341
Db 357 QDPSLPTYPPLPALQFQWASPSTAXTSRDLATEPKXIAPSPSLSTLATIK 405

RESULT 12
AAE23290
ID AAE23290 standard; protein; 387 AA.
XX
AC AAE23290;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3beta-FLAGpolyHis fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; fusion protein; asthma.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 1..365
FT /note= "Human nectin-3alpha protein"
FT Region 366..381
FT /note= "FLAG peptide"
FT Region 382..387
FT /note= "PolyHis tag"
XX
WO200228902-A2.
XX
11-APR-2002.
XX
05-OCT-2001; 2001WO-US031392.
XX
05-OCT-2000; 2000US-0238557P.
XX
(IMMV ) IMMUNEX CORP.
XX
Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
WPI; 2002-426103/45.
XX
Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
XX
useful for treating or preventing heart failure, malaria,
XX
glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
XX
sepsis, stroke.
XX
Claim 9; Page 105-107; 141pp; English.
```

CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenesis in a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC FLAGpolyHis fusion protein
XX
SQ Sequence 387 AA;

Query Match 86.9%; Score 1602; DB 5; Length 387;
Best Local Similarity 98.7%; Pred. No. 3.2e-127;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLCNADANP 297
QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 PPTTTT 306
Db 358 VPFKQT 363

RESULT 13
AAE23299
ID AAE23299 standard; protein; 437 AA.
XX
AC AAE23299;
XX
DT 27-AUG-2002 (first entry)
XX
DE Human nectin-3gamma protein.
XX
KW Human; nectin-3gamma; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
FN WO200228902-A2.
XX
PD 11-APR-2002.
XX

PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum FR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
XX N-PSDE; AAD37450.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 125-126; 141pp; English.
XX
CC The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenesis in a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3gamma protein.
CC Human nectin-3gamma gene is located on chromosome 3
XX
SQ Sequence 437 AA;

Query Match 86.9%; Score 1602; DB 5; Length 437;
Best Local Similarity 98.7%; Pred. No. 3.7e-127;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117
QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
QY 121 PDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGVNLCNADANP 297
QY 241 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 PPTTTT 306
Db 358 VPFKQT 363

RESULT 14
AAE23284
ID AAE23284 standard; protein; 504 AA.
XX

AC AAE23284;
XX 27-AUG-2002 (first entry)
DT Human deleted nectin-3beta protein.
XX
DE Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
XX WPI; 2002-426103/45.
DR N-PSDB; AAD37443.
DR
XX Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
XX Claim 1; Page 89-91; 141pp; English.
PS
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,
CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is human nectin-3beta protein
CC containing 6 amino acids deleted from the N-terminal end. Human nectin-
CC 3beta gene is located on chromosome 3
XX
SQ Sequence 504 AA;
Query Match 86.9%; Score 1602; DB 5; Length 504;
Best Local Similarity 98.7%; Pred. NO. 4.5e-127;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 GPIIIVPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFVSQGEY 60
DB 52 GPIIIVPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHPQYGFVSQGEY 111
QY 61 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG 120
DB 112 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTVTVLVEPTVSLIKG 171
QY 121 PDSLIDGGNETVAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPPTR 180

Db 172 PDSLIDGGNETVAATGKPVAHIDWEGDLGEMESTTSPNETATIIISQYKLFPPTR 231
QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 240
Db 232 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFGVGRKGVNLKCNADANP 291
QY 241 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTENYSGVYICKVTNSLGQSRSDQKVIYISD 300
Db 292 PPFKSVWSRLDQGWPDGLLASDNTLHFVHPLTENYSGVYICKVTNSLGQSRSDQKVIYISD 351
QY 301 PPTTTT 306
Db 352 VPFKQT 357
RESULT 15
AAE23285
ID AAE23285 standard; protein; 510 AA.
XX
AC AAE23285;
XX 29-AUG-2003 (revised)
DT 27-AUG-2002 (first entry)
XX
DE Mouse nectin-3-human nectin-3beta fusion protein.
XX
KW Human; nectin-3beta; therapy; cell adhesion; cell proliferation; sepsis;
KW paracellular transport disorder; kidney; diabetic retinopathy; allergy;
KW allograft rejection; metastasis; restenosis; inflammatory bowel disease;
KW oedema; atherosclerosis; ischaemia-reperfusion injury; thrombosis;
KW stroke; tumour; cancer; herpesvirus infection; asthma; chromosome 3.
XX
OS Homo sapiens.
OS Mus musculus.
OS Chimeric.
XX
XX Key Location/Qualifiers
FT Region 1..6
FT /note= "Mouse nectin-3 pprotein"
FT Region 7..510
FT /note= "Human nectin-3beta protein"
XX
PN WO200228902-A2.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2001; 2001WO-US031392.
XX
PR 05-OCT-2000; 2000US-0238557P.
XX
XX (IMMV) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Lofton TE, Sorensen EA, Youakim A;
XX
DR WPI; 2002-426103/45.
DR N-PSDB; AAD37444.
XX
PT Novel purified nectin-3 and nectin-4 polypeptides which bind to nectin-1,
PT useful for treating or preventing heart failure, malaria,
PT glomerulonephritis, endometriosis, leukemia, asthma, allergy, edema,
PT sepsis, stroke.
XX
PS Claim 1; Page 94-95; 141pp; English.
XX The invention relates to a substantially purified nectin3alpha, beta,
CC gamma and nectin-4 polypeptides and their corresponding polynucleotides.
CC Nectin DNA and protein are useful for treating a disease associated with
CC cell adhesion activity, adherens junction formation activity, epithelial
CC or endothelial barrier function activity, endothelial proliferation or
CC migration activity, viral polypeptide binding activity. The epithelial or
CC endothelial barrier function disorder which is treated by the above
CC mentioned method is inflammation, sepsis, oedema, diabetic retinopathy,
CC asthma, allergy, allograft rejection, metastasis of cancer cells,

CC paracellular transport disorders such as magnesium transport defects in
CC the kidney or inflammatory bowel disease. Nectin DNA is also useful for
CC inhibiting angiogenesis in a mammal and treating endothelial migration,
CC proliferation or angiogenic condition of a tissue or a subject, such as
CC ischaemia, atherosclerosis, ischaemia-reperfusion injury, thrombosis,
CC stroke, restenosis, tumour growth and treating herpesvirus infection.
CC Nectin is also useful for modulating proliferation or migration of an
CC endothelial cell, an epithelial cell or a smooth muscle cell (vascular
CC smooth muscle cell). The present sequence is a fusion protein encoding 6
CC amino acids from mouse nectin-3 protein and the rest form human nectin-
CC 3beta protein. Human nectin-3beta gene is located on chromosome 3.
CC (Updated on 29-AUG-2003 to standardise OS field)

XX

SQ Sequence 510 AA;

Query Match 86.9%; Score 1602; DB 5; Length 510;
Best Local Similarity 98.7%; Pred. No. 4.6e-127;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db	58	GPIIVEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAHHPOYGFSVQGEY	117
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	120
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG	177
QY	121	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTR	180
Db	178	PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTR	237
QY	181	FARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP	240
Db	238	FARGRRITCVVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANP	297
QY	241	PPFKSVWSRLDQWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD	300
Db	298	PPFKSVWSRLDQWPDGILLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRSDQKVIYISD	357
QY	301	PPTTTT	306
Db	358	VPFKQT	363

Search completed: April 12, 2004, 09:38:31
Job time : 42.9091 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:45:21 ; Search time 29 Seconds
(without alignments)
3146.189 Million cell updates/sec

Title: US-09-972-268-4_COPY_58_404
Perfect score: 1844
Sequence: 1 GPIIVEPHVTAVGKNVSLK.....KKLPFLTLATIKDDTIAT 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1073127 seqs, 262937947 residues

Total number of hits satisfying chosen parameters: 1073127

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1844	100.0	426	10	US-09-972-268-15
2	1844	100.0	542	10	US-09-972-268-2
3	1844	100.0	549	10	US-09-972-268-4
4	1844	100.0	549	10	US-09-972-268-6
5	1844	100.0	549	14	US-10-161-572-45
6	1844	100.0	634	10	US-09-972-268-13
7	1767	95.8	549	10	US-09-959-845-2
8	1767	95.8	549	10	US-09-972-268-17
9	1602	86.9	387	10	US-09-972-268-16
10	1602	86.9	437	10	US-09-972-268-31
11	1602	86.9	504	10	US-09-972-268-8
12	1602	86.9	510	10	US-09-972-268-10
13	1602	86.9	510	10	US-09-972-268-12
14	1602	86.9	595	10	US-09-972-268-14
15	1567	85.0	438	10	US-09-959-845-6

16	1567	85.0	438	10	US-09-972-268-19	Sequence 19, Appl
17	1567	85.0	510	10	US-09-959-845-4	Sequence 4, Appli
18	1567	85.0	510	10	US-09-972-268-18	Sequence 18, Appl
19	594	32.2	258	15	US-10-264-237-2626	Sequence 2626, Ap
20	538.5	29.2	458	10	US-09-972-268-21	Sequence 21, Appl
21	538.5	29.2	514	14	US-10-161-572-60	Sequence 60, Appl
22	538.5	29.2	517	10	US-09-972-268-20	Sequence 20, Appl
23	516	28.0	518	9	US-09-919-172-20	Sequence 20, Appl
24	476.5	25.8	314	10	US-09-766-511B-36	Sequence 36, Appl
25	476.5	25.8	479	10	US-09-766-511B-35	Sequence 35, Appl
26	476.5	25.8	497	10	US-09-972-268-37	Sequence 37, Appl
27	476.5	25.8	510	10	US-09-766-511B-33	Sequence 33, Appl
28	476.5	25.8	510	12	US-10-058-270A-54	Sequence 54, Appl
29	476.5	25.8	510	14	US-10-161-572-55	Sequence 55, Appl
30	476.5	25.8	510	14	US-10-241-220-94	Sequence 94, Appl
31	476.5	25.8	510	15	US-10-295-027-66	Sequence 66, Appl
32	476.5	25.8	510	15	US-10-173-999-76	Sequence 76, Appl
33	474.5	25.7	510	10	US-09-972-268-24	Sequence 24, Appl
34	474.5	25.7	510	14	US-10-161-572-54	Sequence 54, Appl
35	470	25.5	498	10	US-09-972-268-39	Sequence 39, Appl
36	470	25.5	511	10	US-09-972-268-34	Sequence 34, Appl
37	470	25.5	580	10	US-09-972-268-36	Sequence 36, Appl
38	401.5	21.8	538	10	US-09-972-268-23	Sequence 23, Appl
39	401.5	21.8	538	10	US-09-984-130-138	Sequence 138, App
40	401.5	21.8	538	10	US-09-836-353A-138	Sequence 138, App
41	401.5	21.8	538	14	US-10-161-572-61	Sequence 61, Appl
42	401.5	21.8	538	15	US-10-411-010-17	Sequence 17, Appl
43	396.5	21.5	479	10	US-09-972-268-22	Sequence 22, Appl
44	396.5	21.5	479	14	US-10-161-572-62	Sequence 62, Appl
45	394.5	21.4	522	15	US-10-264-049-2969	Sequence 2969, Ap

ALIGNMENTS

RESULT 1
US-09-972-268-15
; Sequence 15, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-alpha-FLAGpolyHis
US-09-972-268-15

Query Match	100.0%;	Score 1844;	DB 10;	Length 426;
Best Local Similarity	100.0%;	Pred. No. 1.6e-160;		
Matches	347;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY	60	
Db	58	GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTAVVHHPQYGFVSQGEY	117	
QY	61	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG	120	
Db	118	QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTTLVVEPTVSLIKG	177	

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QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 357
QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 404

RESULT 2
US-09-972-268-2
; Sequence 2, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 542
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-972-268-2

Query Match 100.0%; Score 1844; DB 10; Length 542;
Best Local Similarity 100.0%; Pred. No. 2.3e-160;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 51 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 110
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QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
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QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
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QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 347
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RESULT 3
US-09-972-268-4
; Sequence 4, Application US/09972268
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; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: nucleotides 1-21 are from Mus musculus Nectin-3, the rest are fr
; OTHER INFORMATION: m human Nectin-3 alpha
US-09-972-268-4

Query Match 100.0%; Score 1844; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.3e-160;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
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Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIIISQYKLFPTTR 237
QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVGRKGVNLKCNADANP 297
QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVIYISD 300
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QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 404

RESULT 4
US-09-972-268-6
; Sequence 6, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 549
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TYPE: PRT
ORGANISM: homo sapiens
US-09-972-268-6

Query Match 100.0%; Score 1844; DB 10; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.3e-160;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKG 120
Db 118 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKG 177

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Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

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Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGKGVNLKCNADANP 297

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Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 357

QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 404

RESULT 5
US-10-161-572-45
Sequence 45, Application US/10161572
Publication No. US20030087266A1
GENERAL INFORMATION:
APPLICANT: EXELIXIS, INC.
TITLE OF INVENTION: IGS AS MODIFIERS OF THE p53 PATHWAY AND METHODS OF USE
FILE REFERENCE: EX02-097C-PC
CURRENT APPLICATION NUMBER: US/10/161,572
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 60/296,076
PRIOR FILING DATE: 2001-06-05
PRIOR APPLICATION NUMBER: US 60/328,605
PRIOR FILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: US 60/338,733
PRIOR FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/357,253
PRIOR FILING DATE: 2002-02-15
PRIOR APPLICATION NUMBER: US 60/357,600
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 549
TYPE: PRT
ORGANISM: Homo sapiens
US-10-161-572-45

Query Match 100.0%; Score 1844; DB 14; Length 549;
Best Local Similarity 100.0%; Pred. No. 2.3e-160;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 58 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

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Db 118 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

QY 191 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 357

QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 404

RESULT 6
US-09-972-268-13
Sequence 13, Application US/09972268
Publication No. US20030044893A1
GENERAL INFORMATION:
APPLICANT: Baum, Peter R.
APPLICANT: Fanslow, William C.
APPLICANT: Lofton, Timothy E.
APPLICANT: Sorensen, Eric A.
APPLICANT: Youakim, Adel
TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
FILE REFERENCE: 3101-A
CURRENT APPLICATION NUMBER: US/09/972,268
CURRENT FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/238,557
PRIOR FILING DATE: 2000-10-05
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 634
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: fusion protein: human Nectin-3-alpha-Fc
US-09-972-268-13

Query Match 100.0%; Score 1844; DB 10; Length 634;
Best Local Similarity 100.0%; Pred. No. 2.8e-160;
Matches 347; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 58 GPIIVEPHVTAVGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 117

QY 61 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKG 120
Db 118 QGRVLFKNVSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSITTVLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180
Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGKGVNLKCNADANP 240
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIQYAPEVSVTGYDGNWVFGKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 300
Db 298 PPFKSVWSRLDQWPDGLLASDNTLHFVHPLTFNYSVGYICKVTNSLGORSQDKVIYISD 357

QY 301 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 347
Db 358 PPTTTTLOPTIQWHPSTADIEDLATEPKLPFPLSTLATIKDDTIAT 404

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US-09-959-845-2
; Sequence 2, Application US/09959845
; Publication No. US20030008334A1
; GENERAL INFORMATION:
; APPLICANT: Yoshiaki TAKAI
; APPLICANT: Hiroaki NAKANISHI
; APPLICANT: Kenko SATO
; APPLICANT: Kenichi TAKAHASHI
; TITLE OF INVENTION: Protein Nectin-3
; FILE REFERENCE: 2001-1678A/LC/00653
; CURRENT APPLICATION NUMBER: US/09/959,845
; CURRENT FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: PCT/JP01/01871
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: JP 2000-065595
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 2
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Mouse
US-09-959-845-2

Query Match          95.8%; Score 1767; DB 10; Length 549;
Best Local Similarity 94.2%; Pred. No. 2.7e-153;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
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Db 58 GSIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
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Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 237
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QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 297
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 PPTTTTLQPTIQWHPSPADVDIATEHKKLPFPLSTLATIKDDTIAT 404
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 GSIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 237
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 297
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
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QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 PPTTTTLQPTIQWHPSPADVDIATEHKKLPFPLSTLATIKDDTIAT 404
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RESULT 8
US-09-972-268-17
; Sequence 17, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-15

Query Match          86.9%; Score 1602; DB 10; Length 387;
Best Local Similarity 98.7%; Pred. No. 2.3e-138;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 GSIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 237
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 297
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
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QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 PPTTTTLQPTIQWHPSPADVDIATEHKKLPFPLSTLATIKDDTIAT 404
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-15
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; TYPE: PRT
; ORGANISM: mus musculus
US-09-972-268-17

Query Match          95.8%; Score 1767; DB 10; Length 549;
Best Local Similarity 94.2%; Pred. No. 2.7e-153;
Matches 327; Conservative 13; Mismatches 7; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
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Db 58 GSIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 237
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 297
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
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Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
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QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347
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Db 358 PPTTTTLQPTIQWHPSPADVDIATEHKKLPFPLSTLATIKDDTIAT 404
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RESULT 9
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-15

Query Match          86.9%; Score 1602; DB 10; Length 387;
Best Local Similarity 98.7%; Pred. No. 2.3e-138;
Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60
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Db 58 GSIIVEPHVTAVWGKNSLKLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120
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Db 118 QGRVLFKNYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177
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QY 121 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 180
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Db 178 PDSLIDGGNETVAAICIAATGKPVVAHIDWEGDLGEMESTTSPNETATIISQYKLFPTTR 237
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 240
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 238 FARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFVGRKGNLKCNDANP 297
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 300
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSDDQKVIYISD 357
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 301 PPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIAT 347
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 PPTTTTLQPTIQWHPSPADVDIATEHKKLPFPLSTLATIKDDTIAT 404
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RESULT 9
US-09-972-268-16
; Sequence 16, Application US/09972268
; Publication No. US20030044893A1
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter R.
; APPLICANT: Fanslow, William C.
; APPLICANT: Lofton, Timothy E.
; APPLICANT: Sorensen, Eric A.
; APPLICANT: Youakim, Adel
; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE
; FILE REFERENCE: 3101-A
; CURRENT APPLICATION NUMBER: US/09/972,268
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 60/238,557
; PRIOR FILING DATE: 2000-10-05
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 387
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: fusion protein: human Nectin-3-beta-FLAGpolyHis
US-09-972-268-15
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Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

QY 301 PPTTTT 306

Db 358 VPFKQT 363

RESULT 10

US-09-972-268-31

; Sequence 31, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 31

; LENGTH: 437

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-972-268-31

Query Match 86.9%; Score 1602; DB 10; Length 437;

Best Local Similarity 98.7%; Pred. No. 2.7e-138;

Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60

Db 58 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 117

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 118 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 177

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180

Db 178 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 237

QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 240

Db 238 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 297

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300

Db 298 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 357

QY 301 PPTTTT 306

Db 358 VPFKQT 363

RESULT 11

US-09-972-268-8

; Sequence 8, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 8

; LENGTH: 504

; TYPE: PRT

; ORGANISM: homo sapiens

US-09-972-268-8

Query Match 86.9%; Score 1602; DB 10; Length 504;

Best Local Similarity 98.7%; Pred. No. 3.3e-138;

Matches 302; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 60

Db 52 GPIIPEPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPOYGFVSQGEY 111

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 120

Db 112 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKG 171

QY 121 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 180

Db 172 PDSLIDGGNETVAAICIAATGKPVAHIDWEGDLGEMESTTTSFPNETATIISQYKLFPTTR 231

QY 181 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 240

Db 232 FARGRRITCVVKKHPALEKDIRYSFILDIOYAPEVSVTGYDGNWVFGVGRKGVNLKCNADANP 291

QY 241 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 300

Db 292 PPFKSVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISD 351

QY 301 PPTTTT 306

Db 352 VPFKQT 357

RESULT 12

US-09-972-268-10

; Sequence 10, Application US/09972268

; Publication No. US20030044893A1

; GENERAL INFORMATION:

; APPLICANT: Baum, Peter R.

; APPLICANT: Fanslow, William C.

; APPLICANT: Lofton, Timothy E.

; APPLICANT: Sorensen, Eric A.

; APPLICANT: Youakim, Adel

; TITLE OF INVENTION: NECTIN POLYPEPTIDES, POLYNUCLEOTIDES, METHODS OF MAKING AND USE

; FILE REFERENCE: 3101-A

; CURRENT APPLICATION NUMBER: US/09/972,268

; CURRENT FILING DATE: 2001-10-05

; PRIOR APPLICATION NUMBER: 60/238,557

; PRIOR FILING DATE: 2000-10-05

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: Patentin version 3.1

; SEQ ID NO 10

; LENGTH: 510

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: nucleotides 1-18 are from Mus musculus Nectin-3 DNA, the rest ar

; OTHER INFORMATION: from human Nectin-3 beta

US-09-972-268-10

Query Match	86.9%	Score 1602;	DB 10;	Length 510;
Best Local Similarity	98.7%	Pred. No. 3.4e-138;		
Matches 302; Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

[illegible]

RESULT 13

US-09-972-268-12
; Sequence 12, Application US/09972268
; Publication No. US2003004893A1
; GENERAL INFORMATION:

```

/ APPLICANT: Baum, Peter R.
/
/ APPLICANT: Fanslow, William C.
/
/ APPLICANT: Lofton, Timothy E.
/
/ APPLICANT: Sorensen, Eric A.
/
/ APPLICANT: Youakim, Adel
/
/ TITLE OF INVENTION: NECTIN POLYPEPTIDES,
/
/ FILE REFERENCE: 3101-A
/
/ CURRENT APPLICATION NUMBER: US/09/972,268
/
/ CURRENT FILING DATE: 2001-10-05
/
/ PRIOR APPLICATION NUMBER: 60/238,557
/
/ PRIOR FILING DATE: 2000-10-05
/
/ NUMBER OF SEQ ID NOS: 39
/
/ SOFTWARE: PatentIn version 3.1
/

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US-09-972-268-12

Query Match	86.9%;	Score 1602;	DB 10;	Length 510;
Best Local Similarity	98.7%;	Pred. No. 3.4e-138;		
Matches 302: Conservative	0;	Mismatches 4;	Indels 0;	Gaps 0;

QY	1	GPII	VEPH	TAVG	KNVSL	KCLIE	VNET	ITQI	SWEK	IHGK	SSQT	VA	VHH	PQY	GFS	VQGEY	60
Db	58	GPII	VEPH	TAVG	KNVSL	KCLIE	VNET	ITQI	SWEK	IHGK	SSQT	VA	VHH	PQY	GFS	VQGEY	117
QY	61	QGRV	LFNK	YSLN	DATIT	LHNIG	FS	DSGKY	ICKAV	TFPL	GLNA	QS	TTVT	VL	VEPT	VS	LKG 120
Db	118	QGRV	LFNK	YSLN	DATIT	LHNIG	FS	DSGKY	ICKAV	TFPL	GLNA	QS	TTVT	VL	VEPT	VS	LKG 177
QY	121	PDSL	LDGG	NETV	AAIC	AATG	KPVA	HIDW	EGDL	GEMES	TTTS	FPNET	ATII	ISQY	KLF	FPTR	180
Db	178	PDSL	LDGG	NETV	AAIC	AATG	KPVA	HIDW	EGDL	GEMES	TTTS	FPNET	ATII	ISQY	KLF	FPTR	237
QY	181	FARG	RRIT	CVVK	HPAL	EKDIR	YSF	ILDI	QYAP	EVSV	TGYD	GNWF	VG	RGK	GNL	KCNADANP	240

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OM protein - protein search, using sw model

Run on: April 12, 2004, 09:30:41 ; Search time 11.4545 Seconds
(without alignments)
1563.939 Million cell updates/sec

Title: US-09-972-268-4_COPY_58_404
Perfect score: 1844
Sequence: 1 GPIVPHVTVAVGKNVSLK.....KKLPFLSLTIATIKDDTIAT 347

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	538.5	29.2	517	4	US-09-723-368-4
2	535.5	29.0	458	4	US-09-435-956A-1
3	516	28.0	518	4	US-09-919-172-20
4	396.5	21.5	479	4	US-09-723-368-2
5	376	20.4	408	4	US-09-724-864-62
6	287	15.6	440	4	US-09-866-028-61
7	287	15.6	442	4	US-09-778-510-20
8	287	15.6	442	4	US-09-930-803-1
9	284	15.4	423	4	US-09-778-510-22
10	234	12.7	421	2	US-08-659-984A-1
11	234	12.7	421	3	US-08-660-531-1
12	234	12.7	444	2	US-08-659-984A-5
13	234	12.7	444	3	US-08-660-531-5
14	227.5	12.3	398	4	US-09-778-510-4
15	217.5	11.8	398	4	US-09-778-510-6
16	217.5	11.8	398	4	US-09-907-794A-84
17	217.5	11.8	398	4	US-09-905-125A-84
18	217.5	11.8	398	4	US-09-902-775A-84
19	217.5	11.8	432	4	US-09-778-510-2
20	190.5	10.3	227	4	US-09-205-258-947
21	187.5	10.2	274	4	US-09-570-367C-19
22	187.5	10.2	274	4	US-09-915-524-19
23	162.5	8.8	278	4	US-09-570-367C-2
24	162.5	8.8	278	4	US-09-915-524-2
25	160	8.7	477	2	US-08-432-016-3
26	160	8.7	477	2	US-08-684-594-3
27	159.5	8.6	278	4	US-09-570-367C-21

28	159.5	8.6	278	4	US-09-915-524-21	Sequence 21, Appl
29	159	8.6	1101	3	US-08-986-485-2	Sequence 2, Appl
30	158	8.6	642	1	US-08-217-299-1	Sequence 1, Appl
31	158	8.6	698	2	US-08-602-725-36	Sequence 36, Appl
32	158	8.6	734	2	US-08-389-459A-17	Sequence 17, Appl
33	158	8.6	734	3	US-08-987-867A-17	Sequence 17, Appl
34	154.5	8.4	1018	1	US-08-408-093-6	Sequence 6, Appl
35	154.5	8.4	1018	1	US-08-408-420A-6	Sequence 6, Appl
36	154.5	8.4	1018	1	US-08-714-901-6	Sequence 6, Appl
37	154.5	8.4	1018	3	US-08-040-741-6	Sequence 6, Appl
38	151	8.2	467	3	US-09-046-736-2	Sequence 2, Appl
39	147	8.0	313	4	US-09-700-397-4	Sequence 4, Appl
40	147	8.0	344	4	US-09-700-397-3	Sequence 3, Appl
41	145.5	7.9	1651	3	US-09-540-245A-18	Sequence 18, Appl
42	144.5	7.8	605	2	US-08-752-307B-8	Sequence 8, Appl
43	144.5	7.8	605	4	US-09-707-802-8	Sequence 8, Appl
44	144.5	7.8	605	4	US-09-991-326-8	Sequence 8, Appl
45	144.5	7.8	1018	1	US-08-452-052-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-723-368-4
; Sequence 4, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITECK, Charles J.
; APPLICANT: KRUMMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-4

Query Match	29.2%;	Score 538.5;	DB 4;	Length 517;
Best Local Similarity	37.8%;	Pred. No. 5.8e-45;		
Matches	113;	Conservative	56;	Mismatches 119;
				Indels 11;
				Gaps 5;
Qy	14	GKNVSLKCLIE---VN	ETITQISWEKIHGSSQT	VAVHHPQYGFVSQGEYQGRVLFKNYS 70
Db	44	GTDVVLHCSFANPLPS	VKITQVTWQSTNGSKQ	NVAIYNPSMGVSLAPYRERVEFLRPS 103
Qy	71	LNDAITILHNIGFSDG	KYICKAVTFPLGNAQS	STTVTLVEPTVSLIKGPDSDLIDG--- 127
Db	104	FTDGTIRLSLELEDE	GVYICEFATFPTGNRE	SQNLNTVMKPT-NWIEGTQAVLRKKG 162
Qy	128	-GNETVAAICIAATG	KPVAHIDWEGDL-GEM	ESTTTSFPNETATIIISQYKLFPTTFARGR 185
Db	163	QDDKVLVATCTSANG	KPPSVSVSWETRLKGA	EYQEIIRNPNGTIVTISRVLVPSREAHQQ 222
Qy	186	RITCVVKHPALEKDI	RSFILDIQYAPEVSVT	GYDGNWFVGRKGVLNKCNDANPPPFKS 245

Db 223 SLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEY 280
QY 246 VWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVYISDPPTT 304
Db 281 HWTTLNGLPLKGVGAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEFPYT 339

RESULT 2

US-09-435-956A-1
; Sequence 1, Application US/09435956A
; Patent No. 6469155
; GENERAL INFORMATION:
; APPLICANT: Universita degli Studi di Bologna
; APPLICANT: Institut National de la Sante et de la Recherche M
; TITLE OF INVENTION: HIGR and Related V Domain for the Manufacture of a
; TITLE OF INVENTION: Medicament for Preventing or Treating HSV-1, HSV-2 and
; TITLE OF INVENTION: BHV Infections
; FILE REFERENCE: MODIANO
; CURRENT APPLICATION NUMBER: US/09/435,956A
; CURRENT FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Original Source: Hela Cell Line
; OTHER INFORMATION: General Functional Class of Gene: Immunoglobulin
; OTHER INFORMATION: Superfamily
; OTHER INFORMATION: Binding Macromolecules: HSV-gD
; OTHER INFORMATION: Subcellular localisation: Plasma Membrane
; OTHER INFORMATION: Other Information: Viral Receptor
US-09-435-956A-1

Query Match 29.0%; Score 535.5; DB 4; Length 458;
Best Local Similarity 37.7%; Pred. No. 9.5e-45;
Matches 112; Conservative 55; Mismatches 119; Indels 11; Gaps 5;

QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRVERFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQLNLTVMMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWEGDL-GEMESTTTTSFPNETATIIISQYKLFPTTFARGR 185
Db 163 QDDKVLVATCTSANGKPPSVSVSWETRLKGEAEYQEIRNPNGTVTVISRYRLVPSRAHQ 222
QY 186 RITCVVKHPALEKDRIYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNADANPPPKS 245
Db 223 SLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRMVDVKLTCKADANPPATEY 280
QY 246 VWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVYISDPP 302
Db 281 HWTTLNGLPLKGVGAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEVNITEKP 337

RESULT 3

US-09-919-172-20
; Sequence 20, Application US/09919172
; Patent No. 6673545
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary
; APPLICANT: Turner, Christopher M.
; TITLE OF INVENTION: PROSTATE CANCER MARKERS
; FILE REFERENCE: PA-0036 US
; CURRENT APPLICATION NUMBER: US/09/919,172
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: 60/222,469
; PRIOR FILING DATE: 2000-07-28

; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673545 3189059CD1
US-09-919-172-20

Query Match 28.0%; Score 516; DB 4; Length 518;
Best Local Similarity 35.7%; Pred. No. 1e-42;
Matches 110; Conservative 56; Mismatches 114; Indels 28; Gaps 6;
QY 14 GKNVSLKCLIE---VNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNYS 70
Db 44 GTDVLHCSFANPLPSVKITQVTWQKSTNGSKQNVAIYNPSMGVSVLAPYRVERFLRPS 103
QY 71 LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVEPTVSLIKGPDSLIDG--- 127
Db 104 FTDGTIRLSRLEDEGVYICGFATFPTGNRESQLNLTVMMAKPT-NWIEGTQAVLRAKKG 162
QY 128 -GNETVAAICIAATGKPVAHIDWE-----GDLGEMESTTTTSFPNETATIIISQYKL 176
Db 163 QDDKVLVATCTSANGKPPSVSVSWETRLKGEARVPCDSGT-----PMAPVTVISRYRL 214
QY 177 FPTRFARGRRITCVVKHPALEKDRIYSFILDIOYAPEVSVTGYDGNWFWGKGVNLCNNA 236
Db 215 VPSREAHQQSLACIVNYHM--DRFKESLTNLNVQYEPEVTIEGFDGNWYLQRMVDVKLTCKA 272
QY 237 DANPPPKSVWSRLDQGWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLGQRSDQKVI 296
Db 273 DANPPATEYHWTTLNGLSLPKGVGAQNRTLFFKGPINYSLAGTYICEATNPIGTRSGQVEV 332
QY 297 YISDPPTT 304
Db 333 NITEFPYT 340

RESULT 4

US-09-723-368-2
; Sequence 2, Application US/09723368
; Patent No. 6641818
; GENERAL INFORMATION:
; APPLICANT: NORTHWESTERN UNIVERSITY
; APPLICANT: SPEAR, Patricia G.
; APPLICANT: WARNER, Morgyn S.
; APPLICANT: GERAGHTY, Robert G.
; APPLICANT: MARTINEZ, Wanda M.
; APPLICANT: MONTGOMERY, Rebecca I.
; APPLICANT: COHEN, Gary H.
; APPLICANT: EISENBERG, Roselyn J.
; APPLICANT: WHITBECK, Charles J.
; APPLICANT: KRUMMENACHER, Claude
; APPLICANT: UNIVERSITY OF PENNSYLVANIA
; TITLE OF INVENTION: CELLULAR PROTEINS WHICH MEDIATE HERPESVIRUS ENTRY
; FILE REFERENCE: 200290.0050/2U1
; CURRENT APPLICATION NUMBER: US/09/723,368
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. 60/087,862
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: PCT/US99/12235
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-723-368-2

Query Match 21.5%; Score 396.5; DB 4; Length 479;

Best Local Similarity 29.1%; Pred. No. 7.3e-31;
Matches 95; Conservative 57; Mismatches 132; Indels 43; Gaps 9;

QY 5 VEPHVTAVWGKNVSLKCLI---EVNETITQISWEKIHGKSS-QTVAVHHPQYGFVSQGEY 60
Db 38 VLPEVRGQLGGTVELPCHLLPPVPGLYISLVTWQRPDAPANHONVAAFHFKMGPSFPSPK 97

QY 61 QG--RVLF-----KNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVT 108
Db 98 PGSERLSFVSAKQSTGQDTEAELQDATLALHGLTVEDEGNYTCEFFATFPKGSVRGMTWLR 157

QY 109 VLVEP-----TVSLIKGPDSLIDGGNETVAAICIAATGKPVVAHI-----DWEGDLGE 155
Db 158 VIAKPKNQAEAKVTFSPQDP-----TTVALCISKEGRPPARISWLSSLDWEAKETQ 208

QY 156 MESTTTSFPNETATIISQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIOYAPEVS 215
Db 209 VSGTLAG---TVTVTSRFTLVPSGRADGVTVTCKVEHESFEERALIPVTLVRYPPPEVS 264

QY 216 VTGYDGNWVFVGRKGVNLKCNADANPPPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNY 275
Db 265 ISGYDDNWYLGRTDALSCDVRSNPEPTGYDWSITSGTFPTSAAVQGSQ-L-VIHAVDSL 323

QY 276 SGVYICKVTNSLQSRDQKVIYISDPP 302
Db 324 NTTFVCTVTNAVGMGRAEQVIFVRETP 350

RESULT 5
US-09-724-864-62
; Sequence 62, Application US/09724864
; Patent No. 6380362
; GENERAL INFORMATION:
; APPLICANT: Watson, James D
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Polynucleotides, polypeptides expressed
; TITLE OF INVENTION: by the polynucleotides and methods for their use.
; FILE REFERENCE: 11000.1050U1
; CURRENT APPLICATION NUMBER: US/09/724,864
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 6380362 60/171,678
; PRIOR FILING DATE: 1999-12-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Mouse
US-09-724-864-62

Query Match 20.4%; Score 376; DB 4; Length 408;
Best Local Similarity 32.5%; Pred. No. 6.3e-29;
Matches 102; Conservative 53; Mismatches 137; Indels 22; Gaps 10;

QY 3 IIVEPHVTAVWGKNVSLKCLIEVNE--TITQISW-EKIHGKSSQTVAVHHPQYGFVSQGE 59
Db 32 VLVPYNSTGVLGSTTLHCSLTSNENVTITQITWMKSDSGSHALVAVFHPKKGPNKEP 91

QY 60 YQGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEP--TVSL 117
Db 92 ERVKFLAAQQDLRNASLAISNLVSVEDEGIYECQIATFPRGSRSTNAWLKVQARPKNTAE 151

QY 118 IKGPDSLI--DGGNETVAAICIAATGKPVVAHI---EGDLGEMESTTTSFPNETATII 171
Db 152 LEPSFTLILQD-----VAKCISANGHPPGRISWPSNVNNGSHREMKE-PGSQPG-TTIVT 203

QY 172 SQYKLFPTRFARGRRITCVVKHPALEKDIRYSFILDIOYAPE-VSVTYDGNWVFVGRKGV 230
Db 204 SYLSMVPSRQADGKNITCTVEHESLQELDQLLVTLVSQPYPPENVSISGYDGNVYGLTNL 263

QY 231 NLKCNADANPPPFKS--VMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLG 288
Db 264 TLTCEAHSKPAPDMAGYNWSTNTGDFPNSVKRQGNMLLISTVEDGLNNTVIVCEVTNALG 323

QY 289 QRSQKQKVIYISDPP 302
Db 324 SGQGQVHIIVKEKP 337

RESULT 6
US-09-866-028-61
; Sequence 61, Application US/09866028
; Patent No. 6642360
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul
; APPLICANT: Grimaldi, Christopher
; APPLICANT: Gurney, Austin
; APPLICANT: Hillan, Kenneth
; APPLICANT: Kljavin, Ivar
; APPLICANT: Napier, Mary
; APPLICANT: Roy, Margaret
; APPLICANT: Tumas, Daniel
; APPLICANT: Wood, William
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P2548P1C1
; CURRENT APPLICATION NUMBER: US/09/866,028
; CURRENT FILING DATE: 2001-05-25
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 61
; LENGTH: 440
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-866-028-61

Query Match 15.6%; Score 287; DB 4; Length 440;
Best Local Similarity 26.5%; Pred. No. 5.3e-20;
Matches 92; Conservative 66; Mismatches 145; Indels 44; Gaps 14;

QY 9 VTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKN 68
Db 50 VTVIEGEVATISC--QVNKSDDSVI--QLLNPNRQTI-----YFRDFRPLKDSRFQLLN 99

QY 69 YSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIK-GPDSLIDG 127
Db 100 FSSSELKVSLTNVSIISDEGRYFCQLYTDP--PQESYTTITVLVPPRNLMDIQDQTAVEG 157

QY 128 GNETVAAICIAATGKPVVAHI---EGDL-----GEMESTTTSFPNETATIISQYKLFPTRF 181
Db 158 --EEIEVNCTAMASKPATITIRWFKGNTTELKGSVEVEWSDMY-----TVTSQLMLKVHKE 210

QY 182 ARGRRITCVVKHPALEKDIRYSFILDIOYAPEVSVTYDGNWVFVGRKG--VNLKCNADAN 239
Db 211 DDGVPVICQVEHPAVTGNLQTRYLEVQYKPVQVHIQMTYPLQGLTREGDALELTCEAIGK 270

QY 240 PPPFKSVMSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQSRDQKVIYIS 299
Db 271 POPVMVTWVRVDDMPQHAVLSGNL-FINNLNKNTDNGTYRCEASNIVGKAHSDYMLYVY 329

QY 300 DPPTTTTLQPTIQWHPSTADIEDLATEPKKLPFPLSTLATIKDDTIA 346
Db 330 DPP--TTIPP-----PTTTTTTTTTT-----TTILTIITDSRA 361

RESULT 7
US-09-778-510-20
; Sequence 20, Application US/09778510
; Patent No. 6512095


```

/ SEQUENCE INFORMATION DATA.
/ APPLICATION NUMBER: US 08/485,152
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Heslin, James M.
/ REGISTRATION NUMBER: 29,541
/ REFERENCE/DOCKET NUMBER: 15270-002810US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-326-2400
/ TELEFAX: 415-326-2422
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 421 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-659-984A-1

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; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 421 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-531-1

Query Match      12.7%; Score 234; DB 3; Length 421;
Best Local Similarity 23.5%; Pred. No. 9.4e-15;
Matches 84; Conservative 72; Mismatches 160; Indels 42; Gaps 16

QY    1 GPIIVEPHVTAVWGNKNSLKLIEVNETITQISWEKIHGKSQTVAHHHPQYGFVSQGEY 60
Db    10 GQPPLTQNVTVEGGTAILTCRVDQNDN-TSLQWS---NPAQQTL-----YFDKKALR 59
      | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY    61 QGRVLFNKYSLNDAITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTLVE-PTVSLIK 119
Db    60 DNRIELVRASWHELSSIVSDVLSDEGYTCFLTMPVKTSKAYLTVLGVPEKPQISGFS 119
      | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY    120 GPDSLIDGNETVAATCIAATGKPVAHIDW--EGDLGEMESTTTSFPN-ETATIISQYK 175
Db    120 SP--VMEG--DLMQLTKTSGSKPAADIRWFKNCKEIKDVLYLKEEDANRKCTFTVSSILD 175
      | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY    176 LFPTRFARRRITCVVKHPPALEKDRIYSF-ILDIQYAPEVSVT-----GYDGNWVFVGRKG 229
Db    176 FRVDRSDDGVAVICRVDHESLNATPQAMQVLEIHYTPSVKLIIPSTPFPEGQPLI---- 231
      | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
QY    230 VNLKCNDANPNPPFKSVWSRLDGQW--PDGLLASDNTHLVFVHPLTFNYSGVYICKVTNSL 287
Db    232 --LTCSKGPPLPEPVLWTGDGGLPDPDRMVVSGRELNIIF-LNKTDNGTYRCEATNTI 288
      | : ||| | | | | | | | | | | | | | | | | | | | | | | | | | |

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US-660-531-1		12.7%; Score 234; DB 3; Length 421;		
Query Match		23.5%; Pred. No. 9.4e-15;		
Best Local Similarity		Matches 84; Conservative 72; Mismatches 160; Indels 42; Gaps 16		
QY	1	GPIIVEPHVTA	VWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHHPQYGFSVQGEY	60
Db	10	GQFPLTQNVTV	VEGGTAILTCRVDQNDN-TSLQWS---NPAQQTIL-----YFDDKKALR	59
QY	61	QGRVLFKNYS	LNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVE-PTVSLIK	119
Db	60	DNRIELVRAS	WHELSSIVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKPOISGFS	119
QY	120	GPDSLIDGNET	VAAICIAATGKPVAHIDW---EGDLGEMESTTTSFPN-ETATIIISQYK	175
Db	120	SP--VMEG--	DLMQLTCKTSGSKPAADIRWFKNDKEIKDVKYLKEEDANRKCTFTVSSITLD	175
QY	176	LFPTRFARRR	ITCVVKHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWFVGRKG	229
Db	176	FRVDRSDDG	VAVICRVDHESLNATPQVAMQVLEIHYTPSVKLIIPSTFPFQEGOPLI-----	231
QY	230	VNLKCNADAN	PPPKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL	287
Db	232	--LTCSKGP	LPBPVLWTKDGGELPDPDRMVVSGRELNIIF-LNKTDNGTYRCEATNTI	288

QY 288 QQRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKKLPFPLSLATIKD 342
Db 289 QQSSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVA-ITTSPT---TSATTSIRD 341

RESULT 12
US-08-659-984A-5
; Sequence 5, Application US/08659984A
; Patent No. 5942400
; GENERAL INFORMATION:
; APPLICANT: Anderson, John P.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Jacobson-Croak, Kirsten L.
; TITLE OF INVENTION: Assays for Detecting Beta-Secretase
; TITLE OF INVENTION: Inhibition
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/659,984A
; FILING DATE: 07-JUN-1996
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,152
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002810US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-659-984A-5

Query Match 12.7%; Score 234; DB 2; Length 444;
Best Local Similarity 23.5%; Pred. No. 1e-14;
Matches 84; Conservative 72; Mismatches 160; Indels 42; Gaps 16;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 33 GQFPLTQNTVVEGGTALTTCRVDQNDN-TSLQWS---NPAQQTLL-----YFDDKKALR 82

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVE-PTVSLIK 119
Db 83 DNRIELVRASWHELSSISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFS 142

QY 120 GPDSLIDGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSPFN-ETATIIISQYK 175
Db 143 SP--VMEG--DLMQLTCKTSGSKPAADIRWFKNDEIKDKVYLKEEDANRKTFTVSSTLD 198

QY 176 LFPTRFARRRITCVVKHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWVGRKG 229
Db 199 FRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKIIPTSTFPFQEGQPLI---- 254

QY 230 VNLKCNADANPPFKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287

Db 255 --LTCESKGKPLPEPVLWTKDGGELPDPDRMVVSGRELNILF-LNKTDNGTYRCEATNTI 311
QY 288 QQRSDQKVIYISDPPTT---TTLQPTIQWHPSTADIEDLATEPKKLPFPLSLATIKD 342
Db 312 QQSSAEYVLIVHDVPNTLLPTTIIPSLTTATVTTTVA-ITTSPT---TSATTSIRD 364

RESULT 13
US-08-660-531-5
; Sequence 5, Application US/08660531
; Patent No. 6221645
; GENERAL INFORMATION:
; APPLICANT: Chrysler, Susanna M.S.
; APPLICANT: Sinha, Sukanto
; APPLICANT: Keim, Pamela S.
; APPLICANT: Anderson, John P.
; TITLE OF INVENTION: Beta-Secretase
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Ctr., 8th Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/660,531
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/480,498
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Heslin, James M.
; REGISTRATION NUMBER: 29,541
; REFERENCE/DOCKET NUMBER: 15270-002210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-660-531-5

Query Match 12.7%; Score 234; DB 3; Length 444;
Best Local Similarity 23.5%; Pred. No. 1e-14;
Matches 84; Conservative 72; Mismatches 160; Indels 42; Gaps 16;

QY 1 GPIIIVPHVTAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEY 60
Db 33 GQFPLTQNTVVEGGTALTTCRVDQNDN-TSLQWS---NPAQQTLL-----YFDDKKALR 82

QY 61 QGRVLFKNYSLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVE-PTVSLIK 119
Db 83 DNRIELVRASWHELSSISVSDVSLSDGQYTCSLFTMPVKTSKAYLTVLGVPEKQISGFS 142

QY 120 GPDSLIDGNETVAAICIAATGKPVAHIDW---EGDLGEMESTTTSPFN-ETATIIISQYK 175
Db 143 SP--VMEG--DLMQLTCKTSGSKPAADIRWFKNDEIKDKVYLKEEDANRKTFTVSSTLD 198

QY 176 LFPTRFARRRITCVVKHPALEKDIRYSF-ILDIQYAPEVSVT-----GYDGNWVGRKG 229
Db 199 FRVDRSDDGVAVICRVDHESLNATPQVAMQVLEIHYTPSVKIIPTSTFPFQEGQPLI---- 254

QY 230 VNLKCNADANPPPFKSVWSRLDGQW--PDGLLASDNTLHFVHPLTFNYSGVYICKVTNSL 287
Db 255 --LTCSKSGKPLPEPVLWTKDGGELPDPRMVVSGRELNILF-LNKTDNGTYRCEATNTI 311
QY 288 QORSQDKVIYISDPPTT---TTLQPTIQHPSTADIEDLATEPKKLPPFLSTLATIKD 342
Db 312 GOSSAEYVLVHDVNTLLPTTIIIPSLTATVTTVA-ITTSPT-----TSATTSSIRD 364

RESULT 14
US-09-778-510-4
; Sequence 4, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-778-510-4

Query Match 12.3%; Score 227.5; DB 4; Length 398;
Best Local Similarity 26.6%; Pred. No. 3.8e-14;
Matches 79; Conservative 52; Mismatches 145; Indels 21; Gaps 11;

QY 10 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNY 69
Db 39 TVVAGGTVVLKQVKDHED-SSLQWS---NPAQQTLL-----YFGEKRALRDNRIQLVSS 88

QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGN 129
Db 89 TPHELSSISISNVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145

QY 130 ETVAACIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIISQYKLFPTRFARGR 185
Db 146 ETATLNCQSSGSKPAALQLTWRKGDQELHGDQTRIQEDPNKGTFTVSSSVSFQVTREDDGA 205

QY 186 RITCVVKHPALE-KDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFK 244
Db 206 NIVCSVNHESLKGADRSTSQRIEVLTYPTAMIRPEPAHPREGQK-LLLHCEGRGNPVPQQ 264

QY 245 SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDP 301
Db 265 YVWVK-EGSEPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYTAYFTLNNDP 319

RESULT 15
US-09-778-510-6
; Sequence 6, Application US/09778510
; Patent No. 6512095
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; TITLE OF INVENTION: Molecules Designated B7L1
; FILE REFERENCE: 2844-US
; CURRENT APPLICATION NUMBER: US/09/778,510
; CURRENT FILING DATE: 2001-02-07
; PRIOR APPLICATION NUMBER: PCT/US99/17906
; PRIOR FILING DATE: 1999-08-05
; PRIOR APPLICATION NUMBER: 60/095,663
; PRIOR FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6

; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-778-510-6

Query Match 11.8%; Score 217.5; DB 4; Length 398;
Best Local Similarity 25.9%; Pred. No. 3.8e-13;
Matches 77; Conservative 52; Mismatches 147; Indels 21; Gaps 11;

QY 10 TAVWGKNVSLKCLIEVNETITQISWEKIHGKSSQTVAVHHPQYGFVSQGEYQGRVLFKNY 69
Db 39 TVVAGGTVVLKQVKDHED-SSLQWS---NPAQQTLL-----YFGEKRALRDNRIQLVTS 88

QY 70 SLNDATITLHNIGFSDSGKYICKAVTFPLGNAQSSTTVTVLVEPTVSLIKGPDSDLIDGN 129
Db 89 TPHELSSISISNVALADEGEYTCSTFTMPVRTAKS--LVTVLGIPQKPIITGYKSSL-REK 145

QY 130 ETVAACIAATGKPVAHIDWEGDLGEMESTTTSF---PN-ETATIISQYKLFPTRFARGR 185
Db 146 DTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKGTFTVSSSVTFQVTREDDGA 205

QY 186 RITCVVKHPALE-KDIRYSFILDIOYAPEVSVTGYDGNWFVGRKGVNLKCNADANPPPFK 244
Db 206 SIVCSVNHESLKGADRSTSQRIEVLTYPTAMIRPDPPHPREGQK-LLLHCEGRGNPVPQQ 264

QY 245 SVWSRLDGQWPDGLLASDNTLHFVHPLTFNYSGVYICKVTNSLQORSQDKVIYISDP 301
Db 265 YLWEK-EGSVPLKMTQESALIFPF-LNKSDSGTYGCTATSNMGSYKAYYTLNVNDP 319

Search completed: April 12, 2004, 09:49:21
Job time : 12.4545 secs